

```

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
XX [1]
XX 1-6
RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferstr. 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by DKFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No. 31 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
XX Key Location/Qualifiers
XX
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone_lib="434 (synonym: hles3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX
XX Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;
XX
Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 5 g 5

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RESULT 31
BE726686/c
LOCUS BE726686 6 bp mRNA linear EST 14-SEP-2000
DEFINITION Chlamydomonas reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Grossman A., Davies J., Federspiel N., Harris E., Lefebvre P.,
AUTHORS McDermott J.P., Silflow C., Stern D., and Surzycki R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
JOURNAL Unicellular System for Analyzing Gene Function and Regulation in
COMMENT Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 2 G 2

RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST: 7 BP.
XX
AC AL042562;
XX
SV AL042562.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX
DE EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
DB 1 G 1

RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST: 7 BP.
XX
AC AL042652;
XX
SV AL042652.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX
DE EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"

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FT      /dev_stage="adult"
FT      /tissue_type="testis"
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SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      2 G 2

RESULT 37
HSM007502/c standard; RNA; EST: 7 BP.
XX
AC      AL042652;
XX
SV      AL042652.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX
KW      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OS
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      [1]
XX      RP 1-7
XX      RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..7
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434N1921"
FT      DH10B; sites NotI + SalI
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      1 G 1

RESULT 38
CS8888

LOCUS      CS8888
DEFINITION      C58888 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
ACCESSION      C58888
VERSION      C58888
KEYWORDS      C58888.1 GI:2417593
SOURCE      EST.
ORGANISM      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Rhabditidae; Peloderiinae; Caenorhabditis.
REFERENCE      1 (bases 1 to 7)
AUTHORS      Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
JOURNAL      Expression map of the C.elegans genome
COMMENT      Unpublished (1996)
CONTACT      Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..7
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK383a7"
/clone_id="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT      2 a 0 c 1 g 3 t 1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 1; DB 10; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      7 G 7

RESULT 39
HSM001420/c standard; RNA; EST: 8 BP.
XX
AC      AL037095;
XX
SV      AL037095.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
XX
KW      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OS
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      [1]
XX      RP 1-8
XX      RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX      sequencing consortium of the German Genome Project

```

```

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key
FH Location/Qualifiers
FT
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L0771"
FT /clone_11b="564 (synonym: hfbz2). Vector pAMP1: host
FT x1-2blue: sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 8 BP: 2 A; 3 C; 0 G; 3 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 7 G 7

RESULT 40
HSM001743/c
ID HSM001743 standard; RNA; EST; 8 BP.
XX
AC AL037413:
XX
SV AL037413.1
XX
UT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp564L0771_s1 (from clone DKFZp564L0771)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
FH (1)
FH 1-8
FH Key
FH Location/Qualifiers
FT
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L0771"
FT /clone_11b="564 (synonym: hfbz2). Vector pAMP1: host
FT x1-2blue: sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 8 BP: 1 A; 7 C; 0 G; 0 T; 0 other:

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 7 G 7

RESULT 41
HSM004451/c
ID HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975:
XX
SV AL039975.1
XX
UT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
FH (1)
FH 1-8
FH Key
FH Location/Qualifiers
FT
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434K0712"
FT /clone_11b="434 (synonym: htes3). Vector pSport1: host
FT DH10B: sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP: 2 A; 2 C; 2 G; 2 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 42
HSM004451/c
ID HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975:
XX

```

```

SV      AL039975.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KM      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      (1)
RP      1-8
RA      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..8
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434K0712"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 8 BP; 2 A; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
        |
Db      8 G 8

RESULT 43
HSM007277
ID      HSM007277 standard; RNA; EST; 8 BP.
AC      AL042427;
XX
SV      AL042427.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KM      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      (1)
RP      1-8
RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..8
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434C2421"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

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RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..8
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434C2421"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 8 BP; 2 A; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
        |
Db      1 G 1

RESULT 44
HSM007277/c
ID      HSM007277 standard; RNA; EST; 8 BP.
AC      AL042427;
XX
SV      AL042427.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KM      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      (1)
RP      1-8
RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key
FH      Location/Qualifiers
FT      source
FT      1..8
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434C2421"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

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FT DH10B: sites NotI + SalI\*  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX

Search completed: July 15, 2002, 20:07:36  
 Job time: 14494 sec

SQ Sequence 8 BP: 2 A: 2 C: 2 G: 2 T: 0 other:

Query Match Best Local Similarity 100.0%; Score 1: DB 2: Length 8:  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
 DB 8 C 8

RESULT 45

HSMD007323  
 ID HSM007323 standard; RNA; EST; 8 BP.  
 XX

AC AL042473:

XX AL042473.1

SV 12-MAR-1999 (Rel. 59, Created)

XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFP434F0121\_r1 (from clone DKFP434F0121)

XX EST; expressed sequence tag.

KW Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX

RN

RP

RA

RT Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopperspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FT

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OY 1 g 1  
 DB 1 G 1

Sequence 8 BP: 2 A: 2 C: 2 G: 2 T: 0 other:

Query Match Best Local Similarity 100.0%; Score 1: DB 2: Length 8:  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 Seconds

(without alignments)  
2.105 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3141\_3141

Sequence: 1 g 1

Scoring table:

Gapco 60.0, Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Pending Patents, NA, New:\*\*  
1: /cgn2\_6/ptodata/2/pna/PT\_NEW\_COMB.seq:\*\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1	100.0	2	6	US-10-027-632-51869
C 2	1	100.0	2	6	US-10-027-632-52280
C 3	1	100.0	2	6	US-10-027-632-52357
C 4	1	100.0	2	6	US-10-027-632-53003
C 5	1	100.0	2	6	US-10-027-632-58305
C 6	1	100.0	2	6	US-10-027-632-175312
C 7	1	100.0	2	6	US-10-027-632-175312
C 8	1	100.0	2	6	US-10-027-632-175337
C 9	1	100.0	2	6	US-10-027-632-175354
C 10	1	100.0	2	6	US-10-027-632-175401
C 11	1	100.0	2	6	US-10-027-632-175403
C 12	1	100.0	2	6	US-10-027-632-175415
C 13	1	100.0	2	6	US-10-027-632-175419
C 14	1	100.0	2	6	US-10-027-632-175426
C 15	1	100.0	2	6	US-10-027-632-175433
C 16	1	100.0	2	6	US-10-027-632-175849
C 17	1	100.0	2	6	US-10-027-632-175849
C 18	1	100.0	2	6	US-10-027-632-175849
C 19	1	100.0	2	6	US-10-027-632-175880
C 20	1	100.0	2	6	US-10-027-632-178420
C 21	1	100.0	2	6	US-10-027-632-178440
C 22	1	100.0	2	6	US-10-027-632-178440
C 23	1	100.0	2	6	US-10-027-632-178617
C 24	1	100.0	2	6	US-10-027-632-178640
C 25	1	100.0	3	1	PCT-US02-00351-20
C 26	1	100.0	3	6	US-10-027-632-52136
					US-10-027-632-52402

C 27	1	100.0	3	6	US-10-027-632-52403	Sequence 52403, A
C 28	1	100.0	3	6	US-10-027-632-52404	Sequence 52404, A
C 29	1	100.0	3	6	US-10-027-632-52410	Sequence 52410, A
C 30	1	100.0	3	6	US-10-027-632-52417	Sequence 52417, A
C 31	1	100.0	3	6	US-10-027-632-52418	Sequence 52418, A
C 32	1	100.0	3	6	US-10-027-632-52419	Sequence 52419, A
C 33	1	100.0	3	6	US-10-027-632-52425	Sequence 52425, A
C 34	1	100.0	3	6	US-10-027-632-52491	Sequence 52491, A
C 35	1	100.0	3	6	US-10-027-632-52495	Sequence 52495, A
C 36	1	100.0	3	6	US-10-027-632-52496	Sequence 52496, A
C 37	1	100.0	3	6	US-10-027-632-52508	Sequence 52508, A
C 38	1	100.0	3	6	US-10-027-632-52512	Sequence 52512, A
C 39	1	100.0	3	6	US-10-027-632-52513	Sequence 52513, A
C 40	1	100.0	3	6	US-10-027-632-52615	Sequence 52615, A
C 41	1	100.0	3	6	US-10-027-632-52633	Sequence 52633, A
C 42	1	100.0	3	6	US-10-027-632-52651	Sequence 52651, A
C 43	1	100.0	3	6	US-10-027-632-52753	Sequence 52753, A
C 44	1	100.0	3	6	US-10-027-632-52758	Sequence 52758, A
C 45	1	100.0	3	6	US-10-027-632-52761	Sequence 52761, A

## ALIGNMENTS

```
RESULT 1
US-10-027-632-51869/c
: Sequence 51869, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE OF INVENTION: Polymorphisms in the Human Genome
: TITLE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 51869
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-51869

Query Match
Best Local Similarity 100.0%: Score 1: DB 6: Length 2:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 2 G 2

RESULT 2
US-10-027-632-52280/c
: Sequence 52280, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
```

```
RESULT 3
US-10-027-632-52357/c
Sequence 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
```

```
Db 2 g 2
RESULT 4
US-10-027-632-53003/c
Sequence 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 g 2
```

```
RESULT 5
US-10-027-632-58305/c
Sequence 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218.006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198.676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193.483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185.218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167.363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156.358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146.002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58305
```



LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-58305

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 6  
US-10-027-632-175312  
Sequence 175312, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175312  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175312

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 7  
US-10-027-632-175337  
Sequence 175337, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175337  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175337

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 8  
US-10-027-632-175354  
Sequence 175354, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175354  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175354

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 9  
US-10-027-632-175401  
Sequence 175401, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db       1 g 1
```

```
RESULT 10
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db       1 g 1
```

```
RESULT 11
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db       1 g 1
```

```
RESULT 12
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 13
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 14
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 15
US-10-027-632-175849
; Sequence 175849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 16
US-10-027-632-176848
; Sequence 176848, Application US/10027632
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176848
```

```

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
         |
Db       1 g 1
```

```

RESULT 17
US-10-027-632-176849
; Sequence 176849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176849
```

Query Match 100.0%; Score 1; DB 6; Length 2;

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
         |
Db       1 g 1
```

```

RESULT 18
US-10-027-632-176880
; Sequence 176880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176880
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176880
```

```

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
         |
Db       1 g 1
```

```

RESULT 19
US-10-027-632-178420
; Sequence 178420, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
```

```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```
RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```
RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       2 g 2
```

```
RESULT 22
US-10-027-632-178617
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       2 g 2
```

RESULT 23

```
US-10-027-632-178640
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 g 2
```

```
RESULT 24
PCT-US02-00351-20/c
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ian
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
PCT-US02-00351-20
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 3 g 3
```

RESULT 25

```
US-10-027-632-52136
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 3 g 3
```

```
RESULT 26
US-10-027-632-52402/c
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402
```

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

RESULT 27  
US-10-027-632-52403/c  
; Sequence 52403, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52403  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52403

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

RESULT 28  
US-10-027-632-52404/c  
; Sequence 52404, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52404  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52404

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

RESULT 29  
US-10-027-632-52410/c  
; Sequence 52410, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52410  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52410

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 3 G 3

RESULT 30  
US-10-027-632-52417/c  
; Sequence 52417, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632

```
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 52417
;; LENGTH: 3
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-52417
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 31
US-10-027-632-52418/c
;; Sequence 52418, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 52418
;; LENGTH: 3
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-52418
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 32
US-10-027-632-52419/c
;; Sequence 52419, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 52419
;; LENGTH: 3
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-52419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 G 2
```

```
RESULT 33
US-10-027-632-52425/c
;; Sequence 52425, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 52425
;; LENGTH: 3
;; TYPE: DNA
;; ORGANISM: Human
```



US-10-027-632-52425

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 3 g 3

RESULT 34  
US-10-027-632-52491

; Sequence 52491, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 52491  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52491

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 2 g 2

RESULT 35  
US-10-027-632-52495/C

; Sequence 52495, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 52495  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52495

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 3 g 3

RESULT 36  
US-10-027-632-52496

; Sequence 52496, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 52496  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52496

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 2 g 2

RESULT 37  
US-10-027-632-52508

; Sequence 52508, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52508
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

```

RESULT 38
US-10-027-632-52512/c
: Sequence 52512, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52512
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52512
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

Db 3 G 3

```

RESULT 39
US-10-027-632-52513
: Sequence 52513, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52513
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52513
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 2 g 2
```

```

RESULT 40
US-10-027-632-52615
: Sequence 52615, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52615
: LENGTH: 3
```

TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52615

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 41  
US-10-027-632-52633

Sequence 52633, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52633  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52633

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 42  
US-10-027-632-52651

Sequence 52651, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52651  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52651

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 43  
US-10-027-632-52753

Sequence 52753, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52753  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52753

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 44

US-10-027-632-52758/c  
Sequence 52758, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758

```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
        |
Db       1 G 1

```

```

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761

```

```

OY      1 g 1
        |
Db       1 G 1

```

Search completed: July 16, 2002, 02:57:00  
Job time: 24558 sec

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

---

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 : Search time 12941.8 Seconds

(without alignments)  
1.672 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3141\_3141

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table: OLIGO\_NUC

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/US05 COMB.seq:\*

2: /cgn2\_6/ptodata/2/pna/US05 COMB.seq:\*

3: /cgn2\_6/ptodata/2/pna/US07 COMB.seq:\*

4: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

5: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

6: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

7: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

8: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

9: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

10: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

11: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

12: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

13: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

14: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

15: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

16: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

17: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

18: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

19: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

20: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

21: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

22: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

23: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

24: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

25: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

26: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

27: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

28: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

29: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

30: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

31: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

32: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

33: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

34: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

35: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

36: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

37: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

38: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

39: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

40: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

41: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

42: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

43: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	100.0	2	3	US-07-934-385-14	Sequence 14, Appl
2	100.0	2	5	US-08-107-721-46	Sequence 16, Appl
3	100.0	2	5	US-08-107-721-46	Sequence 16, Appl
4	100.0	2	15	US-09-172-828-15	Sequence 15, Appl
5	100.0	2	16	US-09-284-725-201	Sequence 20, Appl
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45	1	100.0	2	24	US-09-634-306B-178617	Sequence 178617

## ALIGNMENTS

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1 RESULT 1
2
3 : Sequence 14: Application US/07934385
4 : GENERAL INFORMATION:
5 : APPLICANT: LATHAM, JOHN
6 : APPLICANT: LEUNG, LAWRENCE
7 : TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
8 : TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES
9 : NUMBER OF SEQUENCES: 177
10 : CORRESPONDENCE ADDRESS:
11 : ADDRESSEE: MORRISON & FOERSTER
12 : STREET: 755 Page Mill Road
13 : City: Palo Alto
14 : STATE: California
15 : COUNTRY: USA
16 : ZIP: 94304-1018
17 :
18 : COMPUTER READABLE FORM:
19 : MEDIUM TYPE: Floppy disk
20 : COMPUTER: IBM PC compatible
21 : OPERATING SYSTEM: PC-DOS/MS-DOS
22 : SOFTWARE: Patent In Release #1.0, Version #1.25
23 : CURRENT APPLICATION DATA:
24 : APPLICATION NUMBER: US/07/934,385
25 : FILING DATE: 19920821
26 : CLASSIFICATION: 435
27 :
28 : ATTORNEY/AGENT INFORMATION:
29 : NAME: GRACEY, NANCY J.
30 : REGISTRATION NUMBER: 28,216
31 : REFERENCE/DOCKET NUMBER: 24610-2002.22
32 : TELECOMMUNICATION INFORMATION:
33 : TELEPHONE: (415) 494-0792
34 : TELEFAX: (415) 494-0792
35 :
36 : TELEX: 706141
37 :
38 : INFORMATION FOR SEQ ID NO: 14:
39 : SEQUENCE CHARACTERISTICS:
40 : LENGTH: 2 base pairs
41 : TYPE: NUCLEIC ACID
42 : STRANDEDNESS: single
43 : TOPOLOGY: linear
44 :
45 : FEATURE:
46 : NAME/KEY: misc_difference
47 : LOCATION: replace(1,"")
48 : OTHER INFORMATION: /note="This position is a
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Best Local Similarity	100.0%	Pred. No. 0;		
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	1		0;	Gaps
db	2 G 2			

RESULT 2  
US-08-107-721-46  
; Sequence 46, Application US/08107721  
; GENERAL INFORMATION.

APPLICANT: TOOLE, JOHN J.  
 APPLICANT: GRIFFIN, LINDA C.  
 APPLICANT: BOCK, LOUIS C.  
 APPLICANT: LATHAM, JOHN A.  
 APPLICANT: MUENCHAU, DARL. D.  
 APPLICANT: KRANCZYK, STEVEN  
 TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
 TITLE OF INVENTION: METHODS OF MARKING  
 NUMBER OF SEQUENCES: 109  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GILEAD SCIENCES, INC.  
 STREET: 344 LAKESIDE DRIVE  
 CITY: FOSTER CITY  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/107,721  
 FILING DATE: 20-AUG-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GRACEY, NANCY J.  
 REGISTRATION NUMBER: 28216  
 REFERENCE/DOCKET NUMBER: 24610-20022.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)574-3000  
 TELEFAX: (415)578-9284  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1  
 OTHER INFORMATION: /note="This is a biotin-17  
 OTHER INFORMATION: nucleotide stretch of abasic residues."  
 US-08-107-721-46

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Query Match      100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Qy      1 g 1
Db      2 G 2

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RESULT      3
US-08-107-721B-46
: Sequence 46, Application US/08107721B
: GENERAL INFORMATION:
: APPLICANT: TOOLE, JOHN J.
: APPLICANT: GRIFFIN, LINDA C.
: APPLICANT: BOCK, LOUIS C.
: APPLICANT: LATHAM, JOHN A.
: APPLICANT: MUENCHAU, DARYL D.
: APPLICANT: KRANCZYK, STEVEN
: TITLE OF INVENTION: APHARMOS SPECIFIC FOR BIOMOLECULES AND
: TITLE OF INVENTION: METHODS OF MAKING

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NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GILEAD SCIENCES, INC.  
STREET: 344 LAKE SIDE DRIVE  
CITY: FOSTER CITY  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,721B  
FILING DATE: 20-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28216  
REFERENCE/DOCKET NUMBER: 24610-20022.20  
TELEPHONE: (415)574-3000  
TELEFAX: (415)578-9264  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: /note= "This is a bictln-17  
US-08-107-721B-46  
nucleotide stretch of abasic residues."

Query Match 100.0%; Score 1; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 G 2

RESULT 4  
US-09-172-828-15  
Sequence 15, Application US/09172828  
GENERAL INFORMATION:  
APPLICANT: Children's Medical Center Corporation  
APPLICANT: Klagsbrun, Michael  
APPLICANT: Elenius, Klaus  
APPLICANT: Corfas, Gabriel  
TITLE OF INVENTION: Novel Human EGF Receptors and Use  
FILE REFERENCE: 47758-PCT  
CURRENT APPLICATION NUMBER: US/09/172,828  
CURRENT FILING DATE: 1998-10-15  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 2  
TYPE: DNA  
ORGANISM: mouse  
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 1 g 1

RESULT 5  
US-09-284-725-201/c  
Sequence 201, Application US/09284725  
GENERAL INFORMATION:  
APPLICANT: Quint, Wilhelmus  
APPLICANT: Van Doorn, Leendert  
TITLE OF INVENTION: Probes, methods and kits for detection and  
TITLE OF INVENTION: typing of Helicobacter pylori nucleic acids in biological  
NUMBER OF SEQUENCES: 280  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobb, Martens, Olson & Bear, LLP  
STREET: 620 Newport Center Drive, 16th floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/284,725  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP96/870131.8  
FILING DATE: 16-OCT-1996  
APPLICATION NUMBER: PCT/EP97/05614  
FILING DATE: 10-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: INNOG2.001APC  
TELEPHONE: (949) 760-0404  
TELEFAX: (949) 760-9395  
INFORMATION FOR SEQ ID NO: 201:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-284-725-201

Query Match 100.0%; Score 1; DB 16; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 G 2

RESULT 6  
US-09-306-333A-32  
Sequence 32, Application US/09306333A  
GENERAL INFORMATION:  
APPLICANT: Academy of Applied Science  
TITLE OF INVENTION: BRCAl and hMLH1 Gene Primer Sequences and Method for  
TITLE OF INVENTION: Testing  
FILE REFERENCE: BRCAl  
CURRENT APPLICATION NUMBER: US/09/306,333A  
CURRENT FILING DATE: 1999-05-06



PRIOR APPLICATION NUMBER: PCT/IB00/01607  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-333A-32

Query Match  
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 g 2

RESULT 7  
US-09-306-333A-32/c  
Sequence 32, Application US/09306333A  
GENERAL INFORMATION:  
APPLICANT: Academy of Applied Science  
TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for  
FILE REFERENCE: BRCA1  
CURRENT APPLICATION NUMBER: US/09/306,333A  
PRIOR FILING DATE: 1999-05-06  
PRIOR APPLICATION NUMBER: PCT/IB00/01607  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-333A-32

Query Match  
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 1 g 1

RESULT 8  
US-09-387-777-2/c  
Sequence 2, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-8907X  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
to an ASCII file

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 17; Length 2;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 g 2

RESULT 9  
US-09-387-777-3  
Sequence 3, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-8907X  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
to an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 10  
US-09-387-777-5/c  
Sequence 5, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 1 G 1

RESULT 11

US-09-387-777-6/c  
Sequence 6, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 12  
US-09-387-777-7  
Sequence 7, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Friedmann, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-387-777-7

Query Match 100.0%; Score 1: DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

## RESULT 13

US-09-387-777-7/C

Sequence 7, Application US/09387777  
GENERAL INFORMATION:

APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESS: Mark M. Friedmann c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Friedmann, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SPO ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-387-777-7

Query Match 100.0%; Score 1: DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

## RESULT 14

US-09-387-777-8/C

Sequence 8, Application US/09387777  
GENERAL INFORMATION:

APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESS: Mark M. Friedmann c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Friedmann, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-387-777-8

Query Match 100.0%; Score 1: DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 G 1

RESULT 15

US-09-387-777-9

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 G 1

RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 G 1

RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Friedmam, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 18  
US-09-387-777-11  
Sequence 11, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedmam, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-11

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 1 G 1

RESULT 19  
US-09-387-777-12  
Sequence 12, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedmam c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedmam, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-12

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 1 G 1

RESULT 20  
US-09-387-777-14/c  
Sequence 14, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEO ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

RESULT 21  
US-09-387-777-15  
Sequence 15, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEO ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

RESULT 22  
US-09-472-035A-19  
Sequence 19, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kashi et al.  
TITLE OF INVENTION: ABUNDANT, WELL-DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472,035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEO ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-19

Query Match 100.0%; Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 1 g 1

RESULT 23  
US-09-472-035A-20/C  
Sequence 20: Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kasht et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
Zip: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead Slimnote-8907X  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472,035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-20

Query Match 100.0%; Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 2 g 2  
RESULT 24

US-09-634-306B-51869/C  
Sequence 51869, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51869  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-51869

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 2 g 2

RESULT 25  
US-09-634-306B-52280/C  
Sequence 52280, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52280  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-52280

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 26
US-09-634-306B-52357/C
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 27
US-09-634-306B-53003/C
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      2 g 2
```

```
RESULT 28
US-09-634-306B-58305/C
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 g 1
```

```
RESULT 29
US-09-634-306B-175312
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
```



```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 30
US-09-634-306B-175337
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 31
US-09-634-306B-175354
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 32
US-09-634-306B-175401
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-09-634-306B-175401

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 33

US-09-634-306B-175403  
; Sequence 175403, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 175403  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-175403

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 34

US-09-634-306B-175415  
; Sequence 175415, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175415

LENGTH: 2

TYPE: DNA

ORGANISM: Human

US-09-634-306B-175415

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 35

US-09-634-306B-175419  
; Sequence 175419, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 175419  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-175419

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 36

US-09-634-306B-175426  
; Sequence 175426, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129

```

; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175426
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 1 g 1
```

```

RESULT 37
US-09-634-306B-175433
; Sequence 175433, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175433
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 1 g 1
```

```

Db 1 g 1
RESULT 38
US-09-634-306B-175849
; Sequence 175849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175849
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
Db 1 g 1
```

```

RESULT 39
US-09-634-306B-176848
; Sequence 176848, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2
```

TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176848

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

RESULT 40  
US-09-634-306B-176849  
Sequence 176849, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176849  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176849

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

RESULT 41  
US-09-634-306B-176880  
Sequence 176880, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176880  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176880

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

RESULT 42  
US-09-634-306B-178420  
Sequence 178420, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 178420  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-178420

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

RESULT 43  
US-09-634-306B-178440  
Sequence 178440, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440
```

```

Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
db 1 g 1
```

```

RESULT 44
US-09-634-306B-178440/C
: Sequence 178440, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440
```

```

Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 1 g 1
db 2 g 2
```

```

RESULT 45
US-09-634-306B-178617
: Sequence 178617, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178617
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178617
```

```

Query Match          100.0%: Score 1; DB 24; Length 2:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
db 2 g 2
```

Search completed: July 16, 2002, 02:50:26  
Job time: 31279 sec

\_\_\_\_\_

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds  
(without alignments)  
1.098 Million cell updates/sec

Title: US-09-375-248-1-COPY\_3141\_3141

Sequence score: 1 9 1

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/p/odata/2/1na/5A-COMB.seq:\*  
3: /cgn2\_6/p/odata/2/1na/5B-COMB.seq:\*  
4: /cgn2\_6/p/odata/2/1na/6A-COMB.seq:\*  
5: /cgn2\_6/p/odata/2/1na/6B-COMB.seq:\*  
6: /cgn2\_6/p/odata/2/1na/PCTUS-COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1	100.0	2	1 US-08-268-679B-8	Sequence 8, Appl1
2	1	100.0	2	1 US-08-484-192-16	Sequence 16, Appl1
3	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl1
4	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl1
5	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl1
6	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl1
7	1	100.0	3	1 US-07-791-213D-46	Sequence 62, Appl1
8	1	100.0	3	1 US-07-791-213D-62	Sequence 62, Appl1
9	1	100.0	3	1 US-08-268-679B-7	Sequence 7, Appl1
10	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl1
11	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl1
12	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl1
13	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl1
14	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl1
15	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl1
16	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl1
17	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl1
18	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl1
19	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl1
20	1	100.0	3	3 US-08-873-709-9	Sequence 9, Appl1
21	1	100.0	3	3 US-09-032-365A-36	Sequence 36, Appl1
22	1	100.0	3	4 US-08-793-634B-12	Sequence 12, Appl1
23	1	100.0	3	4 US-08-793-634B-12	Sequence 12, Appl1
24	1	100.0	4	1 US-07-755-462-2	Sequence 55, Appl1
25	1	100.0	4	1 US-07-755-462-2	Sequence 2, Appl1
26	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl1
27	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl1

28	1	100.0	4	1 US-07-630-288A-7	Sequence 7, Appl1
29	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl1
30	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl1
31	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl1
32	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl1
33	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl1
34	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl1
35	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl1
36	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl1
37	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl1
38	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl1
39	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl1
40	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl1
41	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl1
42	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl1
43	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl1
44	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl1
45	1	100.0	4	1 US-08-199-317-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-268-679B-8  
Sequence 8, Application US/08268679B  
Patent No. 5674729  
GENERAL INFORMATION:  
APPLICANT: WINNER, ECKARD, MOLLA,  
AKHTERUZZAMAN, PAUL, ANIKO V.  
TITLE OF INVENTION: DE NOVO CELL-FREE  
SYNTHESIS PICORNAVIRUS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08268,679B  
FILING DATE: 30-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07\846,914  
FILING DATE: 06-MAR-1992  
CLASSIFICATION: 435  
APPLICATION NUMBER: 07\719,761  
FILING DATE: 24-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C. H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 0887-4095 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.  
US-08-268-6798-8

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 1 g 1

RESULT 2  
US-08-484-192-16  
Sequence 16, Application US/08484192  
Patent No. 5756291  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: ALBRECHT, GLENN  
APPLICANT: LATNAM, JOHN  
APPLICANT: LEUNG, LAWRENCE  
APPLICANT: VERMAAS, ERIC  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
TITLE OF INVENTION: METHODS OF MAKING  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,192  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,387  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 246102002221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc.difference  
LOCATION: replace(1,"")  
OTHER INFORMATION: /note= "This is a blotin-17  
OTHER INFORMATION: nucleotide stretch of abasic residues."  
US-08-484-192-16

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 g 1  
Db 1 g 1

Db 2 G 2

RESULT 3  
US-08-361-024-3  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch.  
MEDIUM TYPE: 1.44 Mb  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgeon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 128D-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 1 g 1

RESULT 4  
US-08-361-024-3/C  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence



NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 Mb  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgoon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 128D-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-07-791-213D-46  
Sequence 46, Application US/07/91213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF INVENTIONS: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22133-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-07-791-213D-46/C  
Sequence 46, Application US/07/91213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF INVENTIONS: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22133-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 g 3

RESULT 7  
US-07-791-213D-62  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshihiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 3 g 3

Db 2 g 2

RESULT 8  
US-07-791-213D-62/c  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshihiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 g 3

RESULT 9  
US-08-268-679B-7  
Sequence 7, Application US/08268679B  
Patent No. 5674729  
GENERAL INFORMATION:  
APPLICANT: WIMMER, ECKARD; MOLA,  
APPLICANT: AKTERUZZAMAN; PAUL, ANIRO V.  
TITLE OF INVENTION: DE NOVO CELL-FREE  
TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,679B  
FILING DATE: 30-JUN-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/846,914  
FILING DATE: 06-MAR-1992  
CLASSIFICATION: 435  
APPLICATION NUMBER: 07/719,761  
FILING DATE: 24-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C.H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 0887-4095 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE: N.A.  
POSITION IN GENOME: N.A.  
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 g 2

RESULT 10  
US-08-602-036A-2  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
NUMBER OF SEQUENCES: 23  
METHODS OF INHIBITING METASTATIC CANCER  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 11  
US-08-602-036A-2/c  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
NUMBER OF SEQUENCES: 23  
METHODS OF INHIBITING METASTATIC CANCER  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 3 G 3

RESULT 12  
US-08-293-150A-46  
; Sequence 46, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 G 2

RESULT 13  
US-08-293-150A-46/C  
; Sequence 46, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 3 G 3

RESULT 14  
US-08-293-150A-62  
; Sequence 62, Application US/08293150A  
; Patent No. 5792629

GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
1  
Db 2 G 2

RESULT 15  
US-08-293-150A-62/c  
Sequence 62, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404

CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
1  
Db 3 G 3

RESULT 16  
US-08-502-374A-2  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oeystein  
APPLICANT: Engedaaten, Olav  
APPLICANT: Hovig, Elvind  
APPLICANT: Maelandmo, Gunhild H.  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,374A  
FILING DATE: 14-Jul-1995

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039PDV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 1 g 1

RESULT 17  
US-08-502-374A-2/C  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oeystein  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maeldansmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,374A  
FILING DATE: 14-Jul-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 3 g 3

RESULT 18  
US-08-642-407A-2  
Sequence 2, Application US/08642407A  
Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maeldansmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 1 g 1

RESULT 19  
US-08-642-407A-2/C  
Sequence 2, Application US/08642407A

Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Ooystein, Fodstad  
APPLICANT: Hovig, Eivind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642.407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1  
DB 3 G 3

RESULT 20  
US-08-873-709-9  
Sequence 9, Application US/08873709  
Patent No. 6037126  
GENERAL INFORMATION:  
APPLICANT: Grossman, Abraham  
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND  
APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF  
PROTEIN COMPONENT OF TELOMERASE ENZYME  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abraham Grossman  
STREET: 666 Washington Avenue  
CITY: Pleasantville  
STATE: NY  
COUNTRY: USA  
ZIP: 10570  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873.709  
FILING DATE: 12-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: 0001/002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-747-9108  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-873-709-9

Query Match  
Best Local Similarity 100.0%; Score 1; DB 3; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1  
DB 1 G 1

RESULT 21  
US-09-032-365A-36  
Sequence 36, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Naggart, Juergen  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
NEUROSENSORY DEFECTS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: IBM compatible  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEO-2C1P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-032-365A-36

Query Match 100.0%; Score 1; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 1 g 1

RESULT 22  
US-08-793-634B-12  
Sequence 12, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ. ID NO.: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 2 g 2

RESULT 23  
US-08-973-568-55  
Sequence 55, Application US/08973568B  
Patent No. 6277634  
GENERAL INFORMATION:  
APPLICANT: McCall, Maxine J.  
APPLICANT: Hendry, Philip  
APPLICANT: Lockett, Trevor  
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF  
FILE REFERENCE: 47203bpcus  
CURRENT APPLICATION NUMBER: US/08/973,568B  
CURRENT FILING DATE: 1998-05-18  
NUMBER OF SEQ. ID NOS: 55  
SOFTWARE: Patentin Ver. 2.1  
SEQ. ID NO. 55  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
FEATURE: Synthetic Ribozyme or portion thereof  
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and  
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 1 g 1

RESULT 24  
US-07-755-462-2  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 g 1  
Db 1 g 1

RESULT 25  
US-07-755-462-2/c  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 g 1  
Db 4 g 4

RESULT 26

US-08-169-950-6  
Sequence 6, Application US/08169950  
Patent No. 5366882

GENERAL INFORMATION:

APPLICANT: LUNNEN, KEITH D.

APPLICANT: WILSON, GEOFFREY G.

TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI

TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &

ADDRESSEE: CUSHMAN

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/169,950

FILING DATE: 17-DEC-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, DAVID S.

REGISTRATION NUMBER: 34235

REFERENCE/DOCKET NUMBER: 43959

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 g 1  
Db 1 g 1

RESULT 27

US-08-169-950-6/c

Sequence 6, Application US/08169950

Patent No. 5366882

GENERAL INFORMATION:

APPLICANT: LUNNEN, KEITH D.

APPLICANT: WILSON, GEOFFREY G.

TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI

TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSER: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,950  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1  
|  
DB 4 C 4

RESULT 28  
US-07-630-288A-7  
Sequence 7, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-7

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1  
|  
DB 1 C 1

RESULT 29  
US-07-630-288A-11  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 1 g 1

RESULT 30  
US-07-630-288A-11/C  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630.288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370.218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252.243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1

Db 4 G 4

RESULT 31  
US-07-630-288A-13  
Sequence 13, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630.288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370.218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252.243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-13

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 1 g 1

RESULT 32  
US-07-630-288A-14  
Sequence 14, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-14

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 G 1  
1 G 1

RESULT 33  
US-07-630-288A-14/C  
Sequence 14, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-14

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 G 4  
1 G 1  
4 G 4

RESULT 34  
US-07-630-288A-34  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
Db 2 G 2

RESULT 35  
US-07-630-288A-34/c  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 435  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2430  
TELEFAX: (708) 717-2443  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
Db 4 G 4

RESULT 36  
US-08-126-594-25  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Estraliadis, Aligiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPW/ANC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
Db 3 G 3

RESULT 37  
US-08-126-594-25/c  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Estraliadis, Aligiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 9 1  
|  
Db 4 G 4

RESULT 38  
US-08-188-943-1  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESS: C/O Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 9 1  
|  
Db 3 G 3

RESULT 39  
US-08-188-943-1/c  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESS: C/O Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 q 1  
1  
Db 4 G 4

## RESULT 40

US-08-188-943-2  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 1 q 1  
1  
Db 1 G 1

## RESULT 41

US-08-188-943-2/C  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 1 q 1  
1  
Db 2 G 2

## RESULT 42

US-08-465-811A-25  
Sequence 25, Application US/08465811A  
Patent No. 5637685  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465 811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 3 G 3

RESULT 43  
US-08-465-811A-25/c  
Sequence 25, Application US/08465811A  
Patent No. 5637665  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
NUMBER OF INVENTION: NORMALIZED CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465, 811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 4 G 4

RESULT 44  
US-08-199-317-2  
Sequence 2, Application US/08199317  
Patent No. 5670316  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,317  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,791  
FILING DATE: 09-JUL-1992  
APPLICATION NUMBER: US 07/755,462  
FILING DATE: 04-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 9150-0004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 1 G 1



RESULT 45  
US-08-199-317-2/C  
Sequence 2, Application US/08199317  
Patent No. 5670316  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,317  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,791  
FILING DATE: 09-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,462  
FILING DATE: 04-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 9150-0004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
OY 1 9 1  
DB 4 G 4

Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression

PT useful to inhibit metastatic cancer, partic. osteosarcoma  
XX  
XX Claim 2: Page 56; 70pp; English.  
XX

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
CC expression may include the trinucleotide GUC (AAT33326, given in 5'  
CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
CC other antisense oligonucleotides (AAT33327-36) complementary to  
CC specific regions of the CAPL gene (see also AAT33345), as well as  
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
CC patient as a means of inhibiting metastatic cancer.  
XX  
XX

SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 g 3

RESULT 2  
AAT33326/C  
ID AAT33326 standard; RNA; 3 BP.  
XX  
XX AAT33326;

DT 12-NOV-1996 (first entry)

DE CAPL trinucleotide.

KW CAPL: antisense oligonucleotide; ribozyme; cancer; metastasis;  
osteosarcoma; therapy; ss.

OS Synthetic.

PN MO9625499-A1.

PD 22-AUG-1996.

PF 16-FEB-1996; 96MO-US02108.

PR 17-FEB-1995; 95US-0391375.

PA (HYBR-) HYBRIDON INC.

PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.

PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;  
PI Von Hofe E;

DR WP1: 1996-393400/39.

PT Synthetic oligonucleotide(s) inhibiting CAPL gene expression -  
PT useful to inhibit metastatic cancer, partic. osteosarcoma

PS Claim 2: Page 56; 70pp; English.

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
CC expression may include the trinucleotide GUC (AAT33326, given in 5'  
CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
CC other antisense oligonucleotides (AAT33327-36) complementary to  
CC specific regions of the CAPL gene (see also AAT33345), as well as  
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
CC patient as a means of inhibiting metastatic cancer.  
XX  
XX

SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
1  
Db 1 g 1

RESULT 3  
AAA94655  
ID AAA94655 standard; DNA; 3 BP.  
XX  
XX AAA94655;

DT 15-JAN-2001 (first entry)

DE Human TUB gene probe #2.

KW Human: TULP; neurosensory defect; retina; retinal dystrophy; probe;  
TUB; ss.

OS Homo sapiens.

PN US6114502-A.

PD 05-SEP-2000.

PF 27-FEB-1998; 98US-0032365.

PR 22-AUG-1996; 96US-0701380.

PR 04-SEP-1996; 96US-0706292.

PR 10-APR-1996; 96US-0630592.

PR 17-SEP-1996; 96US-0714991.

PR 30-APR-1997; 97US-0850218.

PR 01-AUG-1997; 97US-0904659.

PR 17-SEP-1997; 97US-0932306.

(AXYS-) AXYS PHARM INC.

PI North M, Nishina P, Noben-Trauth K, Naggett J;

DR WP1: 2000-586483/55.

PT Mammalian proteins expressed in retina and brain, useful for producing  
PT antibodies and for diagnosing neurosensory defects including cochlear  
PT degeneration, peripheral retinal degeneration and cone-rod retinal  
PT dystrophy -

PS Disclosure; Columns 81-82; 61pp; English.

CC The present invention relates to human and murine cDNAs from a  
CC neurosensory defect associated gene family. The novel cDNAs are mouse  
CC tub form I (see AAA94629), mouse tub form II (see AAA94630), human TUB  
CC form 6 (see AAA94632), human TUB form I (see AAA94633), human TULP1 (see  
CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and  
CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as  
CC immunogens to raise antibodies that specifically identify TUB/TULP  
CC expressing cells and in drug screening assays directed at neurosensory  
CC defects. The novel proteins encoded by the present sequence can be used  
CC for the treatment of neurosensory degenerative conditions e.g. retinal  
CC dystrophies. The present sequence is a probe used to isolate the novel  
CC genes of the present invention.  
XX  
XX

SO Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

```

RESULT 4
AAL20244/C
ID AAL20244 standard; CDNA: 3 BP.
XX
AC AAL20244:
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN MO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001MO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Little J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI: 2001-451856/48.
XX
JT New peptide useful as a marker for the diagnosis of breast cancer -
XX
XX Claim 1: Page 2245; 3695pp; English.
XX
PS The invention relates to human breast cancer expressed polynucleotides
XX (AAL07544-AAL26789) and methods of assessing whether a patient is
XX afflicted with breast cancer by examining the correlation between the
XX expression of certain markers and the cancerous state of breast cells
XX The polynucleotides and encoded polypeptides are potential markers for
XX detecting, diagnosing, monitoring, characterising treating and
XX potentially preventing breast cancer. The polynucleotides and encoded
XX polypeptides are also useful for isolating compounds with cytostatic
XX activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match      100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
   |
Db 2 g 2

RESULT 5
AAO81664
ID AAO81664 standard; RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW bubble structure; pseudoknot; receptor; heparin; competition;
XX
XX

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```

KW Inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN MO9500528-A.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
XX (PHAR-) PHARMAGENICS INC.
XX
PI Beutel BA, Joesten ME;
XX
DR WPI: 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity; useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp; English.
XX
XX The sequences given in AAO81642-95 are oligonucleotides which modulate
XX the activity of basic fibroblast growth factor (bFGF) by binding
XX to the bFGF protein. Most esp. the sequences given in AAO81664-67
XX represent core sequences of which at least one is present in each of
XX the binding oligos. These oligonucleotides may form a single
XX strand, double strand, a stem-loop structure, a bubble structure, a
XX pseudoknot or a closed, circular structure. bFGF binds to high
XX affinity receptor and low affinity heparin-like molecules on the
XX cell surface. These oligonucleotides bind to bFGF in competition
XX with its receptor and heparin. These oligonucleotides may inhibit
XX or enhance the activity of bFGF. Particularly, they inhibit
XX CC neovascularisation so they can be used to suppress growth of solid
XX CC tumours and to reduce the risk of metastasis. They can be used as
XX CC diagnostic reagents to determine the presence of thrombin, or used in
XX CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match      100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
   |
Db 1 g 1

RESULT 6
AAO81664/C
ID AAO81664 standard; RNA: 4 BP.
XX
AC AAO81664:
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
XX
XX MO9500528-A.
XX

```

PD 05-JAN-1995.  
XX  
XX  
PF 17-JUN-1994; 94WO-US06884.  
XX  
XX  
PR 18-JUN-1993; 93US-0079677.  
PR 07-JAN-1994; 94US-0179491.  
XX  
PA (PHAR-) PHARMAGENICS INC.  
XX  
XX  
PI Beutel BA, Joesten ME;  
XX  
XX  
DR WPI; 1995-051992/07.  
XX  
XX  
PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
factor - modulating, esp. inhibiting, its activity, useful in  
PT treating cancer, preventing metastasis, and diagnosis.  
XX  
XX  
PS Claim 3; Page 25; 44pp; English.  
XX  
XX  
CC The sequences given in AAQ81642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.  
XX  
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other:  
  
Query Match 100.0%; Score 1; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 g 1  
1  
4 G 4  
Db

RESULT 7  
AAQ81665  
ID AAQ81665 standard; RNA; 4 BP.  
XX  
AC AAQ81665;  
XX  
DT 29-SEP-1995 (first entry)  
XX  
DE bFGF binding oligomer core sequence #2.  
XX  
XX  
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
KW bubble structure; pseudoknot; receptor; heparin; competition;  
KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
KW metastasis; diagnosis; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
PN W09500528-A.  
XX  
PD 05-JAN-1995.  
XX  
XX  
PF 17-JUN-1994; 94WO-US06884.  
XX  
XX  
PR 18-JUN-1993; 93US-0079677.  
PR 07-JAN-1994; 94US-0179491.  
XX

PA (PHAR-) PHARMAGENICS INC.  
XX  
XX  
PI Beutel BA, Joesten ME;  
XX  
XX  
DR WPI; 1995-051992/07.  
XX  
XX  
PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
factor - modulating, esp. inhibiting, its activity, useful in  
PT treating cancer, preventing metastasis, and diagnosis.  
XX  
XX  
PS Claim 3; Page 25; 44pp; English.  
XX  
XX  
CC The sequences given in AAQ81642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.  
XX  
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other:  
  
Query Match 100.0%; Score 1; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 g 1  
1  
3 g 3  
Db

RESULT 8  
AAQ81665/C  
ID AAQ81665 standard; RNA; 4 BP.  
XX  
AC AAQ81665;  
XX  
DT 29-SEP-1995 (first entry)  
XX  
DE bFGF binding oligomer core sequence #2.  
XX  
XX  
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
KW bubble structure; pseudoknot; receptor; heparin; competition;  
KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
KW metastasis; diagnosis; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
PN W09500528-A.  
XX  
PD 05-JAN-1995.  
XX  
XX  
PF 17-JUN-1994; 94WO-US06884.  
XX  
XX  
PR 18-JUN-1993; 93US-0079677.  
PR 07-JAN-1994; 94US-0179491.  
XX  
XX  
PA (PHAR-) PHARMAGENICS INC.  
XX  
XX  
PI Beutel BA, Joesten ME;  
XX  
XX  
DR WPI; 1995-051992/07.  
XX  
XX  
PT New oligo-nucleotide(s) that bind to basic fibroblast growth

PT factor - modulating, esp. inhibiting, its activity, useful in  
PT treating cancer, preventing metastasis, and diagnosis.  
PS Claim 3: Page 25; 44pp; English.  
XX

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AA081644-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC with its receptor and heparin. These oligonucleotides may inhibit  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.  
XX

Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 4 G 4

RESULT 9

AA086385  
ID AA086385 standard; DNA; 4 BP.

AC AA086385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;

KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers

FT modified\_base 1  
FT /\*tag= a  
FT /note= "C-5'phosphate"

PN W09738131-A1.

PD 16-OCT-1997.

PE 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.

PA (IVAN/) IVANOVA E M.

PA (KRIV/) KRIVENKO A A.

PA (KULI/) KULIKOVA V F.

PA (LOKH/) LOKHOV S G.

PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;

PI Likhov SG, Pyshny DV;

WP1: 1997-512737/47.

XX

PT Detection of target nucleic acid sequence - based on ligation of  
PT hybridised short probe to flanking target-complementary sequences  
XX  
PS Example; Page 4; 15pp; Russian.  
XX

CC This sequence represents a probe for the target sequence P0 (shown in  
CC AA086376). This sequence was used to test the method of the invention.  
CC The method of the invention is for detecting a nucleic acid sequence to  
CC be analysed, and comprises hybridisation of an oligonucleotide probe  
CC complementary to the sequence to be analysed and bearing a reporter  
CC group, the novelty is that detection of a sequence is based on the  
CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
CC flanking oligonucleotide sequences (or their derivatives bearing  
CC polycyclic aromatic groups). The method is especially useful for  
CC detecting point mutations. Diagnosis of viral, genetic and other  
CC diseases is also mentioned.  
XX

Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
DB 3 g 3

RESULT 10

AA086385/C  
ID AA086385 standard; DNA; 4 BP.

AC AA086385;

DT 23-APR-1998 (first entry)

DE Probe for target nucleic acid sequence P0.

KW Point mutation detection; nucleic acid sequence analysis; probe;

KW viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

Key Location/Qualifiers

FT modified\_base 1  
FT /\*tag= a  
FT /note= "C-5'phosphate"

PN W09738131-A1.

PD 16-OCT-1997.

PE 11-APR-1996; 96WO-RU00087.

PR 11-APR-1996; 96WO-RU00087.

PA (DYMS/) DYMSHITS G M.

PA (IVAN/) IVANOVA E M.

PA (KRIV/) KRIVENKO A A.

PA (KULI/) KULIKOVA V F.

PA (LOKH/) LOKHOV S G.

PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;

PI Likhov SG, Pyshny DV;

WP1: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of  
PT hybridised short probe to flanking target-complementary sequences  
XX  
PS Example; Page 4; 15pp; Russian.

XX This sequence represents a probe for the target sequence p0 (shown in  
CC AAT66376). This sequence was used to test the method of the invention.  
CC The method of the invention is for detecting a nucleic acid sequence to  
CC be analysed, and comprises hybridisation of an oligonucleotide probe  
CC complementary to the sequence to be analysed and bearing a reporter  
CC group, the novelty is that detection of a sequence is based on the  
CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
CC flanking oligonucleotide sequences (or their derivatives bearing  
CC polycyclic aromatic groups). The method is especially useful for  
CC detecting point mutations. Diagnosis of viral, genetic and other  
CC diseases is also mentioned.

SO Sequence 4 BP: 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 4 C 4

## RESULT 11

AAT77252  
ID AAT77252 standard; DNA: 4 BP.

XX AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;  
KW immune response; antigen; naked gene expression vector; IGE;  
KW antibody; immunotherapy; ss.

XX Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

XX 28-JAN-1997; 97WO-US01277.

XX 30-JAN-1996; 96US-0593554.

XX (REGC ) UNIV CALIFORNIA.

XX Carson DA, Raz E;

XX WPI: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic  
PT polynucleotide - useful for selectively enhancing the TH1 immune  
PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16: Page 15; 102pp; English.

CC This sequence represents a non-coding immunostimulatory polynucleotide  
CC (ISP) comprised of at least one strand of a palindrome, which includes  
CC at least one dinucleotide consisting of adjacent, unethylated cytosine  
CC and guanine residues. ISP's could be used in vaccination methods  
CC for enhancing the immune response of a host to an antigen. Administration  
CC of naked gene expression vectors which encode antigens or their  
CC immunostimulatory fragments suppresses IGE antibody production  
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

SO Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 g 1  
Db 3 g 3

## RESULT 12

AAT77252/C  
ID AAT77252 standard; DNA: 4 BP.

XX AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;  
KW immune response; antigen; naked gene expression vector; IGE;  
KW antibody; immunotherapy; ss.

XX Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

XX 28-JAN-1997; 97WO-US01277.

XX 30-JAN-1996; 96US-0593554.

XX (REGC ) UNIV CALIFORNIA.

XX Carson DA, Raz E;

XX WPI: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic  
PT polynucleotide - useful for selectively enhancing the TH1 immune  
PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16: Page 15; 102pp; English.

CC This sequence represents a non-coding immunostimulatory polynucleotide  
CC (ISP) comprised of at least one strand of a palindrome, which includes  
CC at least one dinucleotide consisting of adjacent, unethylated cytosine  
CC and guanine residues. ISP's could be used in vaccination methods  
CC for enhancing the immune response of a host to an antigen. Administration  
CC of naked gene expression vectors which encode antigens or their  
CC immunostimulatory fragments suppresses IGE antibody production  
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

SO Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

## RESULT 13

AAL17191  
ID AAL17191 standard; CDNA: 4 BP.

XX AAL17191;

DT 07-DEC-2001 (first entry)

PR	14-JAN-2000;	2000US-0176077.
PR	14-MAR-2000;	2000US-0189167.
PR	24-MAR-2000;	2000US-0192099.
PR	29-MAR-2000;	2000US-0193480.
PR	15-MAY-2000;	2000US-0205230.
PR	09-JUN-2000;	2000US-0211315.
PR	25-JUL-2000;	2000US-0220534.
XX		
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PI	Lillie J, Xu Y, Wang Y, Steinmann K;	
DR	WPI: 2001-451856/48.	
XX		
PS	New peptide useful as a marker for the diagnosis of breast cancer .	
PT	Claim 1; Page 1720; 3695pp; English.	
XX		
CC	The invention relates to human breast cancer expressed polynucleotides	
CC	(AAL07544-AAL26789) and methods of assessing whether a patient is	
CC	afflicted with breast cancer by examining the correlation between the	
CC	expression of certain markers and the cancerous state of breast cells.	
CC	The polynucleotides are encoded polypeptides are potential markers for	
CC	detecting, diagnosing, monitoring, characterizing treating and	
CC	potentially preventing breast cancer. The polynucleotides and encoded	
CC	polypeptides are also useful for isolating compounds with cytostatic	
CC	activity.	
XX		
SQ	Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;	
	Query Match	100.0%; Score 1; DB 22; Length 4;
	Best local Similarity	100.0%; Pred. NO. 0;
	Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 g 1	
Dd	3 G 3	
RESULT 15		
AAL24357/C		
ID	AAL24357 standard; cDNA; 4 BP.	
XX		
AC	AAL24357;	
XX		
DT	07-DEC-2001 (first entry)	
XX		
DE	Human breast cancer expressed polynucleotide 16814.	
XX		
OS	Human; breast cancer; cell marker; cytosstatic; ss.	
XX	Homo sapiens.	
XX		
FN	M0200151628-A2.	
CC		
XX		
PD	19-JUL-2001.	
XX		
Pf	10-JAN-2001; 2001MO-US00798.	
XX		
PR	14-JAN-2000; 2000US-0176077.	
PR	14-MAR-2000; 2000US-0189167.	
PR	24-MAR-2000; 2000US-0192099.	
PR	29-MAR-2000; 2000US-0193480.	
PR	15-MAY-2000; 2000US-0205230.	
PR	09-JUN-2000; 2000US-0211315.	
PR	25-JUL-2000; 2000US-0220534.	
XX		
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PI	Lillie J, Xu Y, Wang Y, Steinmann K;	
XX	WPI: 2001-451856/48.	



```

XX New peptide useful as a marker for the diagnosis of breast cancer
PT
XX
XX
PS Claim 1: Page 3087; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAU07544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX
SQ Sequence 4 BP; 0 A; 1 C; 0 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   1
Db 3 G 3

RESULT 16
AA061450
ID AA061450 standard; RNA; 4 BP.
XX
AC AA061450;
XX
XX 18-JUN-2001 (first entry)
DT
XX
XX Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
DE
XX
XX Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
KW cyclin E2F1; vasotrophic; gene therapy; cell cycle arrest; ss.
XX
XX Synthetic.
OS
XX
XX WO200121789-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 22-SEP-1999; 99WO-EP07049.
PF
XX
XX 22-SEP-1999; 99WO-EP07049.
PR
XX
XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
PA
XX
XX Grassi G, Kuhn AC, Kandolf R;
PI
XX
XX WPI: 2001-257985/26.
DR
XX
XX New catalytically acting RNA molecule comprising hammerhead ribozyme
PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
PT inhibiting vascular smooth muscle cell proliferation and restenosis -
PS
XX
XX Claim 12: Page 28; 40pp; German.
XX
XX This invention describes a novel catalytic RNA molecule which is directed
CC against mRNA molecules (1) which encode the cell-relevant protein cyclin
CC E or E2F1. The products of the invention have vasotrophic activity and can
CC be used for gene therapy. The use of (1), or a DNA molecule or a plasmid
CC for inhibiting restenosis is claimed for obtaining a vector for gene therapy and
CC compositons containing these components are also claimed. (1)
CC efficiently induces cell cycle arrest by combined inactivation of cyclin
CC E and E2F1.
XX
XX
SQ Sequence 4 BP; 2 A; 0 C; 1 G; 0 U; 1 other;

```

```

Query Match      100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   1
Db 2 g 2

RESULT 17
AA093676/c
ID AA093676 standard; DNA; 5 BP.
XX
AC AA093676;
XX
XX 24-JUN-1990 (first entry)
DT
XX
XX Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
DE variant (HSV-c) and HSV grape variant (HSV-g).
XX
XX Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
KW
XX
XX Hop growth retarding viroid.
OS
XX
XX JP01040000-A.
PN
XX
XX 10-FEB-1989.
PD
XX
XX 05-AUG-1987; 87JP-0194377.
PF
XX
XX 05-AUG-1987; 87JP-0195377.
PR
XX
XX (YUKI ) YUKI GOSSEI YAKUHIN.
PA
XX
XX WPI: 1989-089715/12.
DR
XX
XX Fractionating and detecting hop growth retarding viroids -
PT using synthetic DNA probe contg. specific base sequence
PT
XX
XX Disclosure; page 3; 5pp; Japanese.
PS
XX
XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
CC probe. The probe is 13-25mer. The probe can be used to diagnose HSV
CC infections in plants.
XX
XX
SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match      100.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   1
Db 5 G 5

RESULT 18
AA068752
ID AA068752 standard; DNA; 5 BP.
XX
XX
XX AA068752;
AC
XX
XX 22-FEB-1995 (first entry)
DT
XX
XX CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.
DE
XX
XX Polymerase chain reaction; primer: PCR; amplify; heavy; light;
KW chain; complementarity determining region; CDR; variable; constant;
KW region; monoclonal antibody; MAb; binding affinity; EDNA; DOTA;

```

KM tumour; cancer; colorectal; breast; metal chelate; hapten; ss.  
XX Synthetic.  
OS  
XX A09350602-A.  
XX  
XX 26-MAY-1994.  
PD  
X  
PF 10-NOV-1993; 93AU-0050602.  
PR  
XX 12-NOV-1992; 92US-0975230.  
XX  
PA (HYBR-) HYBRITECH INC.  
XX  
PI Ahnweiler PM, Moore MD;  
DR WPI: 1994-209063/26.  
XX P-PSDB: AARS4150.  
XX  
PT Polypeptide used in imaging and treatment of carcinomas and  
XX tumours - comprising subunit antibody CDR having binding affinity  
XX for metal chelate of EDTA or DETA or analogues  
XX  
PS Claim 25; Fig 3A; 61pp; English.

The sequences given in AAQ8747-57 encode the wild type and mutagenised versions of the complementarity determining region 1 (CDR1) of the antibody designated CHA255. CHA255 is a murine monoclonal antibody (MAb) which is capable of binding complexes. Mutagenesis of these CDRs causes the production of polypeptides with a particularly high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3 of the heavy chain, and CDR2 and -3 of the light chain were targeted for mutagenesis. Five residues of both CDR1 and -3 of the CHA255 heavy chain, five of seven residues of both CDR1 and -3 of the CHA255 light chain CDR3 residues were specifically targeted for codon-based mutagenesis. The mutagenised MAbs can be used in compositions for in vivo imaging of malignant tissues or tumours. They are also useful for the treatment of malignant tissues or tumours. CC colorectal or breast cancer. Both methods involve the use of CC radionuclides which bind to metal chelates or haptens which are CC specifically delivered to the target site by a targeting molecule. CC derived peptides may be used to construct bi-functional antibodies having dual specificities, or as donor or recipients of CDR sequences.

SO Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 g 1  
|  
Db 1 g 1

RESULT 19  
AAQ81667/c  
ID AAQ81667 standard; RNA; 5 BP.  
XX  
AC AAQ81667;  
XX  
DT 29-SEP-1995 (first entry)  
DE  
XX bfgf binding oligomer core sequence #4.  
XX  
KW Basic: fibroblast growth factor; bfgf; stem-loop structure;  
KW bubble structure; pseudoknot; receptor; heparin; competition;  
KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
KW metastasis; diagnosis; gene therapy; ss.  
XX  
XX Synthetic.

[illegible]

XX (STAD ) AMOCO CORP.  
PA  
XX  
PI Stefano JE;  
XX  
DR WPI: 1996-029807/03.  
XX  
PT Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and  
XX cleavable replicable-inhibiting sequence.  
XX  
PS Claim 4: Column 62; 43pp: English.  
XX  
CC A composition comprises RNA of formula P4-P1-P2-P3 (Ia), a nucleic  
CC acid of formula R1-R2 (Iii), where (Ia) and (Iii) bind to a target  
CC nucleic acid of formula X2-X1-X3 (Ii) to form a hammerhead ribozyme,  
CC where P1 is a MDV-1 sequence capable of autocatalytic replication in  
CC the absence of P3; P2 is a sequence (AA112042 or AA112044) that binds  
CC to (Ii) and forms a cleavage site between P1 and P3; P3 (AA112043)  
CC is an inhibitory element that binds to X2 and interacts with a  
CC nucleotide of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes  
CC nucleotides to form the ribozyme with X1 and P2, or is the terminal  
CC nucleic acid of P1; X1 is a target region of (Ii); X2 and X3 are  
CC terminal nucleotides or second or third target regions of (Ii); R1  
CC is a ribozyme-forming area of (Iii); and R2 is a terminal nucleotide  
CC of R1 or an area of (Iii) that binds to (Ii). X1 and R1 are  
CC mutually exclusive and are represented by the sequences of AA112040 and  
CC AA112041. For hairpin ribozymes, P2 is AA112045 and R1 is AA112046.  
CC Probes bearing ribozymes are produced in a single step by transcription  
CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes  
CC produce specific cleavage events, leading to a product RNA with  
CC defined replication properties.  
XX  
SQ Sequence 5 BP; 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match 100.0%; Score 1; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 5 G 5

RESULT 21  
AAV61663  
ID AAV61663 standard; DNA: 5 BP.  
XX  
AC AAV61663;  
XX  
DT 03-DEC-1998 (first entry)  
XX  
DE Fusarium sp. 18S rRNA DNA fragment #7.  
XX  
KW 18S rRNA: detection: identification: fungus; ss.  
XX  
OS Fusarium sp.  
XX  
PN JP10234380-A.  
XX  
PD 08-SEP-1998.  
XX  
PF 28-FEB-1997; 97JP-0062104.  
XX  
PR 28-FEB-1997; 97JP-0062104.  
XX  
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
XX  
DR WPI: 1998-535034/46.  
XX  
PT Use of oligo:nucleotide for detecting and identification of fungus  
PT of Fusarium genus - as primer or probe to detect of identify  
PT microbes rapidly and exactly

XX  
PS Claim 1: Page 7; 20pp: Japanese.  
XX  
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
CC used in a method for the detection and identification of a fungus of  
CC Fusarium genus. The process can be used to detect or identify microbes  
CC rapidly and exactly.  
XX  
SQ Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 5 G 5

RESULT 22  
AAV61663/C  
ID AAV61663 standard; DNA: 5 BP.  
XX  
AC AAV61663;  
XX  
DT 03-DEC-1998 (first entry)  
XX  
DE Fusarium sp. 18S rRNA DNA fragment #7.  
XX  
KW 18S rRNA: detection: identification: fungus; ss.  
XX  
OS Fusarium sp.  
XX  
PN JP10234380-A.  
XX  
PD 08-SEP-1998.  
XX  
PF 28-FEB-1997; 97JP-0062104.  
XX  
PR 28-FEB-1997; 97JP-0062104.  
XX  
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
XX  
DR WPI: 1998-535034/46.  
XX  
DE Use of oligo:nucleotide for detecting and identification of fungus  
PT of Fusarium genus - as primer or probe to detect of identify  
PT microbes rapidly and exactly  
XX  
PS Claim 1: Page 7; 20pp: Japanese.  
XX  
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
CC used in a method for the detection and identification of a fungus of  
CC Fusarium genus. The process can be used to detect or identify microbes  
CC rapidly and exactly.  
XX  
SQ Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 5 G 5

RESULT 23  
AA196299  
ID AA196299 standard; DNA: 5 BP.  
XX

AC AAT96299;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Fungal telomeric nucleic acid sequence.  
 XX  
 KM Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 KM telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 KM malarial infection; malaria; ss.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN US5695932-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 13-MAY-1993; 93US-0060952.  
 XX  
 PR 13-MAY-1993; 93US-0060952.  
 PR 13-MAY-1992; 92US-0882438.  
 PR 24-MAR-1993; 93US-0038766.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;  
 PI WPI: 1998-041293/04.  
 DR  
 XX  
 PT Detection of eukaryotic pathogens, especially fungal or Plasmodium  
 PT spp. - by detecting telomerase activity  
 XX  
 PS Claim 5: Columns 81-82; 82pp; English.  
 XX  
 CC The present sequence can be used in a novel method for detecting a  
 CC eukaryotic pathogen in a patient. The method comprises obtaining a  
 CC sample of somatic tissue or cells from the patient, determining if  
 CC telomerase activity is present and correlating this with the  
 CC presence of the pathogen. The method is useful for diagnosis of  
 CC fungal infections, especially a fungus of the genus Candida,  
 CC Kluveromyces, Saccharomyces, Sporothrix, Coccidioides,  
 CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,  
 CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially  
 CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.  
 CC  
 SO Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 |  
 Db 2 g 2

RESULT 24  
 AA210695  
 ID AA210695 standard; DNA; 5 BP.  
 XX  
 AC AA210695;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide sequence that increases p53 activity in a cell.  
 XX  
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KM skin cancer; ss.  
 XX  
 OS Synthetic.

XX  
 PN GB2336157-A.  
 XX  
 PD 13-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99GB-0006758.  
 XX  
 PR 26-MAR-1998; 98US-0048927.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 PI Gilchrest BA, Yaar M, Eller M;  
 PI WPI: 1999-543520/46.  
 DR  
 XX  
 PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX  
 PS Claim 11: Page 30; 44pp; English.  
 XX  
 CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.  
 CC  
 SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 |  
 Db 1 g 1

RESULT 25  
 AA210696/c  
 ID AA210696 standard; DNA; 5 BP.  
 XX  
 AC AA210696;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide sequence that increases p53 activity in a cell.  
 XX  
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KM skin cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2336157-A.  
 XX  
 PD 13-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99GB-0006758.  
 XX  
 PR 26-MAR-1998; 98US-0048927.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 PI Gilchrest BA, Yaar M, Eller M;  
 PI WPI: 1999-543520/46.  
 DR  
 XX  
 PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -  
XX Claim 11; Page 30; 44pp: English.

CC AA210692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.

SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 5 G 5

RESULT 26  
AA211611  
ID AA211611 standard; DNA; 5 BP.  
XX  
AC AA211611;

DT 16-NOV-1999 (first entry)  
XX

DE DNA enhancer sequence present in an upstream element.

KW Plant promoter; TATA motif; transcription start site; upstream element;  
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;  
KM ubi-1 promoter; Syn II core promoter; ss.

OS Synthetic.

XX WO9943838-A1.

PN 02-SEP-1999.

PD 23-FEB-1999; 99WO-US03863.

PR 24-FEB-1998; 98US-0028819.

PA (PION-) PIONEER HI-BRED INT INC.

PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

PT WPI: 1999-540601/45.

XX New synthetic promoter functional in plants to provide non-tissue  
XX specific, constitutive expression, particularly of oxalate oxidase for  
XX increased resistance to pathogens.  
PS Claim 39; Page 47; 61pp: English.

CC The invention provides a new synthetic plant promoter that comprises a  
CC TATA motif; a transcription start site (TSS) and a region between TATA  
CC and TSS containing at least 64 percent GC content. The synthetic core  
CC promoter, optionally containing additional upstream elements are used to  
CC increase expression, provides non-tissue specific, constitutive  
CC transcription of heterologous genes in any sort of plant, especially  
CC gene for oxalate oxidase for increasing plant resistance to pathogens.  
CC The upstream activating elements can be used to increase transcription  
CC from any promoter. A combination of the synthetic core promoter with  
CC synthetic upstream elements can induce expression 10 times greater than  
CC that provided by the maize ubi-1 promoter. The present sequence  
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.

XX  
SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 g 2

RESULT 27  
AA211611/C  
ID AA211611 standard; DNA; 5 BP.  
XX  
AC AA211611;

DT 16-NOV-1999 (first entry)  
XX

DE DNA enhancer sequence present in an upstream element.

KW Plant promoter; TATA motif; transcription start site; upstream element;  
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;  
KM ubi-1 promoter; Syn II core promoter; ss.

OS Synthetic.

XX WO9943838-A1.

PN 02-SEP-1999.

PD 23-FEB-1999; 99WO-US03863.

PR 24-FEB-1998; 98US-0028819.

PA (PION-) PIONEER HI-BRED INT INC.

PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

PT WPI: 1999-540601/45.

XX New synthetic promoter functional in plants to provide non-tissue  
XX specific, constitutive expression, particularly of oxalate oxidase for  
XX increased resistance to pathogens.  
PS Claim 39; Page 47; 61pp: English.

CC The invention provides a new synthetic plant promoter that comprises a  
CC TATA motif; a transcription start site (TSS) and a region between TATA  
CC and TSS containing at least 64 percent GC content. The synthetic core  
CC promoter, optionally containing additional upstream elements are used to  
CC increase expression, provides non-tissue specific, constitutive  
CC transcription of heterologous genes in any sort of plant, especially  
CC gene for oxalate oxidase for increasing plant resistance to pathogens.  
CC The upstream activating elements can be used to increase transcription  
CC from any promoter. A combination of the synthetic core promoter with  
CC synthetic upstream elements can induce expression 10 times greater than  
CC that provided by the maize ubi-1 promoter. The present sequence  
CC represents a DNA enhancer OSC-like motif present in an upstream element  
XX sequence.

SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|

Db 5 G 5

RESULT 28  
AAV72347/C  
ID AAV72347 standard; DNA: 5 BP.

XX AAV72347;

XX 28-JUL-1999 (first entry)

DE US5908745 primer #4.

XX DNA sequencing; disease-associated allele; polyacrylamide matrix;  
KM continuous/contiguous stacking hybridization technique; detection;  
KW mutation; diagnosis; primer; ss.

XX Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Parinov SV, Yershov GM;

DR WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous  
stacking hybridization as a diagnostic tool

XX Example 1; Column 9; 16pp; English.

This invention describes novel methods for sequencing and analysing DNA samples to detect disease-associated alleles, by continuous/contiguous stacking hybridization techniques (utilizing universal bases) with oligonucleotides immobilized on polyacrylamide matrices. The methods may be used to detect multiple DNA base mutations which are specific for certain diseases. The methods of the invention provide accurate and efficient and sensitive methods for diagnosing disease by detecting multiple mutation sequences in patient DNA. The method require the minimum number of oligonucleotides and few stacking hybridization steps than prior art methods. The methods are also efficient enough to discriminate between perfect and imperfect duplexes. The methods also obviate the need for the fabrication and array placement of large numbers of immobilized oligomers.

SO Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 5 G 5

RESULT 29

AAV72348

ID AAV72348 standard; DNA: 5 BP.

XX AAV72348;

AC AAV72348;

XX 28-JUL-1999 (first entry)

XX

DE US5908745 primer #5.

XX DNA sequencing; disease-associated allele; polyacrylamide matrix;  
KM continuous/contiguous stacking hybridization technique; detection;  
KW mutation; diagnosis; primer; ss.

XX Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Parinov SV, Yershov GM;

DR WPI: 1999-347002/29.

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SO Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

Db 2 g 2

RESULT 30

AAV72348/C

ID AAV72348 standard; DNA: 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

DE US5908745 primer #5.

XX

KM DNA sequencing; disease-associated allele; polyacrylamide matrix;

KW continuous/contiguous stacking hybridization technique; detection;

XX mutation; diagnosis; primer; ss.

XX Synthetic.

PN US5908745-A.

XX 01-JUN-1999.

```

XX 16-JAN-1996; 96US-0587332.
PF 16-JAN-1996; 96US-0587332.
PR (UYCH-) UNIV CHICAGO.
PA
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
DR WPI: 1999-347002/29.
XX
PT Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
PS Example 1: Column 9; 16pp; English.
XX
CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

```

```

Query Match      100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
DB 5 G 5

```

```

RESULT 31
AAV72349/C
ID AAV72349 standard; DNA: 5 BP.
XX
AC AAV72349;
XX
DT 28-JUL-1999 (first entry)
XX
DE US5908745 primer #6.
XX
KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX
OS Synthetic.
XX
PA US5908745-A.
XX
PN 01-JUN-1999.
XX
PD 16-JAN-1996; 96US-0587332.
PF 16-JAN-1996; 96US-0587332.
XX
PR 16-JAN-1996; 96US-0587332.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
DR WPI: 1999-347002/29.

```

```

XX detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
PS Example 1: Column 9; 16pp; English.
XX
CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

```

```

Query Match      100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 9 1
DB 5 G 5

```

```

RESULT 32
AAV72350/C
ID AAV72350 standard; DNA: 5 BP.
XX
AC AAV72350;
XX
DT 28-JUL-1999 (first entry)
XX
DE US5908745 primer #7.
XX
KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX
OS Synthetic.
XX
PA US5908745-A.
XX
PN 01-JUN-1999.
XX
PD 16-JAN-1996; 96US-0587332.
PF 16-JAN-1996; 96US-0587332.
XX
PR 16-JAN-1996; 96US-0587332.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
DR WPI: 1999-347002/29.
XX
PT Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
PS Example 1: Column 9; 16pp; English.
XX
CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for

```

CC certain diseases. The methods of the invention provide accurate and  
CC efficient and sensitive methods for diagnosing disease by detecting  
CC multiple mutation sequences in patient DNA. The method require the  
CC minimum number of oligonucleotides and few stacking hybridization steps  
CC than prior art methods. The methods are also efficient enough to  
CC discriminate between perfect and imperfect duplexes. The methods also  
CC obviate the need for the fabrication and array placement of large numbers  
CC of immobilized oligomers.

XX  
SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

## Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 5 G 5

## RESULT 33

AA56964  
ID AAX56964 standard; DNA; 5 BP.

AC AAX56964;

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;  
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN W09922772-A1.

XX 14-MAY-1999.

XX 28-OCT-1998; 98WO-US22821.

XX 31-OCT-1997; 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

PT Templin MV;

DR WP1; 1999-313181/26.

XX Liposome-encapsulated oligonucleotides useful for treating or  
preventing cancers associated with ras gene activation

XX Example 1; Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

## Query Match

100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 g 2

## RESULT 34

AA56964/C  
ID AAX56964 standard; DNA; 5 BP.

AC AAX56964;

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;  
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN W09922772-A1.

XX 14-MAY-1999.

XX 28-OCT-1998; 98WO-US22821.

XX 31-OCT-1997; 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

PT Templin MV;

DR WP1; 1999-313181/26.

XX Liposome-encapsulated oligonucleotides useful for treating or  
preventing cancers associated with ras gene activation

XX Example 1; Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

## Query Match

Best Local Similarity 100.0%; Score 1; DB 20; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 4 G 4

## RESULT 35

AA56964/C  
ID AAX21608 standard; DNA; 5 BP.

AC AAX21608;



XX Disclosure: page 22: 97pp: English.  
 CC The invention relates to oligonucleotides, which target a nucleic acid  
 CC encoding human N-ras, and are capable of inhibiting human N-ras  
 CC expression. The antisense oligonucleotides form a pharmaceutical  
 CC composition, which is useful for modulating the expression of human  
 CC N-ras, inhibiting the proliferation of cancer cells, and preventing or  
 CC treating conditions arising from the activation of a human N-ras  
 CC oncogene. The oligonucleotides are also useful in diagnostics,  
 CC therapeutics, and as research reagents and kits. The oligonucleotides  
 CC enable the specific modulation of activated human N-ras expression,  
 CC which is associated with tumour formation. Sequences AAX21601-619  
 CC represent antisense oligonucleotides targeted to mutant H-ras.  
 XX  
 S0 Sequence 5 BP: 1 A; 2 C; 2 G; 0 U; 0 other;

The invention relates to oligonucleotides, which target a nucleic acid encoding human N-ras, and are capable of inhibiting human N-ras expression. The antisense oligonucleotides form a pharmacological composition, which is useful for modulating the expression of human N-ras, inhibiting the proliferation of cancer cells, and preventing or treating conditions arising from the activation of a human N-ras oncogene. The oligonucleotides are also useful in diagnostics, therapeutics, and as research reagents and kits. The oligonucleotides enable the specific modulation of activated human N-ras expression, which is associated with tumour formation. Sequences AAx1601-619 represent antisense oligonucleotides targeted to mutant H-ras.

Sequence 5 BP: 1 A; 2 G; 0 U; 0 other;

```

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX
AC AAA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell cDNA sequence #109.
XX
KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX
OS Homo sapiens.
XX
WO200031259-AZ.
XX
PN
XX
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99WO-US27430.
XX
PR 20-NOV-1998; 98US-0196716.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Simpson AG, Dias Neto E, Brentani RR;
XX
DR WPI: 2000-400100/34.
XX
PT Method for determining open reading frames of the genome of an organism
using primers at low stringency conditions, useful in the construction

```

PT of contigs or constructs of sequenced nucleic acid molecules -  
XX  
PS Example 6: Page 47; 113pp; English.  
XX  
CC The present sequence is a cDNA sequence obtained using a method for  
CC determining open reading frames (ORFs) of the genome of an  
CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse  
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
CC incubated under low stringency conditions to yield single stranded  
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
CC than providing nucleotide sequence information from the non-coding  
CC terminl of nucleic acid molecules, the method provides information on  
CC the more interesting and relevant internal portions, such as ORFs. The  
CC method also permits the construction of contigs of sequenced nucleic  
CC acid molecules.  
XX  
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:  
XX  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 3 g 3  
XX  
RESULT 38  
AA56981/c  
ID AA56981 standard; cDNA; 5 BP.  
XX  
AC AA56981:  
XX  
DT 14-NOV-2000 (first entry)  
XX  
DE Human colon cancer cell cDNA sequence #109.  
XX  
KW Human: arbitrary primer; cDNA synthesis; contig sequence construction;  
KW open reading frame; ORF; low stringency; cDNA sequencing; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200031299-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 19-NOV-1999; 99MO-US27430.  
XX  
PR 20-NOV-1998; 98US-0196716.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Simpson AUG, Dias Neto E, Brentani RR;  
XX  
DR WPI: 2000-400100/34.  
XX  
PT Method for determining open reading frames of the genome of an organism  
PT using primers at low stringency conditions, useful in the construction  
PT of contigs or constructs of sequenced nucleic acid molecules -  
XX  
XX Example 6: Page 47; 113pp; English.  
XX  
CC The present sequence is a cDNA sequence obtained using a method for  
CC determining open reading frames (ORFs) of the genome of an  
CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse  
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
CC incubated under low stringency conditions to yield single stranded  
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
CC than providing nucleotide sequence information from the non-coding  
CC terminl of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The  
CC method also permits the construction of contigs of sequenced nucleic  
CC acid molecules.  
XX  
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:  
XX  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 5 G 5  
XX  
RESULT 39  
AA293601  
ID AA293601 standard; DNA; 5 BP.  
XX  
AC AA293601:  
XX  
DT 24-JUL-2000 (first entry)  
XX  
DE Transcription factor binding site of tobacco gene promoter sequence.  
XX  
KW Regulatory sequence; meristem; genetic engineering;  
KW gene expression; crop protection; transgenic plant; resistance;  
KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.  
XX  
OS Synthetic.  
XX  
OS Nicotiana acuminata.  
XX  
PN WO200012713-A1.  
XX  
PD 09-MAR-2000.  
XX  
PF 26-AUG-1999; 99MO-AU00692.  
XX  
PR 26-AUG-1998; 98AU-0005498.  
XX  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Mudge SR, Birch RG;  
XX  
DR WPI: 2000-237875/20.  
XX  
PF Meristem-expressible nucleic acid sequences, useful for producing  
PF transgenic plants with improved characteristics such as resistance to  
PF pathogens  
XX  
PS Example 9; Page 51; 102pp; English.  
XX  
CC Isolated regulatory sequences of plants that are operable in  
CC dividing cells, in particular the meristem cells of plants are useful  
CC in the genetic engineering of plants. The regulatory sequences can  
CC be used to control the expression of foreign genes placed under their  
CC control. Such methods are useful for producing transgenic plants with  
CC altered shape and/or size. The sequences are also useful for  
CC producing transgenic plants capable of rapid regeneration following  
CC harvest or plants having improved resistance to pathogens. This  
CC sequence has been shown to bind a factor involved in the activation  
CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three  
CC times in the meristem regulatory sequence of Tobacco described in  
CC GENE550 record AA293567.  
XX  
SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other:  
XX  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 5 9 5

## RESULT 40

AA293601/c  
ID AA293601 standard; DNA: 5 BP.

XX  
AC AA293601;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.  
XX  
KW Regulatory sequence; meristem; genetic engineering;  
KW gene expression; crop protection; transgenic plant; resistance;  
KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.  
OS Nicotiana acuminata.  
XX  
PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing  
PT transgenic plants with improved characteristics such as resistance to  
PT pathogens

PS Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in  
CC dividing cells. In particular the meristem cells of plants are useful  
CC in the genetic engineering of plants. The regulatory sequences can  
CC be used to control the expression of foreign genes placed under their  
CC control. Such methods are useful for producing transgenic plants with  
CC altered shape and/or size. The sequences are also useful for  
CC producing transgenic plants capable of rapid regeneration following  
CC harvest or plants having improved resistance to pathogens. This  
CC sequence has been shown to bind a factor involved in the activation  
CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three  
CC times in the meristem regulatory sequence of Tobacco described in  
CC GENESQ record AA293567.  
XX

SO Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 4 6 4

## RESULT 41

AA293602/c  
ID AA293602 standard; DNA: 5 BP.

XX  
AC AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.  
XX

KW Regulatory sequence; meristem; genetic engineering;  
KW gene expression; crop protection; transgenic plant; resistance;  
KW tobacco; transcription factor; NIT2; nitrate; ss.

OS Synthetic.  
OS Nicotiana acuminata.  
XX

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing  
PT transgenic plants with improved characteristics such as resistance to  
PT pathogens

PS Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in  
CC dividing cells. In particular the meristem cells of plants are useful  
CC in the genetic engineering of plants. The regulatory sequences can  
CC be used to control the expression of foreign genes placed under their  
CC control. Such methods are useful for producing transgenic plants with  
CC altered shape and/or size. The sequences are also useful for  
CC producing transgenic plants capable of rapid regeneration following  
CC harvest or plants having improved resistance to pathogens. This  
CC sequence has been shown to regulate nitrate metabolism in the  
CC fungus Neurospora crassa. It occurs multiple times in the meristem  
CC regulatory sequence of Tobacco described in GENESQ record AA293567.  
XX

SO Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 4 6 4

## RESULT 42

AA289330/c  
ID AA289330 standard; DNA: 5 BP.

XX  
AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
KW fat metabolism; ss.

OS Homo sapiens.

PN DE19838837-A1.

PD 02-MAR-2000.

XX 27-AUG-1998; 98DE-1038837.  
XX  
XX 27-AUG-1998; 98DE-1038837.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
XX  
XX Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
XX Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX  
XX Claim 25; Page 12; 38pp; German.  
XX  
XX This invention describes novel recombinant DNA molecules containing  
XX an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
XX cells but not functional in muscle cells or vice versa. The recombinant  
XX DNA molecules are useful for transcription of genes and, with host cells,  
XX to test for substances that can influence transcription. They can also be  
XX used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
XX metabolism and control of the promoter is useful in combating diseases  
XX with inappropriate fat tissue metabolism. This sequence represents a  
XX fragment of the human UCP-3 promoter which is used to illustrate the  
XX method of the invention.  
XX  
XX Sequence 5 BP: 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 2 G 2

RESULT 43  
AA289331  
ID AA289331 standard; DNA: 5 BP.  
XX  
XX AA289331;  
AC  
XX 13-JUN-2000 (first entry)  
DT  
XX Human UCP3 promoter fragment #11.  
DE  
XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
KW fat metabolism; ss.  
XX  
XX Homo sapiens.  
OS  
XX DE19838837-A1.  
PN  
XX 02-MAR-2000.  
PD  
XX 27-AUG-1998; 98DE-1038837.  
PF  
XX 27-AUG-1998; 98DE-1038837.  
PR  
XX 27-AUG-1998; 98DE-1038837.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
XX  
XX Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
XX Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX

PS Claim 28; Page 12; 38pp; German.  
XX  
XX This invention describes novel recombinant DNA molecules containing  
XX an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
XX cells but not functional in muscle cells or vice versa. The recombinant  
XX DNA molecules are useful for transcription of genes and, with host cells,  
XX to test for substances that can influence transcription. They can also be  
XX used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
XX metabolism and control of the promoter is useful in combating diseases  
XX with inappropriate fat tissue metabolism. This sequence represents a  
XX fragment of the human UCP-3 promoter which is used to illustrate the  
XX method of the invention.  
XX  
XX Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 4 g 4

RESULT 44  
AA289332  
ID AA289332 standard; DNA: 5 BP.  
XX  
XX AA289332;  
AC  
XX 13-JUN-2000 (first entry)  
DT  
XX Human UCP3 promoter fragment #12.  
DE  
XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
KW fat metabolism; ss.  
XX  
XX Homo sapiens.  
OS  
XX DE19838837-A1.  
PN  
XX 02-MAR-2000.  
PD  
XX 27-AUG-1998; 98DE-1038837.  
PF  
XX 27-AUG-1998; 98DE-1038837.  
PR  
XX 27-AUG-1998; 98DE-1038837.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
XX  
XX Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
XX Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX  
XX Claim 31; Page 12; 38pp; German.  
XX  
XX This invention describes novel recombinant DNA molecules containing  
XX an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
XX cells but not functional in muscle cells or vice versa. The recombinant  
XX DNA molecules are useful for transcription of genes and, with host cells,  
XX to test for substances that can influence transcription. They can also be  
XX used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
XX metabolism and control of the promoter is useful in combating diseases  
XX with inappropriate fat tissue metabolism. This sequence represents a  
XX fragment of the human UCP-3 promoter which is used to illustrate the  
XX method of the invention.  
XX  
XX Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
 Db 4 g 4

Search completed: July 15, 2002, 23:10:11  
 Job time: 18429 sec

RESULT 45  
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 ID AA248433 standard; DNA: 5 BP.  
 XX  
 AC AA248433:  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE First DNA arm segment.  
 XX  
 KM Microorganism: virus; polymerase chain reaction; food; cosmetic;  
 KM Clinical diagnostic; molecular beacon; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WC9963112-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 18-MAY-1999; 99WO-US10940.  
 XX  
 PR 18-MAY-1998; 98US-0086025.  
 PR 17-MAY-1999; 99US-0086025.  
 XX  
 PA (HUNT-) HUNT WESSON INC.  
 XX  
 PI Romick TL, Fraser MS;  
 DR WPI: 2000-086985/07.  
 XX  
 PT Detection of microorganisms and viruses, for use in the food and  
 PT cosmetic industries and for clinical diagnostics .  
 XX  
 PS Claim 51: Page 40; 63pp: English.  
 XX  
 CC The invention provides a novel in vitro method for the detection of  
 CC microorganisms and viruses. The method comprises: (1) forming a  
 CC polymerase chain reaction (PCR) mixture by combining a predetermined  
 CC volume of a sample to be tested for the presence of a nucleic acid  
 CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer  
 CC comprising 5'-GCTAAGCTCCCAAGT-3', and a second primer comprising  
 CC 5'-AGAACGCTCTCTAAGC-3', and PCR reagents; (2) forming a PCR product by  
 CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,  
 CC to replicate and attain 0.25-1000nmug nucleotide product/mul mixture; (3)  
 CC adding a probe containing DNA comprising 5'-GGTCTCTCTCTAAGCACC-3' to  
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with  
 CC the nucleic acid sequence, if present, and change the conformation of the  
 CC probe; and (4) determining whether or not bacteria are present in the  
 CC sample by detecting the conformational change of the probe, a  
 CC conformational change indicating the presence of bacteria in the sample.  
 CC The methods can be used for the detection of viruses and microorganisms,  
 CC including bacteria, yeast, molds and protoista. They can be used in the  
 CC food and cosmetic industry and in clinical diagnostics. Using the method  
 CC it is not necessary to remove non-hybridized probe from the system.  
 XX  
 SO Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 seconds  
(without alignments)  
2.195 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3141\_3141

Perfect score: 1

Sequence: 1 g 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb-da: \*  
2: gb-hcg: \*  
3: gb-in: \*  
4: gb-om: \*  
5: gb-ov: \*  
6: gb-pat: \*  
7: gb-ph: \*  
8: gb-pl: \*  
9: gb-pr: \*  
10: gb-ro: \*  
11: gb-sts: \*  
12: gb-sy: \*  
13: gb-un: \*  
14: gb-vl: \*  
15: em-ba: \*  
16: em-fun: \*  
17: em-hum: \*  
18: em-in: \*  
19: em-mu: \*  
20: em-om: \*  
21: em-or: \*  
22: em-ov: \*  
23: em-pat: \*  
24: em-ph: \*  
25: em-pl: \*  
26: em-ro: \*  
27: em-sts: \*  
28: em-un: \*  
29: em-vl: \*  
30: em-hcg-hum: \*  
31: em-hcg-inv: \*  
32: em-hcg-other: \*  
33: em-htgo-inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query  
No. Score Match Length DB ID Description

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C	2	1	100.0	2	6	AX092442	Sequence	AX092442	Sequence
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C	4	1	100.0	2	6	AX092444	Sequence	AX092444	Sequence
C	5	1	100.0	2	6	AX092445	Sequence	AX092445	Sequence
C	6	1	100.0	2	6	AX092446	Sequence	AX092446	Sequence
C	7	1	100.0	2	6	AX092447	Sequence	AX092447	Sequence
C	8	1	100.0	2	6	AX092448	Sequence	AX092448	Sequence
C	9	1	100.0	2	6	AX092449	Sequence	AX092449	Sequence
C	10	1	100.0	2	6	AX092450	Sequence	AX092450	Sequence
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
BASE COUNT

AX092441  
Sequence 2 from Patent WO0116366.  
AX092441.1 GI:13444536  
unidentified.  
unclassified.  
1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 2 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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Query Match  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 G 2

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LOCUS AX092442 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 3 from Patent WO0116366.  
ACCESSION AX092442  
VERSION AX092442.1 GI:13444537  
KEYWORDS  
SOURCE  
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AUTHORS  
TITLE  
JOURNAL  
(IL)

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source Location/Qualifiers  
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BASE COUNT 1 a 0 c 1 g 0 t  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 2 G 2

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LOCUS AX092444 2 bp DNA linear PAT 23-MAR-2001  
DEFINITION Sequence 5 from Patent WO0116366.  
ACCESSION AX092444  
VERSION AX092444.1 GI:13444539  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
(IL)

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BASE COUNT 1 a 0 c 1 g 0 t  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 G 1

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LOCUS AX092445 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 6 from Patent WO0116366.  
ACCESSION AX092445  
VERSION AX092445.1 GI:13444540  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
(IL)

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Db 2 G 2

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DEFINITION Sequence 7 from Patent WO0116366.  
ACCESSION AX092446  
VERSION AX092446.1 GI:13444541  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
(IL)

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Db 2 c 2

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DEFINITION Sequence 7 from Patent WO0116366.  
ACCESSION AX092446  
VERSION AX092446.1 GI:13444541  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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LOCUS AX092447 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 8 from Patent WO0116366.  
ACCESSION AX092447  
VERSION AX092447.1 GI:13444542  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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Db 1 c 1

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LOCUS AX092448 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 9 from Patent WO0116366.  
ACCESSION AX092448  
VERSION AX092448.1 GI:13444543  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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OY 1 g 1  
Db 1 c 1

RESULT 9  
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LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 10 from Patent WO0116366.  
ACCESSION AX092449  
VERSION AX092449.1 GI:13444544  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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OY 1 g 1  
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RESULT 10  
AX092449/c

LOCUS

DEFINITION Sequence 10 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 10 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES

source

BASE COUNT

ORIGIN

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2 G 2

RESULT 11

LOCUS

DEFINITION Sequence 11 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 11 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES

source

BASE COUNT

ORIGIN

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2 G 2

RESULT 12

LOCUS

DEFINITION Sequence 15 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 12 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 14 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)DEFINITION Sequence 12 from Patent WO0116366.  
ACCESSION AX092451  
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KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNALTemplate-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 12 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES

source

BASE COUNT

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2 G 2Query Match  
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1  
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RESULT 13

LOCUS

DEFINITION Sequence 14 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 14 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES

source

BASE COUNT

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RESULT 14

LOCUS

DEFINITION Sequence 15 from Patent WO0116366. 2 bp DNA linear PAT 21-MAR-2001

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 15 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 14 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

KEYWORDS  
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AUTHORS  
TITLE  
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unclassified.  
unclassified.  
unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 15 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

Location/Qualifiers  
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/organism="unclassified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

0 a 0 c 1 g 1 t

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 c 2

RESULT 15  
AX092528/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
BASE COUNT  
ORIGIN

AX092528  
Sequence 89 from Patent WO0116366.  
AX092528  
AX092528.1 GI:13444623  
unclassified.  
unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 89 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

Location/Qualifiers  
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/organism="unclassified"  
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/note="synthetic oligonucleotide;"

1 a 1 c 0 g 0 t

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 1 c 1

RESULT 16  
AX092529/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AX092529  
Sequence 90 from Patent WO0116366.  
AX092529  
AX092529.1 GI:13444624  
unclassified.  
unclassified.

unclassified.

unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 90 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

Location/Qualifiers  
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/organism="unclassified"  
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Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 c 2

RESULT 17  
AX092530  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
BASE COUNT  
ORIGIN

AX092530  
Sequence 91 from Patent WO0116366.  
AX092530  
AX092530.1 GI:13444625  
unclassified.  
unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 91 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

Location/Qualifiers  
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/note="synthetic oligonucleotide;"

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Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 c 2

RESULT 18  
AX092538  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AX092538  
Sequence 99 from Patent WO0116366.  
AX092538  
AX092538.1 GI:13444633  
unclassified.  
unclassified.  
1 (bases 1 to 2)  
Kless,H.

TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 99-08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t  
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Best Local Similarity 100.0%; Pred. No. 0;  
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OY 1 g 1  
Db 1 g 1

RESULT 19  
AX175286  
LOCUS AX175286  
DEFINITION Sequence 50 from Patent WO0144465.  
ACCESSION AX175286  
VERSION AX175286.1 GI:14598654  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequence.  
1 (bases 1 to 2)  
REFERENCE  
AUTHORS Phillips,N.C. and Pillon,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 50-21-JUN-2001;  
Bloniche Life Sciences Inc. (CA)  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:32630" 1 t

BASE COUNT 0 a 0 c 1 g 1 t  
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Query Match 100.0%; Score 1; DB 6; Length 2;  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 1 g 1

RESULT 20  
AX175287  
LOCUS AX175287  
DEFINITION Sequence 51 from Patent WO0144465.  
ACCESSION AX175287  
VERSION AX175287.1 GI:14598655  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequence.  
1 (bases 1 to 2)  
REFERENCE  
AUTHORS Phillips,N.C. and Pillon,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 51-21-JUN-2001;  
Bloniche Life Sciences Inc. (CA)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 0 a 0 c 1 g 1 t  
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Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 21  
BD009609/c  
LOCUS BD009609  
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.  
ACCESSION BD009609  
VERSION BD009609.1 GI:18637982  
KEYWORDS JP 2001502536-A/201.  
SOURCE  
ORGANISM  
unidentified.  
unclassified.  
1 (bases 1 to 2)  
REFERENCE  
AUTHORS Quint,W. and Doorn,L.J.V.  
TITLE Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples  
JOURNAL Patent: JP 2001502536-A 201-27-FEB-2001;  
INOGENETICS NV, DDL BV  
COMMENT  
OS Unidentified  
PN JP 2001502536-A/201  
PD 27-FEB-2001  
PF 10-OCT-1997 JP 1998518004  
PR 16-OCT-1996 EP 96870131.8  
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN  
PC C1201/68,C07K14/205,C12N15/11  
CC  
FH Key  
FT source Location/Qualifiers  
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/organism="unidentified".

FEATURES  
source Location/Qualifiers  
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/organism="unidentified"  
/db\_xref="taxon:32644" 0 t 1 others  
BASE COUNT 0 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 g 2

RESULT 22  
CNS01C99  
LOCUS CNS01C99  
DEFINITION Botrytis cinerea strain T4 CDNA library under conditions of nitrogen deprivation.  
ACCESSION AL115237  
VERSION AL115237.1 GI:5829656  
KEYWORDS cdna library; nitrogen deprivation.  
SOURCE Botryotinia fuckeliana.  
ORGANISM Botryotinia fuckeliana  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.  
REFERENCE  
AUTHORS Biton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

```

TITLE      Direct Submission
JOURNAL    Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
REFERENCE   78026 Versailles, France
AUTHORS     2 (bases 1 to 2)
TITLE      Genoscope.
JOURNAL     Direct Submission
            Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 Evry cedex - FRANCE (E-mail : sequefr@genoscope.cns.fr)
            Web : www.genoscope.cns.fr)
            The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSIT
            vector.

FEATURES
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    /organism="Botryotinia fuckeliana"
    /db_xref="taxon:40559"
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  Best Local Similarity 100.0%; Score 1; DB 8; Length 2;
  Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 23
LOCUS      AC079635
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC079635
VERSION     AC079635.3 GI:14647267
KEYWORDS   HTG; HTGS; PHASEO.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 3)
            McCombie,W.R., Baker,J.P., Bahret,A., Yang,C., Ballia,V.,
            Dedhia,N.N., de la Bastide,M., Kuit,K., King,L., Kirchoff,K.A.,
            Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R.,
            Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Palmer,L.,
            Vill.M.D. and Zutavern,F.
            Mouse Genomic Sequence
            Unpublished
            2 (bases 1 to 3)
            McCombie,W.R.
            Direct Submission
            Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
            On Jul 10, 2001 this sequence version replaced gi:14595773.
            * NOTE: This record contains 1 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            1
            3: contig of 3 bp in length.
            This entry has been temporarily removed. An update for RP23-152L20

FEATURES
  source
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    /clone="RP23-152L20"

BASE COUNT
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Query Match
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  Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 3 g 3

RESULT 25
LOCUS      A97991
DEFINITION Sequence 21 from Patent W09914366.
ACCESSION  A97991
VERSION     A97991.1 GI:6781229
KEYWORDS
SOURCE     unidentified.
ORGANISM   unidentified.
  
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unclassified.

REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willense, M.J. and Van, D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)  
FEATURES  
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/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

RESULT 26  
A97991/c

LOCUS A97991 3 bp DNA linear PAT 26-JAN-2000  
DEFINITION Sequence 21 from Patent WO9914366.  
ACCESSION A97991  
VERSION A97991.1 GI:6781229  
KEYWORDS  
SOURCE unidentified.

ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willense, M.J. and Van, D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

RESULT 27  
AX092457/c

LOCUS AX092457 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 18 from Patent WO0116366.  
ACCESSION AX092457  
VERSION AX092457.1 GI:13444552  
KEYWORDS  
SOURCE unidentified.

ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;  
YEIDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)

FEATURES

Location/Qualifiers

source

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/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 g 3

RESULT 28  
AX092458

LOCUS AX092458 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 19 from Patent WO0116366.  
ACCESSION AX092458  
VERSION AX092458.1 GI:13444553  
KEYWORDS  
SOURCE unidentified.

ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;  
YEIDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)

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source 1..3  
Location/Qualifiers  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 1 g 0 t  
ORIGIN

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 g 3

RESULT 29  
AX092460/c

LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 21 from Patent WO0116366.  
ACCESSION AX092460  
VERSION AX092460.1 GI:13444555  
KEYWORDS  
SOURCE unidentified.

ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;  
YEIDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)

FEATURES  
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Location/Qualifiers  
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/db\_xref="taxon:32644"

BASE COUNT 2 a /note="synthetic oligonucleotide;"  
ORIGIN 1 c 0 g 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
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Db 2 G 2

RESULT 30  
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LOCUS  
DEFINITION Sequence 22 from Patent WO0116366.  
ACCESSION AX092461  
VERSION AX092461.1 GI:13444556  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 22 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source Location/Qualifiers  
1..3  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 G 3

RESULT 31  
AX092462 AX092462 3 bp DNA linear PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 23 from Patent WO0116366.  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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source Location/Qualifiers  
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/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
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Db 3 G 3

RESULT 32  
AX092462/c AX092462 3 bp DNA linear PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 23 from Patent WO0116366.  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 G 2

RESULT 33  
AX092463/c AX092463 3 bp DNA linear PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 24 from Patent WO0116366.  
ACCESSION AX092463  
VERSION AX092463.1 GI:13444558  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 24 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
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/note="synthetic oligonucleotide;"  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 2 G 2

RESULT 34  
AX092464  
LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 25 from Patent WO0116366.  
ACCESSION AX092464  
VERSION AX092464.1 GI:13444559  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 25 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

FEATURES  
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Location/Qualifiers  
/organism="unidentified"  
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/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 0 c 1 g 0 t  
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Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 35  
AX092465  
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

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Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 36  
AX092465/c  
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

FEATURES  
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Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 3 G 3

RESULT 37  
AX092466  
LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 27 from Patent WO0116366.  
ACCESSION AX092466  
VERSION AX092466.1 GI:13444561  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE unclassified.  
AUTHORS 1 (bases 1 to 3)  
TITLE Kless,H.  
JOURNAL Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 27 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
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/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 0 c 2 g 0 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2



RESULT 38  
AX092467  
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 28 from Patent WO0116366.  
ACCESSION AX092467  
VERSION AX092467.1 GI:13444562  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 0 c 1 g 1 t  
ORIGIN 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 c 2

RESULT 39  
AX092469  
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 30 from Patent WO0116366.  
ACCESSION AX092469  
VERSION AX092469.1 GI:13444564  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 0 g 1 t  
ORIGIN 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 c 3

RESULT 40

AX092470  
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 31 from Patent WO0116366.  
ACCESSION AX092470  
VERSION AX092470.1 GI:13444565  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 0 c 1 g 1 t  
ORIGIN 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 c 1

RESULT 41  
AX092472  
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 33 from Patent WO0116366.  
ACCESSION AX092472  
VERSION AX092472.1 GI:13444567  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 c 1

RESULT 42  
AX092473  
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 34 from Patent WO0116366.

RESULT	4.3				
AX092474					
LOCUS					
DEFINITION	AX092474	3 bp	DNA	linear	PAT 21-MAR-2001
ACCESSION	Sequence	35	from patent WO0116566.		
VERSION	AX092474				
KEYWORDS	AX092474.1	GI:13444569			
SOURCE					
ORGANISM	unidentified.				
REFERENCE	unidentified.				
AUTHORS	unclassified.				
TITLE	1 (bases 1 to 3)				
JOURNAL	1. H.				
	Template-dependent nucleic acid polymerization using				
	oligonucleotide triphosphates building blocks				
	Patent: WO 0116366-A 35 08-MAR-2001.				
	YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar				
	(IL)				
FEATURES					
source	Location/Qualifiers				
	1..3				
	/organism="unidentified"				
	/db_xref="taxon:32644"				
	/note="synthetic oligonucleotide;"				
	1 a				
	1 c				
	1 g				
	0 t				
BASE COUNT					
ORIGIN					

Query Match	100.0%	Score 1:	DB 6:	Length 3:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches	1:	Conservative 0:	Mismatches 0:	Indels 0:
Gy	1	g 1		
Db	3	g 3		
RESULT 44				
AX092474/c				
LOCUS	AX092474		3 bp	DNA
DEFINITION	Sequence 35 from Patent WO0116366.			linear
ACCESSION	AX092474			
VERSION	AX092474.1		GI:13444569	
KEYWORDS	.			

SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 3)
TITLE	Kless,H.
JOURNAL	Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks Patent: WO 0116366-A 35 08-MAR-2001; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hader (IL)
FEATURES	location/Qualifiers
source	1..3
	/organism="unidentified"
	/db_xref="taxon:32644"
	/note="synthetic oligonucleotide;"
BASE COUNT	1 a 1 c 1 g 0 t
ORIGIN	

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy          1 g 1
            |
Db          1 G 1

```

RESULT	45			
LOCUS	AX092475/c			
DEFINITION	AX092475	3 bp	DNA	linear
ACCESSION	AX092475	Sequence 36 from Patent WO0116366.		PAT 21-MAR-2001
VERSION	AX092475.1			
KEYWORDS	GI:13444570			
SOURCE				
ORGANISM		unidentified.		
REFERENCE		unclassified.		
AUTHORS		1 (bases 1 to 3)		
TITLE		Kless,H.		
JOURNAL		Template-dependent nucleic acid polymerisation using oligonucleotide triphosphates building blocks		
		Patent: WO 0116366-A 36 08-MAR-2001;		
		YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar		
		(IL)		

```
FEATURES
source      Location/Qualifiers
1..3
  /organism="unidentified"
  /db_xref="taxon:32644"
  /note="synthetic oligonucleotide;"
BASE COUNT
1 a      1 c      0 g      1 t
```

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Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 1 g 1

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Search completed: July 15, 2002, 23:28:08  
Job time: 24541 sec

\_\_\_\_\_

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:28 ; Search time 7067.1 Seconds  
(without alignments)  
899.530 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514  
Perfect score: 471  
Sequence: 1 ctgaccatggaagatctgt.....gacctgcattctcgagctg 471

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estha:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: em\_hlc:\*  
10: gb\_estc1:\*  
11: gb\_estc2:\*  
12: gb\_hlc:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_lin:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	30.4	344	9	AA223868 zr10h12.r
2	67	14.2	687	10	BE281514
3	54	11.5	920	10	BE778623
4	27	5.7	189	10	BC815223
5	27	5.7	514	10	BC656884
6	26	5.5	525	9	AA637964
7	26	5.5	542	9	AA911950
8	26	5.5	589	12	AZ645762
9	26	5.5	748	10	BC518797
10	26	5.5	763	10	BI112246
11	26	5.5	789	10	BI158214
12	26	5.5	827	9	A1746873
13	26	5.5	846	10	BE279830
14	26	5.5	869	10	BC870441
15	26	5.5	876	10	BC923284
16	26	5.5	916	10	BF780935
17	26	5.5	1002	10	BF140383

18	25	5.3	722	10	BF320636
19	24	5.1	546	9	BE030526
20	23	4.9	357	9	A1556371
21	23	4.9	409	12	A0136157
22	23	4.9	455	9	AA709653
23	23	4.9	461	9	A1092636
24	23	4.9	498	9	AL039890
25	23	4.9	604	10	BF523018
26	23	4.9	1003	12	CNS04372
27	23	4.9	1099	12	CNS03518
28	22	4.7	658	9	AL642415
29	22	4.7	743	10	BF1556970
30	22	4.7	793	10	BF136721
31	22	4.7	834	10	BI686934
32	22	4.7	888	12	CNS04EJU
33	22	4.7	903	12	CNS02ZER
34	22	4.7	967	12	CNS02YAK
35	22	4.7	978	12	CNS025AS
36	22	4.7	1023	12	CNS01UBA
37	22	4.7	1037	11	BC013342
38	21	4.5	359	9	AA895295
39	21	4.5	458	10	BF147285
40	21	4.5	711	12	AG094291
41	21	4.5	845	10	BI111962
42	21	4.5	945	10	BF119392
43	21	4.5	1019	10	BI153717
44	21	4.5	2564	11	BC018230
45	20	4.2	253	9	AU129676

#### ALIGNMENTS

RESULT 1  
LOCUS AA223868  
DEFINITION zr10h12.r1 Stragatene NT2 neuronal precursor 937230 Homo sapiens  
cDNA clone IMAGE:651143 5' similar to gb:X68203 TYROSINE-PROTEIN  
KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION AA223868  
VERSION AA223868.1 GI:1844453  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maita, M., Matlin  
J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisling, B.,  
White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Willson RK

TITLE  
JOURNAL  
COMMENT Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu

FEATURES  
SOURCE This clone is available royalty-free through LUNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1275 Std Error: 0.00  
Seq Primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 228.  
Location/Qualifiers  
1..344  
/organism="Homo sapiens"  
/db\_xref="GDB:5588193"  
/db\_xref="taxon:9606"  
/clone="IMAGE:651143"  
/clone\_lib="Stragatene NT2 neuronal precursor 937230"  
/tissue\_type="neuroepithelial cells"  
/dev\_stage="Ntera-2 neuroepithelial cells"

/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: brain; Vector: pBluescript SK-; Site: 1;  
EcoRI; Site: 2; XhoI; Cloned unidirectionally. Primer:  
Oligo dt. Uninduced, exponentially growing neuroepithelial  
cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;  
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG  
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'."  
BASE COUNT 65 a 92 c 115 g 66 t 6 others  
ORIGIN

Query Match 30.4%; Score 143; DB 9; Length 344;  
Best Local Similarity 100.0%; Pred. No. 7.3e-62;  
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 tggatggccctgaagaacatcttcgacaaagtgatcacacgacgagatgagtcg 273  
Db 1 tgcattgcccctgaagacatcttcgacaaagtgatcacacgacgagatgagtcg 273  
QY 274 ttgggggtgctctctggagatctctctctggggggcctccgacccctggagtcag 333  
Db 61 ttgtggcctctctctggagatctctctctggggggcctccgacccctggagtcag 333  
QY 334 atcaatgaagatctgcacgag 356  
Db 121 atcaatgaagatctgcacgag 143

RESULT 2  
BE281514 687 bp mRNA linear EST 13-JUL-2000  
LOCUS 601155083f1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3138453 5',  
DEFINITION mRNA sequence.  
ACCESSION BE281514  
VERSION BE281514.1 GI:9156534  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 687)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LCM103 row: f column: 22  
High quality sequence stop: 390.  
location/Qualifiers  
1.687

FEATURES  
source  
1.687

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3138453"  
/clone\_1lb="NIH\_MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: placenta; Vector: pOT7; Site: 1; XhoI;  
Site: 2; EcoRI; cDNA made by oligo-dt priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAGCAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 167 a 183 c 214 g 123 t  
ORIGIN

Query Match 14.2%; Score 67; DB 10; Length 687;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 catacgccgatcatatgctgaactcgtgctcggaagcccaaggagagactgcatc 464  
Db 1 catagccgccatcatgctgactgctgctggaagcccaaggagagactgcatc 60  
QY 465 ggagctg 471  
Db 61 GGAGCTG 67

RESULT 3  
BE778623 920 bp mRNA linear EST 20-OCT-2000  
LOCUS 601466167f1 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:3869200 5',  
DEFINITION mRNA sequence.  
ACCESSION BE778623  
VERSION BE778623.1 GI:10199821  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 920)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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High quality sequence stop: 716.  
location/Qualifiers  
1.920

FEATURES  
source  
1.920

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/clone="IMAGE:3869200"  
/clone\_1lb="NIH\_MGC\_67"  
/tissue\_type="retinoblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1; NotI;  
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."  
BASE COUNT 236 a 240 c 268 g 176 t  
ORIGIN

Query Match 11.5%; Score 54; DB 10; Length 920;  
Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 atgcgaactctgtgctggagagcccaaggcgagaccgcatctcggagctg 471  
Db 1 ATGCTGAACTCTGTGCTCGGAGACCCCAAGCAGACCTGATTCGAGCTG 54

RESULT 4  
BG815223 189 bp mRNA linear EST 22-MAY-2001  
LOCUS dacc02f10.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4405795  
DEFINITION 5' similar to TR-091897 Q91897 FIBROBLAST GROWTH FACTOR RECEPTOR  
PRECURSOR. ;, mRNA sequence.  
ACCESSION BG815223

```

VERSION      BG615223.1  GI:14186203
KEYWORDS     EST.
SOURCE       African clawed frog.
ORGANISM     Xenopus laevis
REFERENCE    Amphibia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Xenopodinae; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 189)
              Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
              Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
TITLE        JOURNAL
COMMENT      Contact: Sandy Clifton, Ph.D.
              Washu Xenopus EST project, 1999
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Library constructed by Life Technologies. DNA Sequencing by:
              Washington University Genome Sequencing Center
              Clone distribution: Xenopus clones from this library are available
              through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov.
              Location/Qualifiers
                1..189
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                /db_xref="taxon:8355"
                /clone_image="4405795"
                /clone_lib="NICHD XCC Emb2"
                /tissue_type="embryo, stage 17/19"
                /lab_host="DH10B (phage-resistant)"
                /note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
                cloned unidirectionally. Primer: Oligo dT. Average insert
                size 2.1 kb. Constructed by Life Technologies."
                size 2..48 c 50 g 42 t

BASE COUNT   49 a 48 c 50 g 42 t
ORIGIN

Query Match      5.7%: Score 27; DB 10; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtcacccacagagaccgtgcgc 95
|||||
DB 125 AAAGTCATCCACAGACCTGCTGC 151

RESULT 5
BG656884 514 bp mRNA linear EST 26-APR-2001
LOCUS     BG656884
DEFINITION d125g11.y1 Wellcome CRC PRN3 St10 5 Xenopus laevis cDNA clone
FACITOR RECEPTOR PRECURSOR. ; mRNA sequence.
ACCESSION BG656884
VERSION    BG656884.1 GI:13796416
KEYWORDS  EST.
SOURCE     African clawed frog.
ORGANISM  Xenopus laevis
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 514)
              Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
              Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
TITLE      JOURNAL
COMMENT    Contact: Sandy Clifton, Ph.D.
              Washu Xenopus EST project, 1999

```

```

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 506.
Location/Qualifiers
  1..514
  /organism="Xenopus laevis"
  /db_xref="taxon:8355"
  /clone_image="3558357"
  /clone_lib="Wellcome CRC PRN3 St10 5"
  /tissue_type="embryo, stage 10.5"
  /lab_host="DH10B (phage-resistant)"
  /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
  were oligo-dT primed and directionally cloned. Staging
  according to Neukoop and Faber. Library was constructed
  by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon
  (Wellcome/CRC Institute)."

BASE COUNT   148 a 110 c 141 g 114 t 1 others
ORIGIN

Query Match      5.7%: Score 27; DB 10; Length 514;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtcacccacagagaccgtgcgc 95
|||||
DB 444 AAAGTCATCCACAGACCTGCTGC 470

RESULT 6
AA637964 525 bp mRNA linear EST 22-OCT-1997
LOCUS     AA637964
DEFINITION vt30a02.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone
IMAGE:1122122 5' similar to gb:M44489 EXTRACELLULAR
SIGNAL-REGULATED KINASE 2 (HUMAN); gb:X58712 mouse MAPK mRNA for
mitogen-activated protein kinase (MOUSE); mRNA sequence.
ACCESSION AA637964
VERSION    AA637964.1 GI:2561552
KEYWORDS  EST.
SOURCE     house mouse.
ORGANISM  Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.
              The Washu-HMI Mouse EST Project
              Unpublished (1996)
              Contact: Maria M/Mouse EST Project
              Washu-HMI Mouse EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:611458
              Seq primer: -28m13 rev2 ET from Amersham
              High quality sequence stop: 313.
              Location/Qualifiers

```

```
source
1..525
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone_image="1122122"
/clone_lib="Barestead mouse myotubes MPLB85"
/cell_line="C2C12"
/lab_host="DH10B"
/notice="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTTCACATCTGACATGACGACGCCGCCCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[AAATCCGATCCTTG], digested with Not I and cloned into the
library constructed by Bob Barestead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT      143 a      125 c      115 g      142 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 26; DB 9; Length 525;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtaccttgacctgccg 155
      |||
Db 232 AAGATCTGTGACTTTGGCCTTGCCCG 257

RESULT 7
LOCUS AW911950 542 bp mRNA linear EST 25-MAY-2000
DEFINITION ur89e03.y1 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE:3157468 5'
similar to gb:X58712 Mouse MARK mRNA for mitogen-activated protein
kinase (MOUSE);, mRNA sequence.
ACCESSION AW911950
VERSION AW911950.1 GI:8077468
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 542)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other-ESTs: ur89e03.x1
Contact: Robert Strausberg, Ph.D.
Email: rgs@pds-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.llnl.gov/image/html/tresources.shtml
MGI:1060224
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1..542
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="3157468"
/clone_lib="NCI-CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"

source
/dev_stage="5 months"
/lab_host="DH10B"
/notice="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      150 a      133 c      113 g      145 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 26; DB 9; Length 542;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtaccttgacctgccg 155
      |||
Db 98 AAGATCTGTGACTTTGGCCTTGCCCG 123

RESULT 8
LOCUS AZ645762/c 589 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0511E24F Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0511E24 F, DNA sequence.
ACCESSION AZ645762
VERSION AZ645762.1 GI:11775570
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Dunn,D., Longacre,A., Barber,M., Becorn,T., Duval,B., Hamli,C.,
Islam,H., Rose,M., Rose,R., Mahmod,M., Meenen,E., Pedersen,T., Reilly
and Wright,D., Weiss,R.
TITLES Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: E column: 24
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 589.
Location/Qualifiers
1..589
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="UGCCIM0511E24"
/clone_lib="Mouse 10kb plasmid UGCCIM library"
/sex="Male"
/lab_host="E. COLI strain XL10-Gold, T1-resistant, F-"
/notice="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
```

of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 133 a 149 c 161 g 146 t

ORIGIN

Query Match 5.5%: Score 26; DB 12; Length 589;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 caccagagactgctgctcggaacat 104  
|||||  
DB 257 CACAGACACCTGCTCGGACAT 232

RESULT 9  
BC518797 748 bp mRNA linear EST 02-APR-2001  
LOCUS 60257830F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3491663 5'  
DEFINITION mRNA sequence.  
ACCESSION BC518797  
VERSION BC518797.1 GI:13514016  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 748)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8536 row: c column: 24  
High quality sequence stop: 735.

FEATURES  
Source Location/Qualifiers  
1..748

/organism="Mus musculus"  
/strain="C57BL/6J (feta1)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3491663"  
/clone\_1ib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: PCMV-SPORT6; Site:1; Salt: 1M; Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 215 a 180 c 156 g 197 t

ORIGIN

Query Match 5.5%: Score 26; DB 10; Length 748;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgctgctccg 155  
|||||  
DB 185 AACATCTGACTTGGCTTCCCG 210

RESULT 10  
B1112246 763 bp mRNA linear EST 26-JUN-2001  
LOCUS B1112246

DEFINITION 602899921F1 NCI\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5029733 5',  
mRNA sequence.  
B1112246  
B1112246.1 GI:14563147

ACCESSION B1112246  
VERSION B1112246.1  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 763)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11083 row: j column: 06  
High quality sequence stop: 761.

FEATURES  
Source Location/Qualifiers  
1..763

/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5029733"  
/clone\_1ib="NCI\_CGAP\_Mam3"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"

/note="Organ: mammary; Vector: PCMV-SPORT6; Site:1; Salt: 1M; Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 222 a 179 c 159 g 203 t

ORIGIN

Query Match 5.5%: Score 26; DB 10; Length 763;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgctgctccg 155  
|||||  
DB 200 AACATCTGACTTGGCTTCCCG 225

RESULT 11  
B1158214 789 bp mRNA linear EST 05-JUL-2001  
LOCUS B1158214

DEFINITION 602920679F1 NIH\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5060946 5',  
mRNA sequence.  
B1158214  
B1158214.1 GI:14618215

ACCESSION B1158214  
VERSION B1158214.1  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 789)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.



Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L14M1164 row: n column: 19  
 High quality sequence start: 3  
 High quality sequence stop: 672.  
 Location/Qualifiers  
 1..789  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_image="5060946"  
 /clone\_lib="NIH\_CGAP\_Mam3"  
 /tissue\_type="tumor, gross tissue"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-Sport6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert 2 kb. Library constructed by Life  
 Technologies, catalog #12017-018. Investigators providing  
 samples: Lochar Hennighausen/Chu-Xia Deng, NIH Reference  
 for transgenic model: Xu et al., Nature Genetics 22, 37-43  
 (1999). Note: this is a NCI-CGAP Library."

BASE COUNT 221 a 187 c 176 g 205 t  
 ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 0.024;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgacttgactgcgcg 155  
 Db 33 AAGATCTGTGACTTGGCTTGCCTGCCG 58

RESULT 12 827 bp mRNA linear EST 22-JUN-1999  
 A1746873  
 LOCUS u108e07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone  
 DEFINITION IMAGE:2076228.5 similar to gb:X58712 Mouse MAPK mRNA for  
 A1746873  
 accession A1746873.1 GI:5125137  
 VERSION EST.  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 827)  
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person  
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
 Waterston,R. and Wilson,R.  
 The WashU-NCI Mouse EST Project 1999  
 TITLE Unpublished (1999)  
 JOURNAL Other\_ESTS: u108e07.x1  
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MGI:994664  
 Seq primer: custom primer used  
 High quality sequence stop: 510.  
 Location/Qualifiers

## FEATURES

## source

1..827  
 /organism="Mus musculus"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone\_image="2076228"  
 /clone\_lib="Sugano mouse embryo mewa"  
 /dev\_stage="embryo, 14 dpc"  
 /lab\_host="DH10B"  
 /note="Vector: pME18-FL3; Site:1: DraIII (CACTGCTG);  
 Site:2: DraIII (CACCATGTG); 1st strand cDNA was primed  
 with an oligo(dT) primer [ATGGGCTTTTCTTTTCTTTT];  
 double-stranded cDNA was ligated to a DraIII adaptor  
 [TGTGGCTTACTG], digested and cloned into distinct DraIII  
 sites of the pME18-FL3 vector (5' site CACTGCTG, 3' site  
 CACCATGTG). XhoI should be used to isolate the cDNA  
 insert. Size selection was performed to exclude fragments  
 <1.5kb. Library constructed by Dr. Sumio Sugano  
 (University of Tokyo Institute of Medical Science).  
 Custom primers for sequencing: 5' end primer  
 CTTCTGCTTAAGCTGCG and 3' end primer  
 CGACTGCACTGACGACA."

BASE COUNT 199 a 226 c 223 g 179 t  
 ORIGIN

Query Match 5.5%; Score 26; DB 9; Length 827;  
 Best Local Similarity 100.0%; Pred. No. 0.024;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgacttgactgcgcg 155  
 Db 698 AAGATCTGTGACTTGGCTTGCCTGCCG 723

RESULT 13 846 bp mRNA linear EST 13-JUL-2000  
 BE279830  
 LOCUS BE279830  
 DEFINITION mRNA sequence.  
 BE279830  
 VERSION BE279830.1 GI:9154825  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 846)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: L14M108 row: p column: 13  
 High quality sequence stop: 85.  
 Location/Qualifiers  
 1..846  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="3140604"  
 /clone\_lib="NIH\_MGC\_21"  
 /tissue\_type="choriocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: placenta; Vector: pORF7; Site:1: XhoI;  
 Site:2: EcoRI; cDNA made by oligo-dT priming.  
 directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAC(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by

## FEATURES

## source

Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 149 a 263 c 200 g 233 t 1 others

ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 846;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 436 ggaagcccaaggcgagactgcattc 461  
|||||  
Db 32 GGACACCCCAAGCGACGACCTGCAATT 57

RESULT 14  
BC870441 869 bp mRNA linear EST 29-MAY-2001  
LOCUS 602791353F1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4922605 5',  
DEFINITION mRNA sequence.  
ACCESSION BC870441  
VERSION BC870441 GI:14220981  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM10842 row: 1 column: 14  
High quality sequence stop: 709.

FEATURES  
source Location/Qualifiers

1..869  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4922605"  
/lab\_host="NCI\_CGAP\_SG2"  
/note="Organ: salivary gland; Vector: PCWV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 248 a 229 c 184 g 208 t

Query Match 5.5%; Score 26; DB 10; Length 869;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgcgcg 155  
|||||  
Db 482 AAGATCTGTGACTTGGCCTTGCCCG 507

RESULT 15  
BG923284 876 bp mRNA linear EST 05-JUN-2001  
LOCUS 602825245F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:4954067 5',  
DEFINITION mRNA sequence.

ACCESSION BG923284  
VERSION BG923284.1 GI:14303760  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM10914 row: 1 column: 12  
High quality sequence stop: 716.

FEATURES  
source Location/Qualifiers

1..876  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4954067"  
/lab\_host="NCI\_CGAP\_Mam6"  
/sex="female; virgin"  
/tissue="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/note="Organ: mammary; Vector: PCWV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. providing samples: Jeffrey Green, M.D., NIH"  
BASE COUNT 219 a 250 c 224 g 183 t

Query Match 5.5%; Score 26; DB 10; Length 876;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgcgcg 155  
|||||  
Db 583 AAGATCTGTGACTTGGCCTTGCCCG 608

RESULT 16  
BF780935 916 bp mRNA linear EST 12-JAN-2001  
LOCUS 602105430F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:4223556  
DEFINITION 5', mRNA sequence.  
ACCESSION BF780935  
VERSION BF780935.1 GI:12085968  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9812 row: C column: 13  
High quality sequence stop: 677.  
Location/Qualifiers  
1..916

FEATURES  
source  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_image="4223556"  
/lab\_host="NCI\_CGAP\_Kid14"  
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library." 1"

BASE COUNT 238 a 228 c 215 g 235 t

ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 916;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgacttgccctggccg 155  
|||||  
Db 158 AAGATCTGACTTGGCCTTGCCG 183

RESULT 17  
BF140383 1002 bp mRNA linear EST 24-OCT-2000  
LOCUS 601787895F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4015703 5'  
DEFINITION mRNA sequence.  
VERSION BF140383.1 GI:10979423  
ACCESSION  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1002)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9261 row: n column: 24  
High quality sequence start: 3  
High quality sequence stop: 556.  
Location/Qualifiers  
1..1002

FEATURES  
source  
/organism="Mus musculus"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone\_image="4015703"  
/lab\_host="NCI\_CGAP\_Lu30"  
/issue\_type="tumor, metastatic to mammary"  
/note="Organ: Lung; Vector: pCMV-SPORT6; Site:1; NotI; Site:2; SalI; Transgenic model MMTV-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 287 a 245 c 231 g 239 t

ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgacttgccctggccg 155  
|||||  
Db 79 AAGATCTGACTTGGCCTTGCCG 104

RESULT 18  
BF320636 722 bp mRNA linear EST 29-DEC-2000  
LOCUS BF320636  
DEFINITION u255b06.y1 NCI\_CGAP Mam6 Mus musculus cDNA clone IMAGE:3672947 5'  
similar to SW:MK01\_MOUSE P27703 MITOGEN-ACTIVATED PROTEIN KINASE 1  
; mRNA sequence.  
VERSION BF320636.1 GI:11269633  
ACCESSION  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 722)  
NCI-CGAP http://www.nci.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Other-ESTs: u255b06.x1  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov/image/html/lresources.shtml  
MGI:1433715

FEATURES  
source  
High quality sequence stop: 460.  
Location/Qualifiers  
1..722

BASE COUNT 168 a 201 c 196 g 154 t  
ORIGIN  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_image="3672947"  
/sex="female, virgin"  
/issue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; SalI; Site:2; NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

Query Match 5.3%; Score 25; DB 10; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 agatctgacttgccctggccg 155  
|||||  
Db 685 AGATCTGACTTGGCCTTGCCG 709

RESULT 19  
BE030526

LOCUS BE030526 546 bp mRNA linear EST 09-JUL-2000

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 T 1

RESULT 29  
US-08-188-943-2  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 4 T 4

RESULT 30  
US-08-188-943-2/c  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

RESULT 31  
US-08-199-317-2  
; Sequence 2, Application US/08199317  
; Patent No. 5670316  
; GENERAL INFORMATION:  
; APPLICANT: Sena, Elissa P.  
; APPLICANT: Calhoun, Cornelia J.  
; APPLICANT: Zarling, David A.  
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
; TITLE OF INVENTION: Formation  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/199,317  
; FILING DATE: 25-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/910,791  
; FILING DATE: 09-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,462  
; FILING DATE: 04-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520,321  
; FILING DATE: 07-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 9150-0004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
; US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

Db 3 t 3

RESULT 32  
US-08-199-317-2/c  
; Sequence 2, Application US/08199317  
; Patent No. 5670316  
; GENERAL INFORMATION:  
; APPLICANT: Sena, Elissa P.  
; APPLICANT: Calhoun, Cornelia J.  
; APPLICANT: Zarling, David A.  
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
; TITLE OF INVENTION: Formation  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/199,317  
; FILING DATE: 25-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/910,791  
; FILING DATE: 09-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,462  
; FILING DATE: 04-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520,321  
; FILING DATE: 07-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 9150-0004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
; US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 2 t 2

RESULT 33  
US-08-393-219-11  
; Sequence 11, Application US/08393219  
; Patent No. 5689040

GENERAL INFORMATION:  
APPLICANT: HARADA, John J.  
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES USEFUL FOR GENE  
NUMBER OF INVENTION: EXPRESSION IN SEEDS AND SEEDLINGS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower, 20th  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,219  
FILING DATE: 23-FEB-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Baslian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 2307E-581  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-393-219-11

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 3 t 3

RESULT 34  
US-08-510-032A-9  
Sequence 9, Application US/08510032A  
Patent No. 5712126  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Yarlindra Prashar  
TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-  
NUMBER OF INVENTION: end Restriction Fragments of cDNA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/510,032A  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-510-032A-9

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 3 t 3

RESULT 35  
US-08-510-032A-9/c  
Sequence 9, Application US/08510032A  
Patent No. 5712126  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Yarlindra Prashar  
TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-  
NUMBER OF INVENTION: end Restriction Fragments of cDNA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/510,032A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-510-032A-9

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 T 2

RESULT 36

US-08-468-049-7/C  
Sequence 7, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468.049

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/630,288

FILING DATE: 17-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: No. 5763171val B. Galloway

REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: CN 581903

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-468-049-7

Query Match

Best Local Similarity 100.0%; Score 1; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 4 T 4

RESULT 37

US-08-468-049-11

Sequence 11, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468.049

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/630,288

FILING DATE: 17-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218

FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/252,243

FILING DATE: 30-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: No. 5763171val B. Galloway

REGISTRATION NUMBER: 33,595

REFERENCE/DOCKET NUMBER: CN 581903

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443

TELEFAX: (708) 717-2430

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-468-049-11

Query Match

Best Local Similarity 100.0%; Score 1; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 3 T 3

RESULT 38

US-08-468-049-11/C

Sequence 11, Application US/08468049

Patent No. 5763171

GENERAL INFORMATION:

APPLICANT: Stefano, James E.

TITLE OF INVENTION: Nucleic Acid Structures with Catalytic

TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5763171val B. Galloway

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.

CITY: Naperville

STATE: IL

COUNTRY: USA

ZIP: 60563

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,049  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/630,288  
FILING DATE: 17-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5763171val B. Galloway  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: CN 581903  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-468-049-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 2 t 2

RESULT 39  
US-08-468-049-34  
Sequence 34, Application US/08468049  
Patent No. 5763171  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5763171val B. Galloway  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,049  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/630,288  
FILING DATE: 17-DEC-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5763171val B. Galloway  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: CN 581903  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-468-049-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 1 u 1

RESULT 40  
US-08-468-049-34/C  
Sequence 34, Application US/08468049  
Patent No. 5763171  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5763171val B. Galloway  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,049  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/630,288  
FILING DATE: 17-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5763171val B. Galloway  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: CN 581903  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443



TELEFAX: (708) 717-2430  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
US-08-468-049-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
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Db 3 t 3

RESULT 41  
US-08-488-015B-5  
; Sequence 5, Application US/08488015B  
; Patent No. 5780272  
; GENERAL INFORMATION:  
; APPLICANT: Jarrell, Kevin A.  
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES  
; NUMBER OF INVENTION: AND REAGENTS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,015B  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HUV-008.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEFAX: (617) 832-1000  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-488-015B-5

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
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Db 2 u 2

RESULT 42

US-08-488-015B-12  
; Sequence 12, Application US/08488015B  
; Patent No. 5780272  
; GENERAL INFORMATION:  
; APPLICANT: Jarrell, Kevin A.  
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES  
; NUMBER OF INVENTION: AND REAGENTS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,015B  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HUV-008.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEFAX: (617) 832-1000  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-488-015B-12

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
|  
Db 1 t 1

RESULT 43  
US-08-351-365-3  
; Sequence 3, Application US/08351365  
; Patent No. 5781681  
; GENERAL INFORMATION:  
; APPLICANT: Matusik, Robert J  
; TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES  
; NUMBER OF INVENTION: OF RAT PROBASTIN GENE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,365  
; FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-351-365-3

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 t 1

RESULT 44  
US-08-351-365-3/C  
Sequence 3, Application US/08351365  
Patent No. 5783681  
GENERAL INFORMATION:  
APPLICANT: Matusik, Robert J  
TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES  
NUMBER OF INVENTION: OF RAT PROBASIN GENE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,365  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-351-365-3

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 2 t 2

RESULT 45  
US-08-351-365-4  
Sequence 4, Application US/08351365  
Patent No. 5783681  
GENERAL INFORMATION:  
APPLICANT: Matusik, Robert J  
TITLE OF INVENTION: ANDROGEN REGULATION WITH DNA SEQUENCES  
NUMBER OF INVENTION: OF RAT PROBASIN GENE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,365  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1887-116 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-351-365-4

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 2 t 2

Search completed: July 15, 2002, 23:07:38  
Job time: 22991 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 ; Search time 12941.8 Seconds

(without alignments)  
1.672 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3150\_3150

Perfect score: 1 t 1

Scoring table: OLIGO-MNC

Gapop 60.0 , Gapept 60.0

Searched: 21979536 seqs, 1081749327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending Patents\_NA\_Main:\*

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31: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq:\*

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33: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*

34: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*

35: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*

36: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq:\*

37: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*

38: /cgn2\_6/ptodata/2/pna/US100\_COMB.seq:\*

39: /cgn2\_6/ptodata/2/pna/US101\_COMB.seq:\*

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42: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*

43: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*

44: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

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2	100.0	1	2	7	US-08-392-180-271	Sequence 271, App	
3	100.0	1	2	13	US-08-964-265-271	Sequence 271, App	
4	100.0	1	2	15	US-09-172-826-15	Sequence 15, App1	
5	100.0	1	2	16	US-09-227-782-16	Sequence 16, App1	
6	100.0	1	2	17	US-09-387-777-1	Sequence 1, App1	
7	100.0	1	2	17	US-09-387-777-3	Sequence 3, App1	
8	100.0	1	2	17	US-09-387-777-4	Sequence 4, App1	
9	100.0	1	2	17	US-09-387-777-5	Sequence 5, App1	
10	100.0	1	2	17	US-09-387-777-8	Sequence 8, App1	
11	100.0	1	2	17	US-09-387-777-9	Sequence 9, App1	
12	100.0	1	2	17	US-09-387-777-12	Sequence 12, App1	
13	100.0	1	2	17	US-09-387-777-13	Sequence 13, App1	
14	100.0	1	2	17	US-09-387-777-14	Sequence 14, App1	
15	100.0	1	2	17	US-09-387-777-15	Sequence 15, App1	
16	100.0	1	2	17	US-09-387-777-16	Sequence 16, App1	
17	100.0	1	2	18	US-09-472-035A-19	Sequence 19, App1	
18	100.0	1	2	24	US-09-634-306B-51869	Sequence 20, App1	
19	100.0	1	2	24	US-09-634-306B-52011	Sequence 51869, A	
20	100.0	1	2	24	US-09-634-306B-52015	Sequence 52011, A	
21	100.0	1	2	24	US-09-634-306B-52280	Sequence 52015, A	
22	100.0	1	2	24	US-09-634-306B-52357	Sequence 52280, A	
23	100.0	1	2	24	US-09-634-306B-58305	Sequence 52357, A	
24	100.0	1	2	24	US-09-634-306B-58424	Sequence 53022, A	
25	100.0	1	2	24	US-09-634-306B-58424	Sequence 58305, A	
26	100.0	1	2	24	US-09-634-306B-58424	Sequence 58424, A	
27	100.0	1	2	24	US-09-634-306B-58424	Sequence 58424, A	
28	100.0	1	2	24	US-09-634-306B-58424	Sequence 58424, A	
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30	100.0	1	2	24	US-09-634-306B-58424	Sequence 58424, A	
31	100.0	1	2	24	US-09-634-306B-58424	Sequence 58424, A	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 33 1 100.0 2 24 US-09-634-306B-58508 Sequence 58508, A  
C 34 1 100.0 2 24 US-09-634-306B-58508 Sequence 58508, A  
C 35 1 100.0 2 24 US-09-634-306B-58520 Sequence 58520, A  
C 36 1 100.0 2 24 US-09-634-306B-58520 Sequence 58520, A  
C 37 1 100.0 2 24 US-09-634-306B-58578 Sequence 58578, A  
C 38 1 100.0 2 24 US-09-634-306B-58578 Sequence 58578, A  
C 39 1 100.0 2 24 US-09-634-306B-58585 Sequence 58585, A  
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C 41 1 100.0 2 24 US-09-634-306B-75842 Sequence 75842, A  
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C 43 1 100.0 2 24 US-09-634-306B-75902 Sequence 75902, A  
C 44 1 100.0 2 24 US-09-634-306B-75923 Sequence 75923, A  
C 45 1 100.0 2 24 US-09-634-306B-75923 Sequence 75923, A

## ALIGNMENTS

RESULT 1  
US-08-241-388-16/c  
Sequence 16, Application US/08241388  
GENERAL INFORMATION:  
APPLICANT: Scott, Jeffrey G.  
TITLE OF INVENTION: Tomita, Takashi  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,388  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1304  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Musca domestica  
STRAIN: Learn-Pyr  
DEVELOPMENTAL STAGE: Adult  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Chromosome 1  
US-08-241-388-16

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 T 2

RESULT 2  
US-08-392-180-271  
Sequence 271, Application US/08392180  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Deleagene, Angelo M.  
APPLICANT: Bills, Pamela Kay  
APPLICANT: Pham, Mino Thu  
TITLE OF INVENTION: SMALL INTESTINE CELL-DERIVED POLYPEPTIDES  
NUMBER OF SEQUENCES: 1369  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,180  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PD-0023 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: 232362  
US-08-392-180-271

Query Match 100.0%; Score 1; DB 7; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 T 1  
Db 1 T 1

RESULT 3  
US-08-964-265-271  
Sequence 271, Application US/08964265  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Deleagene, Angelo M.  
APPLICANT: Bills, Pamela Kay  
APPLICANT: Pham, Mino Thu  
TITLE OF INVENTION: SMALL INTESTINE CELL-DERIVED POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: AND POLYPEPTIDES  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILVIEW AVENUE

CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,265  
FILING DATE: 04-NOV-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: 08/392,180  
APPLICATION NUMBER: 08/392,180  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PD-0023 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONING: 232362  
US-08-964-265-271

Query Match 100.0%; Score 1; DB 13; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 1 t 1

RESULT 4  
US-09-172-828-15  
Sequence 15, Application US/09172828  
GENERAL INFORMATION:  
APPLICANT: Children's Medical Center Corporation  
APPLICANT: Klagsbrun, Michael  
APPLICANT: Elenius, Klaus  
APPLICANT: Corfas, Gabriel  
TITLE OF INVENTION: Novel Human EGF Receptors and Use  
TITLE OF INVENTION: Theroel  
FILE REFERENCE: 47758-PCF  
CURRENT APPLICATION NUMBER: US/09/172,828  
CURRENT FILING DATE: 1998-10-15  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSP for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 2  
TYPE: DNA  
ORGANISM: mouse  
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 2 t 2

RESULT 5  
US-09-227-782-16  
Sequence 16, Application US/09227782  
GENERAL INFORMATION:  
APPLICANT: Kawasaki, Andrew M  
APPLICANT: Fraser, Allister S  
APPLICANT: Manoharan, Muthiah  
APPLICANT: Cook, Phillip D  
APPLICANT: Prakash, Thazha P  
TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides  
FILE REFERENCE: ISIS3315  
CURRENT APPLICATION NUMBER: US/09/227,782  
CURRENT FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 16  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy  
OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
US-09-227-782-16

Query Match 100.0%; Score 1; DB 16; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 1 t 1

RESULT 6  
US-09-387-777-1/C  
Sequence 1, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-1

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 t 1  
Db 2 t 2

RESULT 7  
US-09-387-777-2/c  
Sequence 2, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-2

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 t 1

Db 1 t 1

RESULT 8  
US-09-387-777-3/c  
Sequence 3, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 t 1  
Db 1 t 1

RESULT 9  
US-09-387-777-4  
Sequence 4, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington

```

: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: word for windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
:
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-4
:
: Query Match 100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 t 1
: |
: Db 2 t 2
:
: RESULT 10
: US-09-387-777-4/c
: Sequence 4; Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: word for windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
:
: US-09-387-777-4
```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
:
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-4
:
: Query Match 100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy 1 t 1
: |
: Db 1 t 1
:
: RESULT 11
: US-09-387-777-5/c
: Sequence 5; Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: twinhead* slimote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: word for windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
:
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-5
```



Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 2 t 2

RESULT 12  
US-09-387-777-8  
Sequence 8, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-8  
Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 t 1  
1  
Db 2 t 2  
RESULT 13  
US-09-387-777-9/c  
Sequence 9, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-9  
Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 t 1  
1  
Db 2 t 2  
RESULT 14  
US-09-387-777-12  
Sequence 12, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

```

: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-12
```

```

Query Match          100.0%: Score 1; DB 17; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 t 1
    |
Db 2 T 2
```

```

RESULT 15
US-09-387-777-13
: Sequence 13, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-14
```

```

: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-13
```

```

Query Match          100.0%: Score 1; DB 17; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 t 1
    |
Db 2 T 2
```

```

RESULT 16
US-09-387-777-13/C
: Sequence 13, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Mark M. Friedmam c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedmam, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-387-777-13
```

```

Query Match          100.0%: Score 1; DB 17; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 t 1
    |
Db 2 T 2
```

```

RESULT 17
US-09-387-777-14
: Sequence 14, Application US/09387777
```

GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 1 1  
1 1  
Db 1 1 1

RESULT 18  
US-09-387-777-15  
Sequence 15, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-15

OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 1 1  
1 1  
Db 1 1 1

RESULT 19  
US-09-387-777-16  
Sequence 16, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:

TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-16

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 1 t 1

RESULT 20  
US-09-472-035A-19  
Sequence 19, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kasht et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472.035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-19

Query Match 100.0%; Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 1 t 1

DB 2 t 2

RESULT 21  
US-09-472-035A-20  
Sequence 20, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kasht et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472.035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-20

Query Match 100.0%; Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 1 t 1

RESULT 22  
US-09-634-306B-51869  
Sequence 51869, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
POLYMORPHISMS IN THE HUMAN GENOME  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218.006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198.676

```

: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 51869
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-51869
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 23
US-09-634-306B-52011
: Sequence 52011, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52011
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-52011
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 24
US-09-634-306B-52015
```

```

: Sequence 52015, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52015
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-52015
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 25
US-09-634-306B-52280/C
: Sequence 52280, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52280
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-52280
```

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 t 1  
Db 1 t 1

RESULT 26  
US-09-634-306B-52357  
; Sequence 52357, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: Fastsq for Windows Version 4.0  
; SEQ ID NO: 52357  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 t 1  
Db 1 t 1

RESULT 27  
US-09-634-306B-53022/c  
; Sequence 53022, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: Fastsq for Windows Version 4.0  
; SEQ ID NO: 53022  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-53022

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 t 1  
Db 2 t 2

RESULT 28  
US-09-634-306B-58305  
; Sequence 58305, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: Fastsq for Windows Version 4.0  
; SEQ ID NO: 58305  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 t 1  
Db 2 t 2

RESULT 29  
US-09-634-306B-58424  
; Sequence 58424, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006

```

: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58424
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 2 t 2
```

```
RESULT 30
: Sequence 58424, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58424
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 1 t 1
```

```
RESULT 31
: Sequence 58496, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58496
```

```
Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
db 2 t 2
```

```
RESULT 32
: Sequence 58496, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-58496
```

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 33  
US-09-634-306B-58508

; Sequence 58508, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 58508  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58508

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 t 2

RESULT 34  
US-09-634-306B-58508/C

; Sequence 58508, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 58508  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58508

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 35  
US-09-634-306B-58520

; Sequence 58520, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 58520  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58520

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 t 2

RESULT 36  
US-09-634-306B-58520/C

; Sequence 58520, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B



```

; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58520
```

```
Query Match          100.0%; Score 1; DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 t 1  
Db 1 t 1

```
RESULT 37
US-09-634-306B-58578
; Sequence 58578, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58578
```

```
Query Match          100.0%; Score 1; DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 t 1  
Db 2 t 2

```
RESULT 38
US-09-634-306B-58578/C
; Sequence 58578, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58578
```

```
Query Match          100.0%; Score 1; DB 24; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 t 1  
Db 1 t 1

```
RESULT 39
US-09-634-306B-75805/C
; Sequence 75805, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75805
; LENGTH: 2
; TYPE: DNA
```

ORGANISM: Human  
US-09-634-306B-75805

Query Match  
Best Local Similarity 100.0%; Score 1: DB 24: Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

## RESULT 40

US-09-634-306B-75814/C  
Sequence 75814, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 75814  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-75814

Query Match  
Best Local Similarity 100.0%; Score 1: DB 24: Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

## RESULT 41

US-09-634-306B-75842/C  
Sequence 75842, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 75842  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-75842

Query Match  
Best Local Similarity 100.0%; Score 1: DB 24: Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

## RESULT 42

US-09-634-306B-75868/C  
Sequence 75868, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 75868  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-75868

Query Match  
Best Local Similarity 100.0%; Score 1: DB 24: Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

## RESULT 43

US-09-634-306B-75889/C  
Sequence 75889, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75889
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75889
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

```
RESULT 44
US-09-634-306B-75902/C
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75902
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75902
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
```

```
Db 1 t 1
```

```
RESULT 45
US-09-634-306B-75923/C
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75923
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-75923
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

Search completed: July 16, 2002, 02:50:26  
Job time: 31279 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 : Search time 808.35 Seconds  
(without alignments)  
2.105 Million cell updates/sec

Title: US-09-375-248-1-COPY\_3150\_3150

Sequence score: 1 t 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Capext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/plodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/plodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/plodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/plodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/plodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/plodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/plodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1	100.0	2	6	US-10-027-632-51869
2	1	100.0	2	6	US-10-027-632-52011
3	1	100.0	2	6	US-10-027-632-52015
4	1	100.0	2	6	US-10-027-632-52280
5	1	100.0	2	6	US-10-027-632-53357
6	1	100.0	2	6	US-10-027-632-53022
7	1	100.0	2	6	US-10-027-632-58305
8	1	100.0	2	6	US-10-027-632-58424
9	1	100.0	2	6	US-10-027-632-58424
10	1	100.0	2	6	US-10-027-632-58496
11	1	100.0	2	6	US-10-027-632-58496
12	1	100.0	2	6	US-10-027-632-58508
13	1	100.0	2	6	US-10-027-632-58508
14	1	100.0	2	6	US-10-027-632-58520
15	1	100.0	2	6	US-10-027-632-58520
16	1	100.0	2	6	US-10-027-632-58520
17	1	100.0	2	6	US-10-027-632-58578
18	1	100.0	2	6	US-10-027-632-58578
19	1	100.0	2	6	US-10-027-632-75805
20	1	100.0	2	6	US-10-027-632-75814
21	1	100.0	2	6	US-10-027-632-75814
22	1	100.0	2	6	US-10-027-632-75868
23	1	100.0	2	6	US-10-027-632-75868
24	1	100.0	2	6	US-10-027-632-75902
25	1	100.0	2	6	US-10-027-632-75923
26	1	100.0	2	6	US-10-027-632-75928

c	27	1	100.0	2	6	US-10-027-632-175337	Sequence 175337,
	28	1	100.0	2	6	US-10-027-632-175354	Sequence 175354,
	29	1	100.0	2	6	US-10-027-632-175401	Sequence 175401,
	30	1	100.0	2	6	US-10-027-632-175403	Sequence 175403,
	31	1	100.0	2	6	US-10-027-632-175419	Sequence 175419,
	32	1	100.0	2	6	US-10-027-632-175419	Sequence 175419,
	33	1	100.0	2	6	US-10-027-632-175426	Sequence 175426,
	34	1	100.0	2	6	US-10-027-632-175433	Sequence 175433,
	35	1	100.0	2	6	US-10-027-632-175433	Sequence 175433,
	36	1	100.0	2	6	US-10-027-632-176011	Sequence 176011,
	37	1	100.0	2	6	US-10-027-632-176011	Sequence 176011,
	38	1	100.0	2	6	US-10-027-632-176848	Sequence 176848,
	39	1	100.0	2	6	US-10-027-632-176849	Sequence 176849,
	40	1	100.0	2	6	US-10-027-632-176880	Sequence 176880,
	41	1	100.0	2	6	US-10-027-632-178008	Sequence 178008,
	42	1	100.0	2	6	US-10-027-632-178104	Sequence 178104,
	43	1	100.0	2	6	US-10-027-632-178104	Sequence 178104,
	44	1	100.0	2	6	US-10-027-632-178114	Sequence 178114,
	45	1	100.0	2	6	US-10-027-632-178114	Sequence 178114,

## ALIGNMENTS

```
RESULT 1
US-10-027-632-51869
; Sequence 51869, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match      100.0%  Score 1:  DB 6:  Length 2;
Best Local Similarity 100.0%:  Pred No. 0;
Matches 1:  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 t 1
Db      1 t 1

RESULT 2
US-10-027-632-52011
; Sequence 52011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
```

```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52011
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 1 t 1
```

```
RESULT 3
US-10-027-632-52015
; Sequence 52015, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52015
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52015
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
```

```
Db 1 t 1
RESULT 4
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 1 t 1
RESULT 5
US-10-027-632-52357
; Sequence 52357, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52357
```

```
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52357
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 1 t 1
```

```
RESULT 6
US-10-027-632-53022/c
; Sequence 53022, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53022
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-53022
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 7
US-10-027-632-58305
; Sequence 58305, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 8
US-10-027-632-58424
; Sequence 58424, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58424
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58424
```

```
Query Match          100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
Db 2 t 2
```

```
RESULT 9
US-10-027-632-58424/c
; Sequence 58424, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58424
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58424
```

```

Query Match      100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      1 T 1
```

```

RESULT 10
US-10-027-632-58496
: Sequence 58496, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58496
```

```

Query Match      100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      2 t 2
```

```

RESULT 11
US-10-027-632-58496/c
: Sequence 58496, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 58496
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-58496
```

```

Query Match      100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 t 1
Db      1 T 1
```

```

RESULT 12
US-10-027-632-58508
: Sequence 58508, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
```



```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 2 t 2
```

```

RESULT 13
; Sequence 58508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58508
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 14
; Sequence 58520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58520
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58520
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 2 t 2
```

```

RESULT 15
; Sequence 58520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58520
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58520
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 t 1
    1
Db 1 t 1
```

```

RESULT 16
; Sequence 58578, Application US/10027632
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58578
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       2 t 2
```

```

RESULT 17
US-10-027-632-58578/c
; Sequence 58578, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 58578
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58578
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
```

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       1 t 1
```

```

RESULT 18
US-10-027-632-75805/c
; Sequence 75805, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 75805
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75805
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
         |
Db       1 t 1
```

```

RESULT 19
US-10-027-632-75814/c
; Sequence 75814, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
```

```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75814
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75814
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1
```

```

RESULT 20
US-10-027-632-75842/c
; Sequence 75842, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75842
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75842
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1
```

```

RESULT 21
US-10-027-632-75868/c
; Sequence 75868, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75868
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75868
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1
```

```

RESULT 22
US-10-027-632-75889/c
; Sequence 75889, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75889
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75889
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 t 1
Db 1 t 1
```

RESULT 23

```
US-10-027-632-75902/C
; Sequence 75902, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75902
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75902
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 24
; Sequence 75923, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75923
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75923
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 25
; Sequence 75928, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75928
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75928
```

```
Query Match      100.0%; Score 1: DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
Db      1 t 1
```

```
RESULT 26
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```
RESULT 27
US-10-027-632-175337/c
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```
RESULT 28
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
```

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```
RESULT 29
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827, 129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```
RESULT 30
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 2 t 2
```

```
RESULT 31
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-175415

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```
RESULT 32
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 6; Length 2;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1
Db 2 t 2
```

```
RESULT 33
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
        |
Db       2 t 2
```

```

RESULT 34
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
        |
Db       2 t 2
```

```

RESULT 35
US-10-027-632-176011
; Sequence 176011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
```

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176011
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
        |
Db       2 t 2
```

```

RESULT 36
US-10-027-632-176011/c
; Sequence 176011, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176011
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176011
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 t 1
        |
```

Db 1 t 1

RESULT 37  
US-10-027-632-176848/c

: Sequence 176848, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176848

: LENGTH: 2

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-176848

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 38  
US-10-027-632-176849/c

: Sequence 176849, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176849

: LENGTH: 2

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-176849

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 39  
US-10-027-632-176880/c

: Sequence 176880, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218

: PRIOR FILING DATE: 2000-02-24

: PRIOR APPLICATION NUMBER: US 60/167,363

: PRIOR FILING DATE: 1999-11-23

: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28

: PRIOR APPLICATION NUMBER: US 60/146,002

: NUMBER OF SEQ ID NOS: 325720

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 176880

: LENGTH: 2

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-176880

Query Match

Best Local Similarity 100.0%; Score 1; DB 6; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

Db 2 t 2

RESULT 40  
US-10-027-632-178008

: Sequence 178008, Application US/10027632

: GENERAL INFORMATION:

: APPLICANT: Wang, David G.

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

: FILE REFERENCE: 108827.129

: CURRENT APPLICATION NUMBER: US/10/027,632

: PRIOR FILING DATE: 2002-04-30

: PRIOR APPLICATION NUMBER: US 60/218,006

: PRIOR FILING DATE: 2000-07-12

: PRIOR APPLICATION NUMBER: US 60/198,676

: PRIOR FILING DATE: 2000-04-20

: PRIOR APPLICATION NUMBER: US 60/193,483

: PRIOR FILING DATE: 2000-03-29

: PRIOR APPLICATION NUMBER: US 60/185,218



```

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178008
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178008
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```

RESULT 41
US-10-027-632-178008/c
; Sequence 178008, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178008
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178008
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 1 t 1
```

```

RESULT 42
US-10-027-632-178104
; Sequence 178104, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178104
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178104
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 t 1
Db 2 t 2
```

```

RESULT 43
US-10-027-632-178104/c
; Sequence 178104, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178104
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178104
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 t 1  
|  
Db 1 t 1

RESULT 44  
US-10-027-632-178114

; Sequence 178114, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 178114  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178114

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 t 2

RESULT 45  
US-10-027-632-178114/c

; Sequence 178114, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 178114  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178114

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

Search completed: July 16, 2002, 02:57:00  
Job time: 24558 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:36 ; Search time 7067.1 Seconds  
(without alignments)

1.910 Million cell updates/sec

Title: us-09-375-248-1\_COPY\_3150\_3150

Perfect score: 1 c 1

Sequence: 1 c 1

Scoring table: OLIGO-NUC  
Capop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	2	HSM003817	A1039341 Homo sapi
2	100.0	1	2	HSM003931	A1039455 Homo sapi
3	100.0	1	2	HSM003931	A1039455 Homo sapi
4	100.0	1	2	HSM007187	A1042337 Homo sapi
5	100.0	1	2	HSM008709	A1043859 Homo sapi
6	100.0	1	2	HSM011919	A1047068 Homo sapi
7	100.0	1	2	B1817789	B1817789 G3-G22 Ax
8	100.0	1	2	C55081	C55081 C55081 Yuj1
9	100.0	1	2	A2463604	A2463604 1M027205
10	100.0	1	2	HSM003852	A1039376 Homo sapi
11	100.0	1	2	HSM003852	A1039376 Homo sapi
12	100.0	1	2	HSM007999	A1043149 Homo sapi
13	100.0	1	2	HSM008070	A1043220 Homo sapi
14	100.0	1	2	AW672605	AW672605 2XA Expla
15	100.0	1	2	A2438202	A2438202 1M0228108
16	100.0	1	2	A2438202	A2438202 1M0228108
17	100.0	1	2	Bg926576	Bg926576 HNC56-1-A

C	18	1	100.0	4	2	Bg926576	Bg926576 HNC56-1-A
C	19	1	100.0	4	2	HSM003901	A1039425 Homo sapi
C	20	1	100.0	4	2	HSM010467	A1045617 Homo sapi
C	21	1	100.0	4	9	AW672622	AW672622 73C Expla
C	22	1	100.0	4	12	CNS004RB	AL054121 Drosophila
C	23	1	100.0	4	12	CNS004RB	AL054121 Drosophila
C	24	1	100.0	5	2	HSM007310	A1042460 Homo sapi
C	25	1	100.0	5	2	HSM007310	A1042460 Homo sapi
C	26	1	100.0	5	2	HSM007835	A1042985 Homo sapi
C	27	1	100.0	5	2	HSM011053	A1046203 Homo sapi
C	28	1	100.0	5	2	HSM011053	A1046203 Homo sapi
C	29	1	100.0	6	2	HSM003844	Bg927410 HNC1-1-G7
C	30	1	100.0	6	2	HSM003844	A1039368 Homo sapi
C	31	1	100.0	6	2	HSM004423	A1039368 Homo sapi
C	32	1	100.0	6	2	HSM004423	A1039947 Homo sapi
C	33	1	100.0	6	2	HSM004423	A1039947 Homo sapi
C	34	1	100.0	6	2	HSM007334	A1042484 Homo sapi
C	35	1	100.0	6	2	HSM007334	A1042484 Homo sapi
C	36	1	100.0	6	2	HSM007683	A1042833 Homo sapi
C	37	1	100.0	6	2	HSM007683	A1042833 Homo sapi
C	38	1	100.0	6	2	HSM008014	A1043164 Homo sapi
C	39	1	100.0	6	2	HSM008014	A1043164 Homo sapi
C	40	1	100.0	7	2	Bg897546	Bg897546 HOA14-1-H
C	41	1	100.0	7	2	Bg897546	Bg897546 HOA14-1-H
C	42	1	100.0	7	2	HSM007412	A1042562 Homo sapi
C	43	1	100.0	7	2	HSM007412	A1042562 Homo sapi
C	44	1	100.0	7	2	HSM007502	A1042652 Homo sapi
C	45	1	100.0	7	10	C58888	C58888 C58888 Yuj1

## ALIGNMENTS

RESULT 1  
ID HSM003817 standard: RNA; EST: 2 BP.  
XX AL039341:  
XX  
SV AL039341.1  
XX  
XX 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX  
DE Homo sapiens mRNA: EST DKFP434F2010\_r1 (from clone DKFP434F2010)  
XX  
KW EST: expressed sequence tag.  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
XX  
RN [1]  
RP 1-2  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.:  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MTPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX  
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No sl sequence available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
XX  
FH key  
FH Location/Qualifiers  
FT source  
FT 1..2  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFP434F2010"  
FT /clone\_11b="434 (synonym: htes3). Vector pSport1; host



```

XX RN 11)
RP 1-2
RA Oltenevelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
KL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Medigenomix within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
FT
FT
XX
SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 1 t 1

```

```

RESULT 5
HSM008709
ID HSM008709 standard; RNA; EST; 2 BP.
XX
AC AL043859;
XX
SV AL043859.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434B2128_r1 (from clone DKFZp434B2128)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
FH [1]
FH
FH
RP 1-2
RA Bioecker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the CDNA
CC sequencing consortium of the German Genome Project
CC s1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key Location/Qualifiers
FH

```

```

FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
FT
FT
XX
SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 1 t 1

```

```

RESULT 6
HSM011919
ID HSM011919 standard; RNA; EST; 2 BP.
XX
AC AL047069;
XX
SV AL047069.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
FH [1]
FH
FH
RP 1-2
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key Location/Qualifiers
FH
FH
FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="586 (synonym: hute1). Vector pSport1; host
FT DH10B; sites NotI + SalI/MluI"
FT /dev_stage="adult"
FT /tissue_type="uterus"
FT
FT
FT
XX
SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 t 1

```

Db 1 T 1

# RESULT 7

Bi817789

LOCUS C3-G22 Axolotl Lambda zap library Ambystoma mexicanum cDNA similar

DEFINITION to Putative ribosomal protein S2, mRNA sequence.

ACCESSION Bi817789

VERSION Bi817789.1 GI:15951401

KEYWORDS EST.

SOURCE axolotl.

ORGANISM Ambystoma mexicanum

REFERENCE 1 (bases 1 to 2)

AUTHORS Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,

TITLE JOURNAL

COMMENT

Expressed sequence tags from an axolotl limb regeneration library  
Unpublished (2001)  
Contact: Voss SR  
Department of Biology  
Colorado State University  
Fort Collins, CO 80523, USA  
Tel: 970 491 4869  
Fax: 970 491 0649  
Email: sross@amar.colostate.edu  
Single pass sequence from 5' end. Low quality sequence was trimmed  
from the ends (PHRED error rate = 5%). Trace file available:  
sross@amar.colostate.edu.

## FEATURES

Location/Qualifiers

1..2

/organism="Ambystoma mexicanum"

/db\_xref="taxon:8296"

/clone\_lib="Axolotl Lambda Zap Library"

/tissue\_type="Regenerating forelimb"

/dev\_stage="Medium-bud blastema"

BASE COUNT 0 a 1 c 0 g 1 t

## ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 2 T 2

# RESULT 8

C55081/c

LOCUS C55081 2 bp mRNA linear EST 16-SEP-1997

DEFINITION C55081 Yujl Kohara unpublished cDNA Caenorhabditis elegans cDNA

ACCESSION clone YK350C9 3', mRNA sequence.

VERSION C55081

KEYWORDS C55081.1 GI:2399682

SOURCE EST.

ORGANISM Caenorhabditis elegans.

REFERENCE 1 (bases 1 to 2)

AUTHORS Kohara,Y., Molohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano

TITLE JOURNAL

COMMENT

Expression map of the C. elegans genome  
Unpublished (1996)  
Contact: Yujl Kohara  
Genome Biology Lab.  
National Institute of Genetics  
Yata 111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.

# FEATURES

Location/Qualifiers

1..2

/organism="Caenorhabditis elegans"

/strain="CB1489 him-8(e1489)"

/db\_xref="taxon:6239"

/clone\_lib="YK350C9"

/clone\_lib="Yujl Kohara unpublished cDNA"

/sex="hermaphrodite, male"

/tissue\_type="whole animal"

/dev\_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 1 T 1

# RESULT 9

AZ463604

LOCUS AZ463604 2 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0272J05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION clone UUGC1M0272J05 R, DNA sequence.

VERSION AZ463604

KEYWORDS AZ463604.1 GI:10621729

SOURCE GSS.

ORGANISM house mouse.

REFERENCE 1 (bases 1 to 2)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.

and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0272 row: J column: 05

Seq primer: CACACGGAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 451.

Location/Qualifiers

1..2

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0272J05"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromatically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 2 t 2

RESULT 10  
HSM003852 standard; RNA; EST; 3 BP.

AC AL039376;  
XX AL039376.1

DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp43412010\_r1 (from clone DKFZp43412010)  
XX EST: expressed sequence tag.

XX Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX 11  
RN 1-3  
RP 1-3  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..3  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp43412010"  
FT /clone\_1lb="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

Sequence 3 BP: 1 A; 0 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 2 t 2

RESULT 11  
HSM003852/c  
ID HSM003852 standard; RNA; EST; 3 BP.

AC AL039376;  
XX AL039376.1

DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp43412010\_r1 (from clone DKFZp43412010)  
XX EST: expressed sequence tag.

XX Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX 11  
RN 1-3  
RP 1-3  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..3  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp43412010"  
FT /clone\_1lb="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

Sequence 3 BP: 1 A; 0 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 1 t 1

RESULT 12  
HSM007999 standard; RNA; EST; 3 BP.

AC AL043149;  
XX AL043149.1



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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434E1923_r1 (from clone DKFZp434E1923)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-3
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..3
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone_lib="DKFZp434E1923"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 3 BP; 0 A; 0 C; 0 G; 2 T; 1 other;
SQ
XX
XX Query Match 100.0%; Score 1; DB 2; Length 3;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 t 1
XX 1 T 1
XX
XX RESULT 13
XX HSM008070/c standard; RNA; EST; 3 BP.
XX
XX AL043220;
XX
XX AL043220.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434I1923_r1 (from clone DKFZp434I1923)
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-3
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL

```

```

RL MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1..3
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone_lib="DKFZp434I1923"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 3 BP; 2 A; 0 C; 0 G; 0 T; 1 other;
SQ
XX
XX Query Match 100.0%; Score 1; DB 2; Length 3;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 t 1
XX 3 T 3
XX
XX RESULT 14
XX AM672605/c
XX LOCUS
XX DEFINITION
XX 2Xa Explanted metanephric mesenchyme induced to differentiate into
XX epithelial structures of the nephron ex vivo. Rattus norvegicus
XX cDNA similar to: gp1AF022811.11AF022811 Mus musculus
XX cornichon mRNA, mRNA sequence.
XX
XX ACCESSION 3 bp mRNA linear EST 26-SEP-2001
XX VERSION AM672605.1 GI:7541085
XX KEYWORDS EST.
XX SOURCE Norway rat.
XX ORGANISM Rattus norvegicus
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
XX Rattus.
XX 1 (bases 1 to 3)
XX REFERENCE
XX Pilssov S.Y., Ivanov S.V., Yoshino K., Dove L.F., Pilssova T.M.,
XX Higginbotham K.G., Karavanova I., Lerman M. and Perantoni A.O.
XX Mesenchymal-epithelial transition in the developing metanephric
XX kidney: gene expression study by differential display
XX Genesis 27 (1), 22-31 (2000)
XX JOURNAL MEDLINE
XX COMMENT
XX Contact: Pilssov S.Y.
XX Laboratory of Comparative Carcinogenesis
XX National Cancer Institute
XX FCRDC, Bldg. 338, Room 205, Frederick, MD 21702, USA
XX Tel: 301 846 1242
XX Fax: 301 846 4956
XX Email: pilssov@mail.ncifcrf.gov
XX PCR Primers
XX FORWARD: ctgaagcttcgcgc
XX BACKWARD: ttaagcttttttttc
XX Insert Length: 350 Std Error: 0.00
XX Seq primer: SP6
XX High quality sequence stop: 261.
XX location/Qualifiers
XX 1..3
XX /organism="Rattus norvegicus"
XX /db_xref="taxon:10116"
XX /clone_lib="Explanted metanephric mesenchyme induced to
XX differentiate into epithelial structures of the nephron ex

```

vivo."  
 /tissue\_type="Metanephric mesenchyme"  
 /cell\_type="Mesenchymal/Epithelial"  
 /dev\_stage="13 dpc-16dpc"  
 /lab\_host="JM109"  
 /note="Organ: Kidney; Vector: pCEM-TEasy (Promega); Restriction Enzymes: 1: ApaI, AclI, SphI, NcoI, BstXI, NotI, SacI, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI. CDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pCEM-TEasy (Promega); Its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

## BASE COUNT

1 a 0 c 2 g 0 t

Query Match 100.0%; Score 1; DB 9; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 t 1  
 Db 2 T 2

## RESULT 15

AZ438202 3 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0228108F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

clone UUCG1M0228108 F, DNA sequence.

ACCESSION AZ438202

VERSION AZ438202.1 GI:10562215

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0228 row: 1 column: 08  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 302.  
 Location/Qualifiers  
 1..3  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0228108"  
 /clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

BASE COUNT  
 ORIGIN 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 12; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
 Db 3 T 3

## RESULT 16

AZ438202/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0228 row: 1 column: 08  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 302.  
 Location/Qualifiers  
 1..3  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0228108"  
 /clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 0 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 2 T 2

RESULT 17  
BC926576 standard; RNA; EST; 4 BP.  
XX BC926576:

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)  
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

XX EST.

OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]  
XX 1-4  
XX MEDLINE: 21482651.  
XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,  
RA Sathe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,  
RT "Identification and initial characterization of 5000 expressed sequenced  
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA  
RT libraries".  
RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109  
CC GlaxoSmithKline  
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
CC Tel: 610-270-7245  
CC Fax: 610-270-5598  
CC Email: sanjay\_kumar-1@sk.com  
CC Seq primer: T7.

XX Key Location/Qualifiers

FT source 1..4  
FT /db\_xref="taxon:9606"  
FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional"  
FT /organism="Homo sapiens"  
FT /clone\_lib="HNC (Human Normal Cartilage)"  
FT /tissue\_type="cartilage"  
FT /lab\_host="E.coli DH10 B"  
XX

SO Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 T 1

RESULT 18  
BC926576/C standard; RNA; EST; 4 BP.  
XX BC926576:

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)  
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

XX EST.

OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]  
XX 1-4  
XX MEDLINE: 21482651.  
XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,  
RA Sathe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,  
RT "Identification and initial characterization of 5000 expressed sequenced  
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA  
RT libraries".  
RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109  
CC GlaxoSmithKline  
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
CC Tel: 610-270-7245  
CC Fax: 610-270-5598  
CC Email: sanjay\_kumar-1@sk.com  
CC Seq primer: T7.

XX Key Location/Qualifiers

FT source 1..4  
FT /db\_xref="taxon:9606"  
FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
FT Directional"  
FT /organism="Homo sapiens"  
FT /clone\_lib="HNC (Human Normal Cartilage)"  
FT /tissue\_type="cartilage"  
FT /lab\_host="E.coli DH10 B"  
XX

SO Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 2 t 2

## RESULT 19

HSMD03901/c standard; RNA; EST; 4 BP.  
ID HSM003901

AC AL039425;  
XX  
SV AL039425.1  
XX

DT 12-MAR-1999 (Rel. 59, Created)  
WT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434L0810\_s1 (from clone DKFZp434L0810)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.

XX [1]

RP 1-4  
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
KT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
XX

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

PH source

FT 1..4  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp434L0810"  
FT DH10B: sites NotI + SalI  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match Best Local Similarity 100.0%; Score 1; DB 2; Length 4;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 3 t 3

## RESULT 20

HSMD010467 standard; RNA; EST; 4 BP.  
ID HSM010467

AC AL045617;  
XX

SV AL045617.1  
XX

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434O245\_r1 (from clone DKFZp434O245)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.

XX [1]

RP 1-4  
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
KT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
XX

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT 1..4  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp434O245"  
FT DH10B: sites NotI + SalI  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

SO Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 1; DB 2; Length 4;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 3 t 3

## RESULT 21

AM672622/c

LOCUS 4 bp mRNA linear EST 26-SEP-2001  
DEFINITION 73C Explanted metanephric mesenchyme induced to differentiate into  
epithelial structures of the nephron ex vivo. Rattus norvegicus

CDNA similar to: emb|AL049970.1|HSM800317 Homo sapiens  
mRNA; CDNA DKFZp564B102 (from clone DKFZp564B102); mRNA sequence.

AM672622  
AM672622.1 GI:7541102

VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Norway rat.  
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 4)

PLISOV,S.Y., IVANOV,S.V., YOSHINO,K., DOVE,L.F., PLISOVA,T.M.,  
HIGINBOTHAM,K.G., KARAVANOVA,I., LERMAN,M. and PERANTONI,A.O.,

Mesenchymal-epithelial transition in the developing metanephric  
kidney: gene expression study by differential display

20321327

CONTACT: Plisov S.Y.  
Laboratory of Comparative Carcinogenesis

National Cancer Institute  
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242  
 Fax: 301 846 4956  
 Email: plisov@mail.ncifcrf.gov  
 PCR primers  
 FORWARD: ctgcagctccgctc  
 BACKWARD: ttaagctttttttt  
 Insert length: 262 Std Error: 0.00  
 Seq primer: SP6  
 High quality sequence stop: 262  
 PolyA-yes

## FEATURES

## source

Location/Qualifiers

1..4  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_lib="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo"  
 /tissue\_type="Metanephric mesenchyme"  
 /cell\_type="Mesenchymal/Epithelial"  
 /dev\_stage="13 dpc-16dpc"  
 /lab\_host="JM109"  
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega); Restriction Enzymes: 1: ApaI, AatII, SphI, NcoI, BstXI, NotI, SacI, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

## BASE COUNT

1 a 0 c 3 g 0 t

## ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 3 t 3

## RESULT 22

## CNS004RB

## LOCUS

4 bp DNA linear GSS 03-JUN-1999

## DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC #

## ACCESSION

BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## VERSION

AL054121 GI:4931932

## KEYWORDS

GSS.

## SOURCE

fruit fly.

## ORGANISM

Drosophila melanogaster

## REFERENCE

Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

## AUTHORS

1 (bases 1 to 4)

## TITLE

Genoscope.

## JOURNAL

Direct Submission

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

Location/Qualifiers

1..4  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCI-98"  
 /clone="BACR10A06"  
 /note="end : TET3"

## BASE COUNT

1 a 1 c 0 g 2 t

## ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1

Db 1 t 1

## RESULT 23

## CNS004RB/c

## LOCUS

4 bp DNA linear GSS 03-JUN-1999

## DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC #

## ACCESSION

BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## VERSION

AL054121 GI:4931932

## KEYWORDS

GSS.

## SOURCE

fruit fly.

## ORGANISM

Drosophila melanogaster

## REFERENCE

Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

## AUTHORS

1 (bases 1 to 4)

## TITLE

Genoscope.

## JOURNAL

Direct Submission

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

Location/Qualifiers

1..4  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCI-98"  
 /clone="BACR10A06"  
 /note="end : TET3"

## BASE COUNT

1 a 1 c 0 g 2 t

## ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 3 T 3

RESULT 24  
ID HSM007310 standard; RNA; EST: 5 BP.  
XX AL042460;  
XX AL042460.1

12-MAR-1999 (Rel. 59, Created)  
12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZP434E1821\_r1 (from clone DKFZP434E1821)  
EST: expressed sequence tag.

Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

11  
RP 1-5  
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX

Clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No st sequence available

This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key Location/Qualifiers

FT source 1..5  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZP434E1821"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 4 T 4

RESULT 25  
ID HSM007310 standard; RNA; EST: 5 BP.  
XX AL042460;  
XX AL042460.1

12-MAR-1999 (Rel. 59, Created)  
12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZP434E1821\_r1 (from clone DKFZP434E1821)  
XX EST: expressed sequence tag.

Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

11  
RP 1-5  
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX

Clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No st sequence available

This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key Location/Qualifiers

FT source 1..5  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZP434E1821"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 3 T 3

RESULT 26  
ID HSM007835 standard; RNA; EST: 5 BP.  
XX AL042985;  
XX AL042985.1

12-MAR-1999 (Rel. 59, Created)  
12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZP434N1522\_r1 (from clone DKFZP434N1522)  
EST: expressed sequence tag.

Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

11  
RP 1-5  
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX

Clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project

```

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH key location/Qualifiers
FH
FT source 1..5
FT /db.xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N152"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 2 T 2

RESULT 27
HSM011053 standard; RNA; EST; 5 BP.
ID HSM011053
AC AL046203;
XX
SV AL046203.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DL 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434D137_r1 (from clone DKFZp434D137)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
FH key location/Qualifiers
FH
FT source 1..5
FT /db.xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
Db 3 T 3

RESULT 29
BG927410 standard; RNA; EST; 6 BP.
ID BG927410
AC BG927410;
XX

```

```

SV      BG927410.1
XX
DT      09-JUN-2001 (Rel. 68, Created)
DT      14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
XX      HNC1-1-C7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX      EST.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      MEDLINE: 21482651.
XX      PUBMED: 11597177.
XX      Kumar S., Connor J.R., Dadds R.A., Halsey W., Van Horn M., Mao J.,
XX      Sahle G.M., Hui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
XX      "Identification and Initial Characterization of 5000 expressed sequenced
XX      tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
XX      libraries";
XX      Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX      Contact: Sanjay Kumar
XX      CC      UN2109
XX      CC      GlaxoSmithKline
XX      CC      709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
XX      CC      Tel: 610-270-7245
XX      CC      Fax: 610-270-5598
XX      CC      Email: sanjay_kumar-1@gsk.com
XX      CC      Seq primer: T7.
XX
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XX      FH      source
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XX      FT      /db_xref="taxon:9606"
XX      FT      /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
XX      FT      Directional"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone_lib="HNC (Human Normal Cartilage)"
XX      FT      /tissue_type="cartilage"
XX      FT      /lab_host="E.coli DH10 B"
XX
XX      SO      Sequence 6 BP: 0 A; 5 C; 0 G; 1 T; 0 other:

Query Match      100.0%; Score 1: DB 2: Length 6:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 t 1
        |
DB      3 t 3

RESULT 30
HSM003844
ID      HSM003844 standard; RNA: EST: 6 BP.
XX
AC      AL039368;
XX
SV      AL039368.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

```

```

OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX      sequencing consortium of the German Genome Project
XX      CC      No s1 sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH      source
XX      FT      1..6
XX      FT      /db_xref="taxon:9606"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFZp434I0110"
XX      FT      /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /tissue_type="testis"
XX
XX      SO      Sequence 6 BP: 2 A; 0 C; 2 G; 2 T; 0 other:

Query Match      100.0%; Score 1: DB 2: Length 6:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 t 1
        |
DB      5 T 5

RESULT 31
HSM003844/C
ID      HSM003844 standard; RNA: EST: 6 BP.
XX
AC      AL039368;
XX
SV      AL039368.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX      sequencing consortium of the German Genome Project
XX      CC      No s1 sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers

```



```

FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J0110"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 4 T 4

```

```

RESULT 32
ID HSM004423 standard; RNA; EST; 6 BP.
XX AL039947;
XX AL039947.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key location/Qualifiers
XX
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J0112"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 5 T 5

```

```

RESULT 33
ID HSM004423/C standard; RNA; EST; 6 BP.
XX AL039947;
XX AL039947.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key location/Qualifiers
XX
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J0112"
XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 t 1
Db 4 T 4

```

```

RESULT 34
ID HSM007334 standard; RNA; EST; 6 BP.
XX AL042484;
XX AL042484.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)

```

```

XX EST: expressed sequence tag.
KM Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434f0321"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 5 T 5

RESULT 35
HSM007334/C
ID HSM007334 standard; RNA; EST; 6 BP.
XX
AC AL042484;
XX
SV AL042484.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434f0321_r1 (from clone DKFZp434f0321)
XX
XX EST: expressed sequence tag.
XX
KW Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available

```

```

CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434f0321"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1
DB 4 T 4

RESULT 36
HSM007683
ID HSM007683 standard; RNA; EST; 6 BP.
XX
AC AL042833;
XX
SV AL042833.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX
XX EST: expressed sequence tag.
XX
KW Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434G1622"
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

```

Query Match 100.0%; Score 1; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 3 t 3  
 Db

RESULT 37  
 HSM007683/C  
 ID HSM007683 standard; RNA; EST; 6 BP.  
 XX  
 AC AL042833;  
 XX  
 SV AL042833.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434G1622\_r1 (from clone DKFZp434G1622)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-6  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferapitz 18a D-82152 Martinsried, GERMANY  
 CC  
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC No s1 sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 CC  
 XX  
 FT key Location/Qualifiers  
 FH  
 FI  
 FT source 1..6  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp434G1622"  
 FT /clone\_11b="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 FT  
 FT  
 SO Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 2 t 2  
 Db

RESULT 38  
 HSM008014  
 ID HSM008014 standard; RNA; EST; 6 BP.  
 XX  
 AC AL043164;  
 XX  
 SV AL043164.1

XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434F1123\_s1 (from clone DKFZp434F1123)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-6  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferapitz 18a D-82152 Martinsried, GERMANY  
 CC  
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC r1 sequence also available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 CC  
 XX  
 FT key Location/Qualifiers  
 FH  
 FI  
 FT source 1..6  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp434F1123"  
 FT /clone\_11b="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 FT  
 FT  
 SO Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 1 t 1  
 Db

RESULT 39  
 HSM008014/C  
 ID HSM008014 standard; RNA; EST; 6 BP.  
 XX  
 AC AL043164;  
 XX  
 SV AL043164.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434F1123\_s1 (from clone DKFZp434F1123)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-6  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

KL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
 CC Clone from S. Wiemann, sequenced by LMU within the CCNA  
 CC sequencing consortium of the German Genome Project  
 CC r1 sequence also available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key Location/Qualifiers  
 FT source 1..6  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSPORT1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 FT  
 XX  
 SO Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 t 1  
 1  
 Db 3 T 3

RESULT 40  
 BG897546 standard; RNA; EST; 7 BP.  
 AC BG897546;  
 XX  
 SV BG897546.1  
 XX  
 DT 09-JUN-2001 (Rel. 68, Created)  
 DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)  
 XX  
 DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA  
 DE sequence.  
 DE  
 XX  
 XX EST.  
 KW Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-7  
 MEDLINE: 21482651.  
 RX PUBMED: 11597177.  
 RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,  
 RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,  
 RT "Identification and initial characterization of 5000 expressed sequenced  
 RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA  
 RT libraries";  
 RL Osteoarthritis Cartilage 9(7):641-653(2001).  
 XX  
 XX  
 CC Contact: Sanjay Kumar  
 CC UW2109  
 CC GlaxoSmithKline  
 CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 CC Tel: 610-270-7245  
 CC Fax: 610-270-5598  
 CC Email: sanjay.kumar-1@gsk.com  
 CC Seq primer: T7.  
 CC  
 XX  
 XX  
 FH Key Location/Qualifiers

FH source 1..7  
 FT /db\_xref="taxon:9606"  
 FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 FT Directional"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
 FT /tissue\_type="Cartilage"  
 FT /lab\_host="E.coli DH10 B"  
 FT  
 XX  
 SO Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 t 1  
 1  
 Db 2 T 2

RESULT 41  
 BG897546/C standard; RNA; EST; 7 BP.  
 ID BG897546  
 XX  
 AC BG897546;  
 XX  
 SV BG897546.1  
 XX  
 DT 09-JUN-2001 (Rel. 68, Created)  
 DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)  
 XX  
 DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA  
 DE sequence.  
 DE  
 XX  
 XX EST.  
 KW Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-7  
 MEDLINE: 21482651.  
 RX PUBMED: 11597177.  
 RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,  
 RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.,  
 RT "Identification and initial characterization of 5000 expressed sequenced  
 RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA  
 RT libraries";  
 RL Osteoarthritis Cartilage 9(7):641-653(2001).  
 XX  
 XX  
 CC Contact: Sanjay Kumar  
 CC UW2109  
 CC GlaxoSmithKline  
 CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 CC Tel: 610-270-7245  
 CC Fax: 610-270-5598  
 CC Email: sanjay.kumar-1@gsk.com  
 CC Seq primer: T7.  
 CC  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT source 1..7  
 FT /db\_xref="taxon:9606"  
 FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 FT Directional"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
 FT /tissue\_type="Cartilage"  
 FT /lab\_host="E.coli DH10 B"  
 FT  
 XX

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other:

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 4 T 4

RESULT 42

HSN007412  
ID HSN007412 standard; RNA; EST; 7 BP.

AC AL042562;

SV AL042562.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434J1721\_r1 (from clone DKFZp434J1721)

KW EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP 1-7

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No st sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source

FT 1..7

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434J1721"

FT DH10B; sites NotI + SalI

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 6 T 6

RESULT 43

HSN007412/C  
ID HSN007412 standard; RNA; EST; 7 BP.

AC AL042562;

XX AL042562.1

SV 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434J1721\_r1 (from clone DKFZp434J1721)

KW EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP 1-7

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No st sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source

FT 1..7

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434J1721"

FT DH10B; sites NotI + SalI

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other:

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 7;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 5 T 5

RESULT 44

HSN007502  
ID HSN007502 standard; RNA; EST; 7 BP.

AC AL042562;

SV AL042562.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434J1921\_r1 (from clone DKFZp434J1921)

KW EST; expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP 1-7

KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
KL MIPS, Am Klopferstr. 18a D-82152 Martinsried, GERMANY  
XX  
CC (clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No. 51 sequence available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
XX  
FH Key Location/Qualifiers  
FH  
FT source 1..7  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp434N1921"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"  
XX  
SQ Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other:

Query Match 100.0%; Score 1; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 t 1  
1  
Db 4 T 4

RESULT 45  
LOCUS C58888 7 bp mRNA linear EST 22-SEP-1997  
DEFINITION C58888 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA  
ACCESSION C58888  
VERSION C58888.1 GI:2417593  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
REFERENCE 1 (bases 1 to 7)  
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
TITLE M., Miyata,A. and Nishigaki,A.  
JOURNAL Expression map of the C. elegans genome  
COMMENT Unpublished (1996)  
CONTACT: Yuji Kohara  
Genome Biology Lab.  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers

FEATURES  
source 1..7  
/organism="Caenorhabditis elegans"  
/strain="CBI489 him-8(e1489)"  
/db\_xref="taxon:6239"  
/clone="YK383a7"  
/clone\_lib="Yuji Kohara unpublished cDNA"  
/sex="hermaphrodite, male"  
/tissue\_type="whole animal"  
/dev\_stage="varied"

BASE COUNT 2 a 0 c 1 g 3 t 1 others  
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 t 1  
1  
Db 4 T 4

Search completed: July 15, 2002, 20:07:36  
Job time: 14494 sec

---







```

XX [1]
RN 1-2
RA Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT :
RI Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the KZPD in Berlin
CC Please contact the KZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
FT source 1..2
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZps86P0517"
FT /clone_1lb="586 (synonym: hute1). Vector pSport1; host
FT DH10B; sites NotI + SalI/MluI"
FT /dev_stage="adult"
FT /tissue_type="uterus"
XX
SO Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
DB 2 c 2

RESULT 5
BI817789 2 bp mRNA linear EST 04-OCT-2001
LOCUS G3-G22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
ACCESSION BI817789
VERSION BI817789.1 GI:15951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
Ambystoma.
1 (bases 1 to 2)
REFERENCE Voss,S.R., Kling,D., Maness,N., Smith,J.J., Rondel,M., Bryant,S.V.,
AUTHORS Gardner,D.M. and Parichy,D.M.
TITLE Expressed sequence tags from an axolotl limb regeneration library
JOURNAL Unpublished (2001)
COMMENT Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: svoss@lamar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
svoss@lamar.colostate.edu.
Location/Qualifiers
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_1lb="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

FEATURES
SOURCE
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_1lb="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 1; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
DB 2 c 2

RESULT 7
BE351920 2 bp mRNA linear EST 18-JUL-2000
LOCUS BE351920/c
DEFINITION 894053D07.y1 C. reinhardtii CC-1690, normalized, lambda zap II
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
1 (bases 1 to 2)

```

**AUTHORS** Grossman, A., Davies, J., Federpiet, N., Harris, E., Lefebvre, P., McDermott, J. P., Sillfow, C., Stern, D. and Surzycki, R.,  
**TITLE** Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants: Project Phase 2  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Elizabeth H. Harris  
 DCMB Box 91000  
 Duke University  
 Durham, NC 27708-1000, USA  
 Tel: 919 613 8164  
 Fax: 919 613 8177  
 Email: chlamy@duke.edu  
 Location/Qualifiers  
 1..2  
 /organism="Chlamydomonas reinhardtii"  
 /strain="CC-1690 wild type mt+ 219r"  
 /db\_xref="taxon:3055"  
 /clone\_lib="C. reinhardtii CC-1690, normalized, lambda Zap II"  
 /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI. This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO<sub>2</sub> and HS medium bubbled with 5% CO<sub>2</sub>. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldi et al (1996) Genome Research 6: 791-806."

**BASE COUNT** 0 a 0 c 2 g 0 t  
**ORIGIN**

Query Match 100.0%; Score 1; DB 10; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 c 1  
 |  
 Db 2 c 2

**RESULT** 8  
**AZ463604/c** 2 bp DNA linear GSS 04-OCT-2000  
**DEFINITION** J06272205R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
**ACCESSION** AZ463604  
**VERSION** AZ463604.1 GI:10621729  
**KEYWORDS** GSS.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 2)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
**CONTACT** Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

**JOURNAL**  
**COMMENT**

**FEATURES**  
 source  
 Location/Qualifiers  
 1..2  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M027205"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (911473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT** 0 a 0 c 1 g 1 t  
**ORIGIN**

Query Match 100.0%; Score 1; DB 12; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 c 1  
 |  
 Db 1 c 1

**RESULT** 9  
**AW672605/c** 3 bp mRNA linear EST 26-SEP-2001  
**DEFINITION** 2Xa explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo. Rattus norvegicus cDNA similar to: gb1AF022811.1|AF022811 Mus musculus cornichon mRNA, mRNA sequence.  
**ACCESSION** AW672605  
**VERSION** AW672605.1 GI:7541085  
**KEYWORDS** EST.  
**SOURCE** Norway rat.  
**ORGANISM** Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 3)  
 Pilsav, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Pilsava, T.M., Higginbotham, K.G., Karavanova, I., Lerman, M. and Perantoni, A.O.  
 Mesenchymal-epithelial transition in the developing metanephric kidney: gene expression study by differential display  
 Genesis 27 (1), 22-31 (2000)  
**CONTACT** Pilsav S.Y.  
 Laboratory of Comparative Carcinogenesis  
 National Cancer Institute  
 FCRC, Bldg. 538, Room 205, Frederick, MD 21702, USA

**JOURNAL**  
**COMMENT**

Tel: 301 846 1242  
 Fax: 301 846 4956  
 Email: plisov@mail.ncifcrf.gov  
 PCR Primers  
 FORWARD: ctcgagcctccgctc  
 BACKWARD: tttagcttcttcttc  
 Insert Length: 350 Std Error: 0.00  
 Seq primer: Sp6  
 High quality sequence stop: 261.  
 Location/Qualifiers  
 1..3  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_1lb="Expanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."  
 /tissue\_type="Metanephric mesenchyme"  
 /cell\_type="Mesenchymal/epithelial"  
 /dev\_stage="13 dpc-16dpc"  
 /lab\_host="JM109"  
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega).; Restriction Enzymes: I, AclI, AclII, SphI, NcoI, BstXI, NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

BASE COUNT  
 ORIGIN  
 1 a 0 c 2 g 0 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 9; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
 1  
 Db 3 c 3

RESULT 10  
 A2438202  
 LOCUS 3 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0228108F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 clone UUCG1M0228108 F, DNA sequence.  
 ACCESSION A2438202  
 VERSION A2438202.1 GI:10562215  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 3)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0228 row: 1 column: 08  
 Seq primer: CGTTGTAAACACGCGCCACT  
 Class: plasmid ends

FEATURES  
 source  
 High quality sequence stop: 302.  
 Location/Qualifiers  
 1..3  
 /organism="Mus musculus"  
 /strain="C57BL/6j"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0228108"  
 /clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b1Af129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 1 a 1 c 0 g 1 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 12; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
 1  
 Db 1 c 1

RESULT 11  
 CNS00RCV/c  
 LOCUS 3 bp DNA linear GSS 03-JUN-1999  
 DEFINITION BACR17D19 of Rpci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION A1077515  
 VERSION A1077515.1 GI:4956992  
 KEYWORDS GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 3)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named Rpci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain yz; cn bw sp, the same strain used for the BDGP's

COMMENT

P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

Location/Qualifiers

source

1..3

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="RPC1-98"

/clone="BACRI7D19"

/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 3 c 3

## RESULT 12

ID BG926576 standard; RNA; EST; 4 BP.

AC BG926576;

XX BG926576.1

SV 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

RT Salhe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

libraries";

KL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

FT source

FT 1..4

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone\_lib="HNC (Human Normal Cartilage)"

FT /tissue\_type="cartilage"

FT /lab\_host="E.coli DH10 B"

XX Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

SO

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 3 c 3

## RESULT 13

ID BG926576/C standard; RNA; EST; 4 BP.

XX BG926576;

XX BG926576.1

SV 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

RT Salhe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

libraries";

XX Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

FT source

FT 1..4

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone\_lib="HNC (Human Normal Cartilage)"

FT /tissue\_type="cartilage"

FT /lab\_host="E.coli DH10 B"

Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 4 C 4

RESULT 14

ID HSM003901/c standard; RNA: EST; 4 BP.

XX AL039425;

SV AL039425.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZp434L0810\_s1 (from clone DKFZp434L0810)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

XX Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Cloned from S. Wiemann, sequenced by Qiagen within the cDNA

XX sequencing consortium of the German Genome Project

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source 1..4

XX /db\_xref="taxon:9606"

XX /organism="Homo sapiens"

XX /clone\_id="DKFZp434L0810"

XX /clone\_1ib="434 (synonym: htes3). Vector pSport1; host

XX DH10B; sites NotI + SalI"

XX /dev\_stage="adult"

XX /tissue\_type="testis"

XX Sequence 4 BP: 2 A: 0 C: 1 G: 0 T: 1 other:

XX Query Match 100.0%; Score 1; DB 2; Length 4;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 4 C 4

XX RESULT 15

ID HSM010467 standard; RNA: EST; 4 BP.

XX AL045617;

SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZp434O245\_r1 (from clone DKFZp434O245)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

XX Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Cloned from S. Wiemann, sequenced by Qiagen within the cDNA

XX sequencing consortium of the German Genome Project

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source 1..4

XX /db\_xref="taxon:9606"

XX /organism="Homo sapiens"

XX /clone\_id="DKFZp434O245"

XX /clone\_1ib="434 (synonym: htes3). Vector pSport1; host

XX DH10B; sites NotI + SalI"

XX /dev\_stage="adult"

XX /tissue\_type="testis"

XX Sequence 4 BP: 0 A: 2 C: 1 G: 1 T: 0 other:

XX Query Match 100.0%; Score 1; DB 2; Length 4;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 C 1

XX RESULT 16

ID HSM010467 standard; RNA: EST; 4 BP.

XX AL045617;

SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZp434O245\_r1 (from clone DKFZp434O245)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

XX Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:

XX Eutheria: Primates: Catarrhini: Homiidae: Homo.

XX [1]

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Cloned from S. Wiemann, sequenced by Qiagen within the cDNA

XX sequencing consortium of the German Genome Project

XX No s1 sequence available

XX This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX Key Location/Qualifiers  
 FH source 1..4  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp4340245"  
 FT /clone\_lib="434 (synonym: htcs). Vector pSport1: host  
 FT DH10B; sites NotI + SalI  
 FT /dev\_stage="adult"  
 FT /issue\_type="testis"  
 XX  
 XX  
 S0 Sequence 4 bp; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
 Db 4 C 4

RESULT 17  
 LOCUS AM672622/C  
 DEFINITION 73C Explaned metanephric mesenchyme induced to differentiate into  
 epithelial structures of the nephron ex vivo. Rattus norvegicus  
 cDNA similar to: embfAL049970.1|HSM800317 Homo sapiens  
 mRNA: CDNA DKFZp5648102 (from clone DKFZp5648102); mRNA sequence.  
 AM672622.1 GI:7541102  
 EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 4)  
 Pilssov, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Pilssova, T.M.,  
 Higginbotham, K.G., Karavanova, I., Lerman, M., and Perantonio, A.O.,  
 Kidney: gene expression study by differential display  
 Genests 27 (1), 22-31 (2000)  
 20321327  
 COMMENT Contact: Pilssov S.Y.  
 Laboratory of Comparative Carcinogenesis  
 National Cancer Institute  
 PCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA  
 Tel: 301 846 1242  
 Fax: 301 846 4956  
 Email: pilssov@mail.ncifcrf.gov  
 PCR Primers  
 FORWARD: ctccagctccctc  
 BACKWARD: ttaagctctctcttcttg  
 Insert Length: 262 Std Error: 0.00  
 Seq primer: SP6  
 High quality sequence stop: 262  
 POLY-A=yes.

FEATURES  
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 Location/Qualifiers  
 1..4  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_lib="Explaned metanephric mesenchyme induced to  
 differentiate into epithelial structures of the nephron ex  
 vivo."  
 /tissue\_type="metanephric mesenchyme"  
 /cell\_type="Mesenchymal/Epithelial"  
 /dev\_stage="13 dpc-16dpc"  
 /lab\_host="JMI09"

/note="Organ: Kidney; Vector: pGEM-Teasy (Promega).;  
 Restriction Enzymes 1: ApaI, AatII, SphI, NcoI, BstZI,  
 NotI, SacII, and EcoRI SpeI, EcoRI, NcoI, BstZI, PstI,  
 SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment  
 PCR-amplified in mRNA differential display analysis;  
 cloned in pGEM-Teasy (Promega); Its expression is  
 developmentally regulated during mesenchymal-epithelial  
 conversion in the metanephric kidney."  
 1 a 0 c 3 g 0 t

Query Match 100.0%; Score 1; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
 Db 4 C 4

RESULT 18  
 LOCUS CNS004RB  
 DEFINITION CNS004RB 4 bp DNA linear GSS 03-JUN-1999  
 Drosophila melanogaster genome survey sequence TERT end of BAC #  
 BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 AL054121  
 AL054121.1 GI:4931932  
 GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 4)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;  
 BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 PL and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library,  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source 1..4  
 Location/Qualifiers  
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 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCI-98"  
 /clone="BACR10A06"  
 /note="end : TERT"  
 BASE COUNT 1 a 1 c 0 g 2 t  
 ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
 Db 4 C 4

Db 4 C 4

RESULT 19

HSM007310/c  
ID HSM007310 standard; RNA: EST: 5 BP.

XX AL042460:

XX AL042460.1

XX 12-MAR-1999 (Rel. 59, Created)

XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434E1821\_r1 (from clone DKFZp434E1821)

XX EST: expressed sequence tag.

XX Homo sapiens (human)  
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

XX sequencing consortium of the German Genome Project

XX No sl sequence available

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source 1..5  
XX /db\_xref="taxon:9606"  
XX /organism="Homo sapiens"  
XX /clone\_lib="434 (synonym: hres3). Vector psportl: hostXX DH10B; sites NotI + SalI"  
XX /dev\_stage="adult"  
XX /tissue\_type="testis"

XX Sequence 5 BP: 2 A: 0 C: 1 G: 2 T: 0 other:

Query Match 100.0%; Score 1: DB 2: Length 5:

Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 1 C 1

RESULT 20

HSM007835  
ID HSM007835 standard; RNA: EST: 5 BP.

XX AL042985:

XX AL042985.1

XX 12-MAR-1999 (Rel. 59, Created)

XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434N1522\_r1 (from clone DKFZp434N1522)

XX EST: expressed sequence tag.

XX

Homo sapiens (human)  
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

XX 1-5

XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

XX sequencing consortium of the German Genome Project

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

XX source 1..5  
XX /db\_xref="taxon:9606"  
XX /organism="Homo sapiens"  
XX /clone\_lib="434 (synonym: hres3). Vector psportl: hostXX DH10B; sites NotI + SalI"  
XX /dev\_stage="adult"  
XX /tissue\_type="testis"

XX Sequence 5 BP: 2 A: 1 C: 0 G: 0 T: 2 other:

Query Match 100.0%; Score 1: DB 2: Length 5:

Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 5 C 5

RESULT 21

HSM011053/c  
ID HSM011053 standard; RNA: EST: 5 BP.

XX AL046203:

XX AL046203.1

XX 12-MAR-1999 (Rel. 59, Created)

XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA: EST DKFZp434D137\_r1 (from clone DKFZp434D137)

XX EST: expressed sequence tag.

XX Homo sapiens (human)  
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

XX 1-5

XX Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by BMF within the CDNA

XX sequencing consortium of the German Genome Project

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059



```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_lib="434 (synonym: hhes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SO Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 22
HG927410 standard; RNA; EST; 6 BP.
XX
AC BG927410;
XX
SV BG927410.1
XX
SV 09-JUN-2001 (Rel. 68, Created)
XX 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE HNC1-1-C7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
XX EST.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX MEDLINE: 21482651.
XX PUBMED: 11597177.
XX
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Salhe G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gonen M., Lark M.W.:
RT "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RL Osteoarthritis Cartilage 9(7):641-653(2001).
XX
CC Contact: Sanjay Kumar
CC UW2109
CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay_kumar-1@gsk.com
CC Seq primer: T7.
XX
FH Key Location/Qualifiers
FH
FT source 1..6
FT /db_xref="taxon:9606"
FT /note="Vector: pSPORT 1; site_1: SalI; site_2: NotI;
FT directional"
FT /organism="Homo sapiens"
FT /clone_lib="HNC (Human Normal Cartilage)"
FT /tissue_type="Cartilage"
XX

```

---

```

FT
XX /lab_host="E.coli DH10 B"
XX
SO Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 1 C 1

RESULT 23
HSM003844/C standard; RNA; EST; 6 BP.
XX
ID HSM003844
XX
AC AL039368;
XX
SV AL039368.1
XX
SV 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX EST: expressed sequence tag.
XX
XX Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopfersplitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434I0110"
FT /clone_lib="434 (synonym: hhes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
DB 2 C 2

RESULT 24
HSM004423/C standard; RNA; EST; 6 BP.
XX
ID HSM004423

```

```

XX AC AL039947;
XX SV AL039947.1
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA: EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN 1-6
XX RP 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
XX source 1..6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434J0112"
XX /clone_1b="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1
Db 2 C 2

RESULT 25
HSM007334/C standard; RNA; EST; 6 BP.
XX ID HSM007334
XX AC AL042484;
XX SV AL042484.1
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA: EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN 1-6
XX RP 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
XX source 1..6
XX /db_xref="taxon:9606"

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
XX source 1..6
XX /db_xref="taxon:9606"

OY 1 C 1
Db 2 C 2

RESULT 26
HSM007683 standard; RNA; EST; 6 BP.
XX ID HSM007683
XX AC AL042833;
XX SV AL042833.1
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA: EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN 1-6
XX RP 1-6
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
XX source 1..6
XX /db_xref="taxon:9606"

```



```
OS Homo sapiens (human)
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia:
OC Eutheria: Primates: Catarrhini: Hominoidea: Homo.
XX
XX
XX (11
XX Poulaka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.:
XX Submitted (12-MAR-1999) to the EMBL/GenBank/ODDB databases.
XX MIPS, Am Klopferstritz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by DKFZ within the CDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source 1. .6
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone_lib="434 (synonym: hses3). Vector pSport1: host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
XX
XX Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;
XX
XX Query Match 100.0%; Score 1; DB 2; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 C 1
XX |
XX Db 6 C 6
XX
XX RESULT 30
XX BE726686 6 bp mRNA linear EST 14-SEP-2000
XX LOCUS 894095D11.Y1 C. reinhardtii CC-1690, normalized, Lambda zap II
XX DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
XX ACCESSION BE726686
XX VERSION BE726686.1 GI:10128110
XX KEYWORDS EST.
XX SOURCE Chlamydomonas reinhardtii.
XX ORGANISM Chlamydomonas reinhardtii.
XX Eukaryota: Viridiplantae: Chlorophyta: Chlorophyceae: Volvocales:
XX Chlamydomonadaceae: Chlamydomonas.
XX 1 (bases 1 to 6)
XX Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
XX McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
XX Analyses of the Chlamydomonas reinhardtii Genome: A Model,
XX Unicellular System for Analyzing Gene Function and Regulation in
XX Vascular Plants; project phase 2
XX Unpublished (2000)
XX CONTACT: Charles Hauser
XX DCMB Box 91000
XX Duke University
XX Durham, NC 27708-1000
XX Tel: 919 613 8159
XX Fax: 919 613 8177
XX Email: chauser@duke.edu.
XX Location/Qualifiers
XX 1. .6
XX /organism="Chlamydomonas reinhardtii"
XX /strain="CC-1690 wild type mt+ 21gr"
XX /db_xref="taxon:3055"
XX /clone_lib="C. reinhardtii CC-1690, normalized, Lambda zap
XX
XX JOURNAL
XX COMMENT
XX
XX FEATURES
XX source
XX 1. .6
XX /organism="Chlamydomonas reinhardtii"
XX /strain="CC-1690 wild type mt+ 21gr"
XX /db_xref="taxon:3055"
XX /clone_lib="C. reinhardtii CC-1690, normalized, Lambda zap
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II"
/note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into Lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exsist4 (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
XX
XX BASE COUNT 0 a 1 c 5 g 0 t
XX ORIGIN
XX
XX Query Match 100.0%; Score 1; DB 10; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 C 1
XX |
XX Db 2 C 2
XX
XX RESULT 31
XX BE726686 6 bp mRNA linear EST 14-SEP-2000
XX LOCUS 894095D11.Y1 C. reinhardtii CC-1690, normalized, Lambda zap II
XX DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
XX ACCESSION BE726686
XX VERSION BE726686.1 GI:10128110
XX KEYWORDS EST.
XX SOURCE Chlamydomonas reinhardtii.
XX ORGANISM Chlamydomonas reinhardtii.
XX Eukaryota: Viridiplantae: Chlorophyta: Chlorophyceae: Volvocales:
XX Chlamydomonadaceae: Chlamydomonas.
XX 1 (bases 1 to 6)
XX Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
XX McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
XX Analyses of the Chlamydomonas reinhardtii Genome: A Model,
XX Unicellular System for Analyzing Gene Function and Regulation in
XX Vascular Plants; project phase 2
XX Unpublished (2000)
XX CONTACT: Charles Hauser
XX DCMB Box 91000
XX Duke University
XX Durham, NC 27708-1000
XX Tel: 919 613 8159
XX Fax: 919 613 8177
XX Email: chauser@duke.edu.
XX Location/Qualifiers
XX 1. .6
XX /organism="Chlamydomonas reinhardtii"
XX /strain="CC-1690 wild type mt+ 21gr"
XX /db_xref="taxon:3055"
XX /clone_lib="C. reinhardtii CC-1690, normalized, Lambda zap
XX
XX JOURNAL
XX COMMENT
XX
XX FEATURES
XX source
XX 1. .6
XX /note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XX XhoI; This library, constructed by John Davies and Jeffrey
XX McDermott, combines cDNAs from CC-1690 cells grown to
XX mid-log phase in TAP (acetate-containing) medium in the
XX light, TAP medium in the dark, HS (minimal) medium in
XX ambient levels of CO2 and HS medium bubbled with 5% CO2.
XX PolyA mRNA was purified from each sample, pooled and cDNA
XX synthesized. The cDNA was directionally cloned into lambda
XX ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
XX pBluescript II SK- plasmids were excised from the lambda
XX ZAP clones by superinfection with Exsist4 (Stratagene)
XX phage. The library was normalized using method 4 described
XX in Bonaldo et al (1996) Genome Research 6: 791-806."
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BASE COUNT 0 a 1 c 5 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 6 c 6

RESULT 32

BC897546 standard; RNA; EST; 7 BP.

AC BC897546;

SV BC897546.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA  
sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

RT Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

11 MEDLINE; 21482651.

PUBMED; 11597177.

Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,  
Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

"Identification and initial characterization of 5000 expressed sequenced  
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA  
libraries";

Osteoarthritic Cartilage 9(7):641-653(2001).

CC Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX

XX

XX

XX

XX

XX

XX

Oy 1 c 1

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1

Db 1 c 1

RESULT 33

BC897546/c standard; RNA; EST; 7 BP.

ID BC897546

AC BC897546;

SV BC897546.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA  
sequence.

DE EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

RT Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

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XX

RESULT 34

HSM007412 standard; RNA; EST; 7 BP.

ID HSM007412

AC AL042562;

SV AL042562.1

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 6 c 6

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J172L_r1 (from clone DKFZp434J1721)
DE Homo sapiens mRNA; EST DKFZp434J172L_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX PH source
XX FT 1..7
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434J1721"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX
XX SO Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 35
HSM007412/C
ID HSM007412 standard; RNA; EST; 7 BP.
XX
XX AL042562;
XX
XX SV AL042562.1
XX
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434J172L_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX PH source
XX FT 1..7
XX FT /db_xref="taxon:9606"
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XX FT /clone="DKFZp434J1721"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX
XX SO Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST; 7 BP.
XX
XX AL042652;
XX
XX SV AL042652.1
XX
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434N192L_r1 (from clone DKFZp434N1921)
XX EST: expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
XX 1-7
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX PH source
XX FT 1..7
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434N1921"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
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XX SO Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

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XX /tissue\_type="testis"  
SO Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
DB 1 C 1

RESULT 37  
HSM007502/c  
ID HSM007502 standard; RNA; EST; 7 BP.  
AC AL042652;  
SV AL042652.1  
SV 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
DE Homo sapiens mRNA: EST DKFZp434N1921\_r1 (from clone DKFZp434N1921)  
XX EST: expressed sequence tag.  
XX Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.  
XX [1]  
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX  
CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No. 51 sequence available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
XX  
XX Key Location/Qualifiers  
FH 1..7  
FT source  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"  
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SQ Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
DB 7 C 7  
RESULT 38  
CS8888/c

LOCUS CS8888 7 bp mRNA linear EST 22-SEP-1997  
DEFINITION C58888 Yui Kohara unpublished cDNA Caenorhabditis elegans CDNA  
clone YK383a7 3', mRNA sequence.  
ACCESSION C58888  
VERSION C58888  
KEYWORDS EST.  
SOURCE  
ORGANISM Caenorhabditis elegans.  
Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea  
; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE  
AUTHORS Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
1 (bases 1 to 7)  
1 (bases 1 to 7)  
TITLE Expression map of the C.elegans genome  
JOURNAL Unpublished (1996)  
COMMENT Contact: Yui Kohara  
Genome Biology Lab.  
National Institute of Genetics  
Yata 111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
FEATURES  
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/sex="hermaphrodite, male"  
/tissue\_type="whole animal"  
/dev\_stage="varied"  
BASE COUNT 2 a 1 g 3 t 1 others  
ORIGIN  
Query Match 100.0%; Score 1; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
DB 7 C 7  
RESULT 39  
HSM001420  
ID HSM001420 standard; RNA; EST; 8 BP.  
XX  
AC AL037095;  
SV AL037095.1  
SV 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX  
DE Homo sapiens mRNA: EST DKFZp564L2064\_r1 (from clone DKFZp564L2064)  
XX EST: expressed sequence tag.  
XX  
XX Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
XX Eutheria; Primates; Catarrhini; Homiidae; Homo.  
XX [1]  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
XX  
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA  
CC sequencing consortium of the German Genome Project

```

CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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PH
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FT /db_xref="taxon:9606"
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FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
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XX
SQ Sequence 8 BP; 2 A; 3 C; 0 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 40
HSM001743
ID HSM001743 standard; RNA; EST; 8 BP.
XX
AC AL037413;
XX
SV AL037413.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA: EST DKFZp564L0771_s1 (from clone DKFZp564L0771)
XX
KM EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
RN [1]
RP 1-8
RA Bloecher H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the CDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
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FT /clone_lib="564 (synonym: hibr2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
FT
XX
SQ Sequence 8 BP; 1 A; 7 C; 0 G; 0 T; 0 other;

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Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 41
HSM004451
ID HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975;
XX
SV AL039975.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA: EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KM EST: expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
RN [1]
RP 1-8
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
PH
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FT /organism="Homo sapiens"
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FT /clone_lib="434 (synonym: hies3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 7 C 7

RESULT 42
HSM004451/C
ID HSM004451 standard; RNA; EST; 8 BP.
XX
AC AL039975;

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SV      AL039975.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
DE      EST: expressed sequence tag.
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      (1)
RN      1-8
RP      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      Clone from S. Wiemann, sequenced by Olagen within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX      Key      Location/Qualifiers
FH      source      1..8
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434K0712"
FT      /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other:

Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 C 1
DB      2 C 2

RESULT 43
HSM007277 standard; RNA; EST; 8 BP.
ID      HSM007277
XX      AL042427;
AC      AL042427.1
SV      AL042427.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
DE      EST: expressed sequence tag.
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      (1)
RN      1-8
RP      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX      Key      Location/Qualifiers
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RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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XX      AL042427;
AC      AL042427.1
SV      AL042427.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
DE      EST: expressed sequence tag.
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX      (1)
RN      1-8
RP      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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Search completed: July 15, 2002, 20:07:36  
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Db 2 C 2

RESULT 45  
HSM007323

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AC AL042473:

SV AL042473.1

XX 12-MAR-1999 (Ref. 59, Created)

DT 12-MAR-1999 (Ref. 59, Last updated, Version 1)

DE Homo sapiens mRNA: EST DKFZP434F0121\_f1 (from clone DKFZP434F0121)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

KN 1-8

RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the cDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

PH source 1..8

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FT DH10B; sites NotI + SalI"

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Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

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Db 7 C 7



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds  
(Without alignments)  
2.195 Million cell updates/sec

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Perfect score: 1  
Sequence: 1 g 1

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: gb\_hlg:\*  
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8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
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17: em\_hum:\*  
18: em\_in:\*  
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24: em\_ph:\*  
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33: em\_hlgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C	2	100.0	2	6	AX092442	AX092442 Sequence
C	3	100.0	2	6	AX092443	AX092443 Sequence
C	4	100.0	2	6	AX092444	AX092444 Sequence
C	5	100.0	2	6	AX092445	AX092445 Sequence
C	6	100.0	2	6	AX092446	AX092446 Sequence
C	7	100.0	2	6	AX092447	AX092447 Sequence
C	8	100.0	2	6	AX092448	AX092448 Sequence
C	9	100.0	2	6	AX092449	AX092449 Sequence
C	10	100.0	2	6	AX092450	AX092450 Sequence
C	11	100.0	2	6	AX092451	AX092451 Sequence
C	12	100.0	2	6	AX092452	AX092452 Sequence
C	13	100.0	2	6	AX092453	AX092453 Sequence
C	14	100.0	2	6	AX092454	AX092454 Sequence
C	15	100.0	2	6	AX092455	AX092455 Sequence
C	16	100.0	2	6	AX092456	AX092456 Sequence
C	17	100.0	2	6	AX092457	AX092457 Sequence
C	18	100.0	2	6	AX092458	AX092458 Sequence
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C	22	100.0	2	6	AX092462	AX092462 Sequence
C	23	100.0	2	6	AX092463	AX092463 Sequence
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C	25	100.0	2	6	AX092465	AX092465 Sequence
C	26	100.0	2	6	AX092466	AX092466 Sequence
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ACCESSION	AX092441								
VERSION	AX092441.1	GI:13444536							
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									

Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 2 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Klees, Hadar (IL)

FEATURES  
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Location/Qualifiers

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ACCESSION AX092442  
VERSION AX092442.1 GI:13444537  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

unidentified.  
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1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 3 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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ACCESSION AX092444  
VERSION AX092444.1 GI:13444539  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

unidentified.  
unclassified.  
1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 5 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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ACCESSION AX092445  
VERSION AX092445.1 GI:13444540  
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AUTHORS  
TITLE  
JOURNAL

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1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 6 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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VERSION AX092446.1 GI:13444541  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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Kless, H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 7 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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VERSION AX092446.1 GI:13444541  
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ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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ACCESSION AX092447  
VERSION AX092447.1 GI:13444542  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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Db 1 G 1

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DEFINITION Sequence 9 from Patent WO0116366.  
ACCESSION AX092448  
VERSION AX092448.1 GI:13444543  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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ACCESSION AX092449  
VERSION AX092449.1 GI:13444544  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)  
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ACCESSION AX092449  
VERSION AX092449.1 GI:13444544  
KEYWORDS  
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JOURNAL  
unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 10 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
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Query Match  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 G 2

RESULT 11  
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DEFINITION Sequence 11 from Patent WO0116366.  
ACCESSION AX092450  
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KEYWORDS  
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REFERENCE  
AUTHORS  
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Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 11 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

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DEFINITION Sequence 12 from Patent WO0116366.  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
unclassified.  
1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 12 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
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BASE COUNT  
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DEFINITION Sequence 14 from Patent WO0116366.  
ACCESSION AX092453  
VERSION AX092453.1 GI:13444548  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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1 (bases 1 to 2)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 14 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
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LOCUS AX092454  
DEFINITION Sequence 15 from Patent WO0116366.  
ACCESSION AX092454  
VERSION AX092454.1 GI:13444549

KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 15 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
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RESULT 15  
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LOCUS AX092528 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 89 from Patent WO0116366.  
ACCESSION AX092528  
VERSION AX092528.1 GI:13444623  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 89 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unclassified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 1 c 1

RESULT 16  
AX092529/c  
LOCUS AX092529 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 90 from Patent WO0116366.  
ACCESSION AX092529  
VERSION AX092529.1 GI:13444624  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.

REFERENCE unclassified.  
1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 90 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unclassified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 2 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 c 2

RESULT 17  
AX092530  
LOCUS AX092530 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 91 from Patent WO0116366.  
ACCESSION AX092530  
VERSION AX092530.1 GI:13444625  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unclassified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 c 2

RESULT 18  
AX092538  
LOCUS AX092538 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 99 from Patent WO0116366.  
ACCESSION AX092538  
VERSION AX092538.1 GI:13444633  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.



TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 99-08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..2  
/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

RESULT 19

LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 50 from Patent WO0144465.  
ACCESSION AX175286  
VERSION AX175286.1 GI:14598654

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

RESULT 20

LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 51 from Patent WO0144465.  
ACCESSION AX175287  
VERSION AX175287.1 GI:14598655

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..2  
/organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 2 g 2

RESULT 21

LOCUS BD009609/c 2 bp DNA linear PAT 31-JAN-2002  
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori, nucleic acids in biological samples.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PN

OS

PD

PR

PI

PC

CC

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,  
78026 Versailles, France  
REFERENCE 2 (bases 1 to 2)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage ;  
CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT The cDNA library to be analyzed within the framework of this  
project was created using a Borealis cDNA library which was grown  
under conditions of nitrogen deprivation, which is the normal  
situation for B. cinerea during its development on its host plant.  
The library was produced in an oriented direction, in the pBSII  
vector.

## FEATURES

source Location/Qualifiers  
1..2  
/organism="Botryotinia fuckeliana"  
/strain="T4"  
/db\_xref="taxon:40559"  
/note="Genoscope sequence ID : M04F091"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

## RESULT 23

AC079635 3 bp DNA linear HTG 14-AUG-2001  
LOCUS Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION AC079635  
ACCESSION AC079635.3 GI:14647267  
VERSION HTG: HTGS. PHASED.  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
AUTHORS 1 (bases 1 to 3)  
McCombie,W.R., Baker,J.P., Bahret,A., Yang,C., Ballja,V.,  
Dechla,N.N., de la Bastide,M., Kuhl,K., King,L., Kirchoff,K.A.,  
Miller,B., Nasclmento,L.O., O'Shaughnessy,A.L., Preston,R.R.,  
Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Palmer,L.,  
Vill,M.D. and Zuber,Vern,T.  
COMMENT Mouse genomic sequence  
Unpublished  
TITLE 2 (bases 1 to 3)  
JOURNAL McCombie,W.R.  
REFERENCE Direct Submission  
AUTHORS Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing  
JOURNAL Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring  
Harbor, NY 11724, USA  
COMMENT On Jul 10, 2001 this sequence version replaced gi:14595773.  
\* NOTE: This record contains 1 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
3: contig of 3 bp in length.  
This entry has been temporarily removed. An update for RP23-152L20

will be submitted as soon as it becomes available.

FEATURES Location/Qualifiers  
source 1..3  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="RP23-152L20"

BASE COUNT 1 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 1 g 1

## RESULT 24

CHKNCAMC5 3 bp DNA linear VRT 17-JUL-2000  
LOCUS Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.  
DEFINITION M23994 J04140  
ACCESSION M23994.1 GI:212442  
VERSION M23994.1 GI:212442  
KEYWORDS 5 of 6  
SEGMENT chicken.  
SOURCE Gallus gallus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Prediger,E.A., Hoffman,S., Edelman,G.M. and Cunningham,B.A.  
TITLE Four exons encode a 93-base-pair insert in three neural cell  
adhesion molecule mRNAs specific for chicken heart and skeletal  
muscle.  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)  
MEDLINE 89071747  
PUBMED 3200847  
COMMENT Exon 12D represents a very small exon.  
FEATURES Location/Qualifiers  
1..3  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pC101B"  
/tissue-type="cardiac muscle"  
/dev-stage="day 10 embryo"  
1..3  
/gene="NCAM"  
/number=12

BASE COUNT 2 a 0 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 5; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 g 3

## RESULT 25

A97991 3 bp DNA linear PAT 26-JAN-2000  
LOCUS A97991  
DEFINITION Sequence 21 from Patent W09914366.  
ACCESSION A97991  
VERSION A97991.1 GI:6781229  
KEYWORDS

SOURCE unidentified.  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willemsse,M.J. and Van,D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 g 2

RESULT 26  
A97991/c  
LOCUS A97991  
DEFINITION Sequence 21 from Patent WO9914366.  
ACCESSION A97991  
VERSION A97991.1 GI:6781229  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willemsse,M.J. and Van,D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 g 1

RESULT 27  
AX092457/c  
LOCUS AX092457  
DEFINITION Sequence 18 from Patent WO0116366.  
ACCESSION AX092457  
VERSION AX092457.1 GI:13444552  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)  
FEATURES  
source Location/Qualifiers

source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 g 3

RESULT 28  
AX092458  
LOCUS AX092458  
DEFINITION Sequence 19 from Patent WO0116366.  
ACCESSION AX092458  
VERSION AX092458.1 GI:13444553  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)  
FEATURES  
source Location/Qualifiers

BASE COUNT 2 a 0 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 g 3

RESULT 29  
AX092460/c  
LOCUS AX092460  
DEFINITION Sequence 21 from Patent WO0116366.  
ACCESSION AX092460  
VERSION AX092460.1 GI:13444555  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar (IL)  
FEATURES  
source Location/Qualifiers

BASE COUNT 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN /note="synthetic oligonucleotide:"

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 c 2

RESULT 30  
AX092461/c 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092461  
DEFINITION Sequence 22 from Patent WO0116366.  
ACCESSION AX092461  
VERSION AX092461.1 GI:13444556  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 22 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 2 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 c 3

RESULT 31  
AX092462 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092462  
DEFINITION Sequence 23 from Patent WO0116366.  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 c 3

RESULT 32  
AX092462/c 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092462  
DEFINITION Sequence 23 from Patent WO0116366.  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 c 2

RESULT 33  
AX092463 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092463  
DEFINITION Sequence 24 from Patent WO0116366.  
ACCESSION AX092463  
VERSION AX092463.1 GI:13444558  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 24 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"

BASE COUNT 1 a 1 c 0 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 2 G 2

RESULT 34  
LOCUS AX092464  
DEFINITION Sequence 25 from Patent WO0116366.  
ACCESSION AX092464  
VERSION AX092464.1 GI:13444559  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 25 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 0 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 2 G 2

RESULT 35  
LOCUS AX092465  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
Db 2 G 2

RESULT 36  
LOCUS AX092465/c  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 3 G 3

RESULT 37  
LOCUS AX092466  
DEFINITION Sequence 27 from Patent WO0116366.  
ACCESSION AX092466  
VERSION AX092466.1 GI:13444561  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 27 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 0 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
Db 2 G 2

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RESULT 38
AX092467
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 39
AX092469
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 40
AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
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Best Local Similarity 100.0%; Pred. No. 0;
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OY 1 g 1
Db 3 G 3

RESULT 41
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LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 42
AX092473
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.
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AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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FEATURES
source
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/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 3 G 3

RESULT 41
AX092472
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
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Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 42
AX092473
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.
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---



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compaq Inc.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:11 ; Search time 932.4 seconds  
(without alignments)  
1.841 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3164\_3164

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*

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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	3	17	AAT33326	CAPL trinucleotide
2	100.0	3	17	AAT33326	CAPL trinucleotide
3	100.0	3	21	AAAG4655	Human TUB gene pro
4	100.0	3	22	AA120244	Human breast cance
5	100.0	4	16	AAO81664	bcrf binding oligo
6	100.0	4	16	AAO81664	bcrf binding oligo
7	100.0	4	16	AAO81665	bcrf binding oligo
8	100.0	4	16	AAO81665	bcrf binding oligo
9	100.0	4	18	AAT86385	Probe for target n

C	10	1	100.0	4	18	AAT86385	Probe for target n
C	11	1	100.0	4	18	AAT77252	Immunostimulatory
C	12	1	100.0	4	18	AAT77252	Immunostimulatory
C	13	1	100.0	4	22	AA117191	Human breast cance
C	14	1	100.0	4	22	AA117191	Human breast cance
C	15	1	100.0	4	22	AA124357	Human breast cance
C	16	1	100.0	4	22	AA124357	Cyclic binding ham
C	17	1	100.0	4	22	AA61450	Synthetic probe fo
C	18	1	100.0	5	15	AA61450	CH255 heavy chain
C	19	1	100.0	5	15	AA61450	Cleavable replicab
C	20	1	100.0	5	15	AA61450	Fusarium sp. 18S r
C	21	1	100.0	5	17	AA61450	Fusarium telomeric n
C	22	1	100.0	5	19	AA6163	Oligonucleotide se
C	23	1	100.0	5	19	AA6163	DNA enhancer sequ
C	24	1	100.0	5	20	AA6163	DNA enhancer sequ
C	25	1	100.0	5	20	AA6163	US5908745 primer
C	26	1	100.0	5	20	AA6163	US5908745 primer
C	27	1	100.0	5	20	AA6163	US5908745 primer
C	28	1	100.0	5	20	AA6163	US5908745 primer
C	29	1	100.0	5	20	AA6163	US5908745 primer
C	30	1	100.0	5	20	AA6163	US5908745 primer
C	31	1	100.0	5	20	AA6163	US5908745 primer
C	32	1	100.0	5	20	AA6163	US5908745 primer
C	33	1	100.0	5	20	AA6163	US5908745 primer
C	34	1	100.0	5	20	AA6163	US5908745 primer
C	35	1	100.0	5	20	AA6163	US5908745 primer
C	36	1	100.0	5	20	AA6163	US5908745 primer
C	37	1	100.0	5	20	AA6163	US5908745 primer
C	38	1	100.0	5	21	AA6163	US5908745 primer
C	39	1	100.0	5	21	AA6163	US5908745 primer
C	40	1	100.0	5	21	AA6163	US5908745 primer
C	41	1	100.0	5	21	AA6163	US5908745 primer
C	42	1	100.0	5	21	AA6163	US5908745 primer
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## ALIGNMENTS

RESULT	1
ID	AAT33326 standard; RNA: 3 BP.
XX	AAT33326;
AC	12-NOV-1996 (first entry)
XX	
DE	CAPL trinucleotide.
XX	
KW	CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
KW	osteosarcoma; therapy; ss.
XX	
OS	Synthetic.
XX	
PN	MO9625499-A1.
XX	
FD	22-AUG-1996.
XX	
PE	16-FEB-1996; 96MO-US02108.
XX	
PR	17-FEB-1995; 95US-0391375.
XX	
PA	(HYBR-) HYBRID INC.
PA	(NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
PI	Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandmo GJ;
PI	Von Hofe E;
XX	
DR	WPI; 1996-393400/39.
XX	
PT	Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

PT useful to inhibit metastatic cancer, partic. osteosarcoma  
PS Claim 2: Page 56; 70pp; English.  
XX  
CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
CC expression may include the trinucleotide GUC (AAT33326, given in 5'  
CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
CC other antisense oligonucleotides (AAT33327-36) complementary to  
CC specific regions of the CAPL gene (see also AAT33345), as well as  
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
CC patient as a means of inhibiting metastatic cancer.  
XX  
SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 3 g 3

RESULT 2  
AAT33326/C  
ID AAT33326 standard; RNA: 3 BP.  
XX  
AC AAT33326;  
XX  
DT 12-NOV-1996 (first entry)  
XX  
HE CAPL trinucleotide.  
XX  
KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;  
XX osteosarcoma; therapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO9625499-A1.  
XX  
PD 22-AUG-1996.  
XX  
PF 16-FEB-1996; 96WO-0502108.  
XX  
PR 17-FEB-1995; 95US-0391375.  
XX  
PA (HYBR-) HYBRIDON INC.  
XX (MORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.  
XX  
PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandsmo GJ;  
XX Von Hofe E;  
XX  
DR WPI: 1996-393400/39.  
XX  
PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -  
XX useful to inhibit metastatic cancer, partic. osteosarcoma  
XX  
PS Claim 2: Page 56; 70pp; English.  
XX  
CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
CC expression may include the trinucleotide GUC (AAT33326, given in 5'  
CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
CC other antisense oligonucleotides (AAT33327-36) complementary to  
CC specific regions of the CAPL gene (see also AAT33345), as well as  
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
CC patient as a means of inhibiting metastatic cancer.  
XX  
SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 1 g 1

RESULT 3  
AAA94655  
ID AAA94655 standard; DNA: 3 BP.  
XX  
AC AAA94655;  
XX

DT 15-JAN-2001 (first entry)  
XX  
DE Human TUB gene probe #2.  
XX  
KW Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;  
XX TUB; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6114502-A.  
XX  
PD 05-SEP-2000.  
XX  
PF 27-FEB-1998; 98US-0032365.  
XX

PR 22-AUG-1996; 96US-0701380.  
XX  
PR 04-SEP-1996; 96US-0706292.  
XX  
PR 10-APR-1996; 96US-0630592.  
XX  
PR 17-SEP-1996; 96US-0714991.  
XX  
PR 30-APR-1997; 97US-0850218.  
XX  
PR 01-AUG-1997; 97US-0904699.  
XX  
PR 17-SEP-1997; 97US-0932306.  
XX

(AXYS-) AXYS PHARM INC.

PI North M, Nishina P, Noben-Trauth K, Naggett J;  
XX  
DR WPI: 2000-586483/55.  
XX

PT Mammalian proteins expressed in retina and brain, useful for producing  
XX antihodies and for diagnosing neurosensory defects including cochlear  
XX degeneration, peripheral retinal degeneration and cone-rod retinal  
XX dystrophy -  
XX

Disclosure; Columns 81-82; 61pp; English.

PS The present invention relates to human and murine cDNAs from a  
XX neurosensory defect associated gene family. The novel cDNAs are mouse  
XX tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB  
XX form 6 (see AAA94632), human TUB form I (see AAA94633), human TULP1 (see  
XX AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and  
XX mouse TULP4 (see AAA94638). The novel coding sequences are useful as  
XX immunogens to raise antibodies that specifically identify TUB/TULP  
XX defects. The novel proteins encoded by the present sequence can be used  
XX for the treatment of neurosensory degenerative conditions e.g. retinal  
XX dystrophies. The present sequence is a probe used to isolate the novel  
XX genes of the present invention.

SO Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

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RESULT 4
AAL20244/C
ID AAL20244 standard: cDNA; 3 BP.
XX
AC AAL20244;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human; breast cancer; cell marker; cytosolic; ss.
XX
OS Homo sapiens.
XX
PM WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI: 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer
XX
PS Claim 1: Page 2245; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;
XX
Query Match 100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
I
Db 2 G 2
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```
RESULT 5
AA081664
ID AA081664 standard: RNA; 4 BP.
XX
AC AA081664;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
XX metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PM WO9500528-A.
XX
```

```
RESULT 6
AA081664/C
ID AA081664 standard: RNA; 4 BP.
XX
AC AA081664;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PM WO9500528-A.
XX
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 g 1
I
Db 1 g 1
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The sequences given in AA081642-95 are oligonucleotides which modulate the activity of basic fibroblast growth factor (bFGF) by binding to the bFGF protein. Most esp. the sequences given in AA081664-67 represent core sequences of which at least one is present in each of the binding oligos. These oligonucleotides may form a single strand, double strand, a stem-loop structure, a bubble structure, a pseudoknot or a closed, circular structure. bFGF binds to high affinity receptor and low affinity heparin-like molecules on the cell surface. These oligonucleotides bind to bFGF in competition with its receptor and heparin. These oligonucleotides may inhibit or enhance the activity of bFGF. Particularly, they inhibit neovascularisation so they can be used to suppress growth of solid tumours and to reduce the risk of metastasis. They can be used as diagnostic reagents to determine the presence of thrombin, or used in gene therapy.

Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

PD 05-JAN-1995.

XX 17-JUN-1994: 94WO-US06884.

XX 18-JUN-1993: 93US-0079677.

PK 07-JAN-1994: 94US-0179491.

XX (PHAR-) PHARMAGENICS INC.

PA Beutel BA, Joesten ME;

XX WPI: 1995-051992/07.

PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
factor - modulating, esp. inhibiting, its activity, useful in  
treating cancer, preventing metastasis, and diagnosis.

PS Claim 3: Page 25: 44pp: English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AA08164-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC with its receptor and heparin. These oligonucleotides may inhibit  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.

SO Sequence 4 BP: 0 A: 1 C: 2 G: 1 U: 0 other:

Query Match 100.0%; Score 1: DB 16: Length 4:  
Best Local Similarity 100.0%; Pred. No. 0:

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
1  
4 G 4

RESULT 7

ID AA081665 standard; RNA: 4 BP.

XX AA081665:

DT 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #2.

KW Basic: fibroblast growth factor; bFGF; stem-loop structure;  
KW bubble structure; pseudoknot; receptor; heparin; competition;  
KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
KW metastasis; diagnosis; gene therapy; ss.

XX Synthetic.

PN WO9500528-A.

PD 05-JAN-1995.

PF 17-JUN-1994: 94WO-US06884.

XX 18-JUN-1993: 93US-0079677.

XX 07-JAN-1994: 94US-0179491.

PA (PHAR-) PHARMAGENICS INC.

PI Beutel BA, Joesten ME;

XX WPI: 1995-051992/07.

PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
factor - modulating, esp. inhibiting, its activity, useful in  
treating cancer, preventing metastasis, and diagnosis.

PS Claim 3: Page 25: 44pp: English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AA08164-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC with its receptor and heparin. These oligonucleotides may inhibit  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.

SO Sequence 4 BP: 0 A: 2 C: 1 G: 1 U: 0 other:

Query Match 100.0%; Score 1: DB 16: Length 4:  
Best Local Similarity 100.0%; Pred. No. 0:

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
1  
3 g 3

RESULT 8

ID AA081665/C standard; RNA: 4 BP.

XX AA081665:

DT 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #2.

KW Basic: fibroblast growth factor; bFGF; stem-loop structure;  
KW bubble structure; pseudoknot; receptor; heparin; competition;  
KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
KW metastasis; diagnosis; gene therapy; ss.

XX Synthetic.

PN WO9500528-A.

PD 05-JAN-1995.

PF 17-JUN-1994: 94WO-US06884.

XX 18-JUN-1993: 93US-0079677.

XX 07-JAN-1994: 94US-0179491.

PA (PHAR-) PHARMAGENICS INC.

PI Beutel BA, Joesten ME;

XX WPI: 1995-051992/07.

PT New oligo-nucleotide(s) that bind to basic fibroblast growth

PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081644-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.

XX Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
 1  
 Db 4 C 4

RESULT 9  
 AAT86385  
 ID AAT86385 standard; DNA: 4 BP.

XX AAT86385;

AC 23-APR-1998 (first entry)

XX Probe for target nucleic acid sequence P0.

DE Point mutation detection; nucleic acid sequence analysis; probe;  
 XX viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /note= "C-5' phosphate"

PN WO9738131-A1.

XX 16-OCT-1997.

XX 11-APR-1996; 96WO-RU00087.

XX 11-APR-1996; 96WO-RU00087.

XX (DYMS/) DYMSHITS G M.  
 PA (IVAN/) IVANOVA E M.  
 PA (KRIV/) KRIVENKO A A.  
 PA (KULI/) KULIKOVA V F.  
 PA (LOKH/) LOKHOV S G.  
 PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;  
 PI Likhov SG, Pyshny DV;  
 XX WPI: 1997-512737/47.  
 XX

PT Detection of target nucleic acid sequence - based on ligation of  
 PT hybridised short probe to flanking target-complementary sequences  
 XX  
 PS Example; Page 4; 15pp; Russian.

CC This sequence represents a probe for the target sequence P0 (shown in  
 CC AAT86376). This sequence was used to test the method of the invention.  
 CC The method of the invention is for detecting a nucleic acid sequence to  
 CC be analysed, and comprises hybridisation of an oligonucleotide probe  
 CC complementary to the sequence to be analysed and bearing a reporter  
 CC group, the novelty is that detection of a sequence is based on the  
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
 CC flanking oligonucleotide sequences (or their derivatives bearing  
 CC polycyclic aromatic groups). The method is especially useful for  
 CC detecting point mutations. Diagnosis of viral, genetic and other  
 CC diseases is also mentioned.

XX Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
 1  
 Db 3 g 3

RESULT 10  
 AAT86385/C  
 ID AAT86385 standard; DNA: 4 BP.

XX AAT86385;

DE 23-APR-1998 (first entry)

XX Probe for target nucleic acid sequence P0.

DE Point mutation detection; nucleic acid sequence analysis; probe;  
 XX viral disease diagnosis; genetic disease diagnosis; ss.

OS Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /note= "C-5' phosphate"

PN WO9738131-A1.

XX 16-OCT-1997.

XX 11-APR-1996; 96WO-RU00087.

XX 11-APR-1996; 96WO-RU00087.

XX (DYMS/) DYMSHITS G M.  
 PA (IVAN/) IVANOVA E M.  
 PA (KRIV/) KRIVENKO A A.  
 PA (KULI/) KULIKOVA V F.  
 PA (LOKH/) LOKHOV S G.  
 PA (PYSH/) PYSHNY D V.

PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;  
 PI Likhov SG, Pyshny DV;  
 XX WPI: 1997-512737/47.  
 XX

PT Detection of target nucleic acid sequence - based on ligation of  
 PT hybridised short probe to flanking target-complementary sequences  
 XX  
 PS Example; Page 4; 15pp; Russian.

XX This sequence represents a probe for the target sequence P0 (shown in  
 CC AAT86376). This sequence was used to test the method of the invention.  
 CC The method of the invention is for detecting a nucleic acid sequence to  
 CC be analysed, and comprises hybridisation of an oligonucleotide probe  
 CC complementary to the sequence to be analysed and bearing a reporter  
 CC group, the novelty is that detection of a sequence is based on the  
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
 CC flanking oligonucleotide sequences (or their derivatives bearing  
 CC polycyclic aromatic groups). The method is especially useful for  
 CC detecting point mutations. Diagnosis of viral, genetic and other  
 CC diseases is also mentioned.

SO Sequence 4 BP: 1 A; 2 G; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 g 1  
 Db 4 G 4

## RESULT 11

AA77252  
 ID AAT77252 standard; DNA: 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;  
 KW immune response; antigen; naked gene expression vector; IgE;  
 KM antibody; immunotherapy; ss.

XX Synthetic.

OS WO9728259-A1.

PN 07-AUG-1997.

PD 28-JAN-1997; 97WO-US01277.

PF 30-JAN-1996; 96US-0593554.

PR (REGC ) UNIV CALIFORNIA.

PA Carson DA, Raz E;

PI WP1: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic

PT polynucleotide - useful for selectively enhancing the TH1 immune

PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide  
 CC (ISP) comprised of at least one strand of a palindrome, which includes  
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine  
 CC and guanine residues. ISP's could be used in vaccination methods  
 CC for enhancing the immune response of a host to an antigen. Administration  
 CC of naked gene expression vectors which encode antigens or their  
 CC immunostimulatory fragments suppresses IgE antibody production  
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.  
 CC Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 3 g 3

## RESULT 12

AA77252/C  
 ID AAT77252 standard; DNA: 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;  
 KW immune response; antigen; naked gene expression vector; IgE;  
 KM antibody; immunotherapy; ss.

XX Synthetic.

OS WO9728259-A1.

PN 07-AUG-1997.

PD 28-JAN-1997; 97WO-US01277.

PF 30-JAN-1996; 96US-0593554.

PR (REGC ) UNIV CALIFORNIA.

PA Carson DA, Raz E;

PI WP1: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic

PT polynucleotide - useful for selectively enhancing the TH1 immune

PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide  
 CC (ISP) comprised of at least one strand of a palindrome, which includes  
 CC at least one dinucleotide consisting of adjacent, unethylated cytosine  
 CC and guanine residues. ISP's could be used in vaccination methods  
 CC for enhancing the immune response of a host to an antigen. Administration  
 CC of naked gene expression vectors which encode antigens or their  
 CC immunostimulatory fragments suppresses IgE antibody production  
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.  
 CC Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 2 G 2

## RESULT 13

AA17191  
 ID AAL17191 standard; CDNA: 4 BP.

AC AAL17191;

DT 07-DEC-2001 (first entry)

PR 14-JAN-2000; 2000US-0176077.  
PR 14-MAR-2000; 2000US-0189167.  
PR 24-MAR-2000; 2000US-0192099.  
PR 29-MAR-2000; 2000US-0193480.  
PR 15-MAY-2000; 2000US-0205230.  
PR 09-JUN-2000; 2000US-0211315.  
PR 25-JUL-2000; 2000US-0220534.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Lillie J, Xu Y, Wang Y, Stelmann K;  
XX  
DR WPI: 2001-451856/48.  
XX  
PT New peptide useful as a marker for the diagnosis of breast cancer -  
PS  
XX Claim 1: Page 1720; 365pp; English.

The invention relates to human breast cancer expressed polynucleotides (AAI07544-AAI26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded CC polypeptides are also useful for isolating compounds with cytostatic CC activity.  
XX

Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

```

Query Match      100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 9 1
        | |
Db       3 G 3

```

XX	RESULT 15
XX	AAI24357/C
XX	ID AAI24357 standard; cDNA; 4 BP.
XX	AC AAI24357;
XX	DT 07-DEC-2001 (first entry)
XX	DE Human breast cancer expressed polynucleotide
XX	XX Human; breast cancer; cell marker; cytosol
XX	XX Homo sapiens.
XX	PN WO200151628-A2.
XX	PD 19-JUL-2001.
XX	PF 10-JAN-2001; 2001WO-US00798.
XX	PR 14-JAN-2000; 2000US-0176077.
PR	14-MAR-2000; 2000US-0189167.
PR	24-MAR-2000; 2000US-0192099.
PR	29-MAR-2000; 2000US-0193480.
PR	15-MAY-2000; 2000US-0205230.
PR	09-JUN-2000; 2000US-0211315.
PR	25-JUL-2000; 2000US-0220534.
XX	XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	XX Lillie J, Xu Y, Wang Y, Steilmann K;
XX	XX WPI: 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer -  
 PS Claim 1: Page 3087: 3695pp: English.

CC The invention relates to human breast cancer expressed polynucleotides  
 CC (AA07544-AA026789) and methods of assessing whether a patient is  
 CC afflicted with breast cancer by examining the correlation between the  
 CC expression of certain markers and the cancerous state of breast cells.  
 CC The polynucleotides and encoded polypeptides are potential markers for  
 CC detecting, diagnosing, monitoring, characterizing treating and  
 CC potentially preventing breast cancer. The polynucleotides and encoded  
 CC polypeptides are also useful for isolating compounds with cytostatic  
 CC activity.

SO Sequence 4 BP: 0 A: 1 C: 0 G: 3 T: 0 other;

Query Match 100.0%; Score 1: DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 3 G 3

#### RESULT 16

ID AAF61450 standard; RNA: 4 BP.

XX AAF61450;

DT 18-JUN-2001 (first entry)

DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.

KM Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;

XX cyclin E2P1; vasotrophic; gene therapy; cell cycle arrest; ss.

OS Synthetic.

PN WO200121789-A1.

XX 29-MAR-2001.

XX 22-SEP-1999; 99WO-EP07049.

XX 22-SEP-1999; 99WO-EP07049.

XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.

XX Grassl G, Kuhn AC, Kandolf R;

XX WPI: 2001-257985/26.

XX Claim 12: Page 28: 40pp: German.

CC This invention describes a novel catalytic RNA molecule which is directed  
 CC against mRNA molecules (11) which encode the cell-relevant protein cyclin  
 CC E or E2P1. The products of the invention have vasotrophic activity and can  
 CC be used for gene therapy. The use of (11), or a DNA molecule or a plasmid  
 CC of the invention is claimed for obtaining a vector for gene therapy and  
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic  
 CC compositions containing these components are also claimed. (11)  
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin  
 CC E and E2P1.

SO Sequence 4 BP: 2 A: 0 C: 1 G: 0 U: 1 other;

Query Match 100.0%; Score 1: DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 2 g 2

#### RESULT 17

ID AAN93676/c

XX AAN93676 standard; DNA: 5 BP.

AC AAN93676;

DT 24-JUN-1990 (first entry)

DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber  
 DE variant (HSV-c) and HSV grape variant (HSV-g).

XX Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.

OS Hop growth retarding viroid.

PN JP01040000-A.

XX 10-FEB-1989.

XX 05-AUG-1987; 87JP-0194377.

XX 05-AUG-1987; 87JP-0195377.

XX (YUKI ) YUKI GOSHI YAKUHIN.

XX WPI: 1989-089715/12.

XX Fractionating and detecting hop growth retarding viroids -

XX using synthetic DNA probe contg. specific base sequence

XX Disclosure: page 3; 5pp: Japanese.

XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.

XX HSV, HSV-c and HSV-g are fractionated and detected using the synthetic

XX probe. The probe is 15-25mer. The probe can be used to diagnose HSV

XX infections in plants.

XX Sequence 5 BP: 1 A: 3 C: 0 G: 1 T: 0 other;

#### RESULT 18

ID AAQ68752 standard; DNA: 5 BP.

XX AAQ68752;

XX 22-FEB-1995 (first entry)

XX CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.

XX Polymerase chain reaction; primer; PCR; amplify; heavy; light;

XX chain; complementarity determining region; CDR; variable; constant;

XX region; monoclonal antibody; Mab; binding affinity; EDTA; DOTA;



KW tumour; cancer; colorectal; breast; metal chelate; hapten; ss.  
 XX  
 OS Synthetic.

XX AU9350602-A.

XX 26-MAY-1994.

XX 10-NOV-1993; 93AU-0050602.

XX 12-NOV-1992; 92US-0975230.

XX (HYBR-) HYBRITTECH INC.

XX Ahrweiler PM, Moore MD;

XX WPI: 1994-209063/26.

XX P-PSDB; AAR54150.

PT Polypeptide used in imaging and treatment of carcinomas and  
 PT tumours - comprising substd antibody CDR having binding affinity  
 PT for metal chelate of EDTA or DETA or analogues

PS Claim 25; Fig 3A: 61pp; English.

CC The sequences given in AA068747-57 encode the wild type and mutagenised  
 CC versions of the complementarity determining region 1 (CDR1) of the  
 CC antibody designated CHA255. CHA255 is a murine monoclonal antibody  
 CC (Mab) which is capable of binding complexes. Mutagenesis of these  
 CC CDRs, causes the production of polypeptides with a particularly  
 CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3  
 CC of the heavy chain, and CDR2 and -3 of the light chain were targeted  
 CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255  
 CC heavy chain, five of seven residues of light chain CDR and six of  
 CC nine light chain CDR3 residues were specifically targeted for  
 CC codon-based mutagenesis. The mutagenised MAB's can be used in  
 CC compositions for in vivo imaging of malignant tissues or tumours. They  
 CC are also useful for the treatment of malignant tissues or tumours. eg.  
 CC colorectal or breast cancer. Both methods involve the use of  
 CC radiolabelled which bind to metal chelates or haptens which are  
 CC specifically delivered to the target site by a targeting molecule. CDR  
 CC derived peptides may be used to construct bi-functional antibodies  
 CC having dual specificities, or as donor or recipients of CDR sequences.

SO Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 Other;

Query Match 100.0%; Score 1; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 1 g 1

RESULT 19  
 AA081667/c  
 ID AA081667 standard; RNA: 5 BP.

XX AA081667;

DT 29-SEP-1995 (first entry)

DE bFGF binding oligomer core sequence #4.

KW Basic: fibroblast growth factor; bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.

OS Synthetic.

PN MO9500528-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94MO-US06884.

XX 18-JUN-1993; 93US-0079677.

XX 07-JAN-1994; 94US-0179491.

XX (PHAR-) PHARMAGENICS INC.

XX Beutel BA, Joesten ME;

XX WPI: 1995-051992/07.

PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.

PS Claim 3; Page 25; 44pp; English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.

SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 Other;

Query Match 100.0%; Score 1; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 5 G 5

RESULT 20  
 AAT12043/c  
 ID AAT12043 standard; RNA: 5 BP.

XX AAT12043;

DT 17-JUL-1996 (first entry)

DE Cleavable replicable-inhibiting sequence.

KW Ribozyme; hairpin; hammerhead; probe; MDV-1; multidomain-1;  
 KW replication; cleavage; ss.

OS Synthetic.

PN US5472840-A.

XX 05-DEC-1995.

XX 30-SEP-1988; 88US-0252243.

XX 17-DEC-1990; 90US-0630288.

XX 30-SEP-1988; 88US-0252243.

XX 22-JUN-1989; 89US-0370218.

XX (STAD ) AMOCO CORP.  
PA Stefano JF;  
XX WPI: 1996-029807/03.  
XX Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and  
PT cleavable replicable-inhibiting sequence.  
PS Claim 4: Column 62; 43pp: English.  
XX  
CC A composition comprises RNA of formula P4-P1-P2-P3 (1a), a nucleic  
CC acid of formula R1-R2 (111), where (1a) and (111) bind to a target  
CC nucleic acid of formula X2-X1-X3 (11) to form a hammerhead ribozyme,  
CC where P1 is a MDV-1 sequence capable of autocatalytic replication in  
CC the absence of P3; P2 is a sequence (AA112042 or AA112044) that binds  
CC to (11) and forms a cleavage site between P1 and P3; P3 (AA112043)  
CC is an inhibitory element that binds to X2 and interacts with a  
CC region of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes  
CC nucleotides to form the ribozyme with X1 and P2, or is the terminal  
CC nucleotide of P1; X1 is a target region of (11); X2 and X3 are  
CC terminal nucleotides or second or third target regions of (11); R1  
CC is a ribozyme-forming area of (111); and R2 is a terminal nucleotide  
CC of R1 or an area of (111) that binds to (11). X1 and R1 are  
CC mutually exclusive and are represented by the sequences of AA112040 and  
CC AA112041. For hairpin ribozymes, P2 is AA112045 and R1 is AA112046.  
CC Probes bearing ribozymes are produced in a single step by transcription  
CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes  
CC produce specific cleavage events, leading to a product RNA with  
CC defined replication properties.  
XX  
SQ Sequence 5 BP: 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 17; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 5 G 5

RESULT 21  
AAV61663  
ID AAV61663 standard; DNA: 5 BP.  
XX  
AC AAV61663;  
XX  
DT 03-DEC-1998 (first entry)  
XX  
DE Fusarium sp. 18S rRNA DNA fragment #7.  
XX  
KW 18S rRNA: detection; identification; fungus; ss.  
XX  
OS Fusarium sp.  
XX  
PN JP10234380-A.  
XX  
PD 08-SEP-1998.  
XX  
PF 28-FEB-1997; 97JP-0062104.  
XX  
PR 28-FEB-1997; 97JP-0062104.  
XX  
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
XX  
DR WPI: 1998-535034/46.  
XX  
PT Use of oligo:nucleotide for detecting and identification of fungus  
PT of Fusarium genus - as primer or probe to detect or identify  
PT microbes rapidly and exactly

XX  
PS Claim 1: Page 7; 20pp: Japanese.  
XX  
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
CC used in a method for the detection and identification of a fungus of  
CC Fusarium genus. The process can be used to detect or identify microbes  
CC rapidly and exactly.  
XX  
SQ Sequence 5 BP: 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 5 G 5

RESULT 22  
AAV61663/C  
ID AAV61663 standard; DNA: 5 BP.  
XX  
AC AAV61663;  
XX  
DT 03-DEC-1998 (first entry)  
XX  
DE Fusarium sp. 18S rRNA DNA fragment #7.  
XX  
KW 18S rRNA: detection; identification; fungus; ss.  
XX  
OS Fusarium sp.  
XX  
PN JP10234380-A.  
XX  
PD 08-SEP-1998.  
XX  
PF 28-FEB-1997; 97JP-0062104.  
XX  
PR 28-FEB-1997; 97JP-0062104.  
XX  
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
XX  
DR WPI: 1998-535034/46.  
XX  
PT Use of oligo:nucleotide for detecting and identification of fungus  
PT of Fusarium genus - as primer or probe to detect or identify  
PT microbes rapidly and exactly  
XX  
PS Claim 1: Page 7; 20pp: Japanese.  
XX  
CC AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
CC used in a method for the detection and identification of a fungus of  
CC Fusarium genus. The process can be used to detect or identify microbes  
CC rapidly and exactly.  
XX  
SQ Sequence 5 BP: 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 19; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 5 G 5

RESULT 23  
AAV62299  
ID AAV62299 standard; DNA: 5 BP.  
XX

```

AC AA196299;
XX
XX 08-APR-1998 (first entry)
XX
XX Fungal telomeric nucleic acid sequence.
XX
XX
XX Detection: eukaryotic pathogen: telomeric nucleic acid sequence;
XX telomerase activity; diagnosis: fungal infection; fungus: fungi;
XX malarial infection; malaria: ss.
XX
XX Saccharomyces cerevisiae.
XX
XX US5695932-A.
XX
XX 09-DEC-1997.
XX
XX 13-MAY-1993: 93US-0060952.
XX
XX 13-MAY-1993: 93US-0060952.
XX 13-MAY-1992: 92US-0862438.
XX 24-MAR-1993: 93US-0038766.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
XX WPI: 1998-041292/04.
XX
XX Detection of eukaryotic pathogens, especially fungal or Plasmodium
XX spp. - by detecting telomerase activity
XX
XX
XX Claim 5: Columns 81-82: 82pp: English.
XX
XX The present sequence can be used in a novel method for detecting a
XX eukaryotic pathogen in a patient. The method comprises obtaining a
XX sample of somatic tissue or cells from the patient, determining if
XX telomerase activity is present and correlating this with the
XX presence of the pathogen. The method is useful for diagnosis of
XX fungal infections, especially a fungus of the genus Candida,
XX Kluveromyces, Saccharomyces, Sporobolix, Coccidioides,
XX Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
XX Aspergillus, Mucor or Rhizopus, or malarial infections, especially
XX Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
XX
XX Sequence 5 BP: 0 A; 0 C; 3 G; 2 T; 0 other:

Query Match          100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   1
Db 2 g 2

RESULT 24
AA10695
ID AA210695 standard; DNA: 5 BP.
XX
XX AA210695;
XX
XX 23-NOV-1999 (first entry)
XX
XX Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX skin cancer; ss.
XX
XX Synthetic.

```

```

XX
XX GB2336157-A.
XX
XX 13-OCT-1999.
XX
XX 24-MAR-1999: 99GB-0006758.
XX
XX 26-MAR-1998: 98US-0048927.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX WPI: 1999-543520/46.
XX
XX DNA fragments useful for increasing p53 activity in a cell and reducing
XX susceptibility to UV-induced hyperproliferative diseases -
XX
XX Claim 11: Page 30; 44pp: English.
XX
XX AA210692-97 represent DNA fragments that are used for increasing p53
XX activity in a cell. The oligonucleotides are UV mimetics and
XX protect cells against subsequent exposure to UV-irradiation or
XX chemicals. The oligonucleotides are useful for increasing p53 activity
XX in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX and reducing susceptibility to skin cancer.
XX
XX Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other:

Query Match          100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
   1
Db 1 g 1

RESULT 25
AA210696/C
ID AA210696 standard; DNA: 5 BP.
XX
XX AA210696;
XX
XX 23-NOV-1999 (first entry)
XX
XX Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX skin cancer; ss.
XX
XX Synthetic.
XX
XX GB2336157-A.
XX
XX 13-OCT-1999.
XX
XX 24-MAR-1999: 99GB-0006758.
XX
XX 26-MAR-1998: 98US-0048927.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX WPI: 1999-543520/46.
XX
XX DNA fragments useful for increasing p53 activity in a cell and reducing

```

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acceptability to UV-induced hyperproliferative diseases -  
claim 11: Page 30: 44pp: English.

claim 11: Page 30: 44pp: English.  
w10692-97 represent DNA fragments that are used for increasing p53  
activity in a cell. The oligonucleotides are UV-irradiation or  
react cells against subsequent exposure to UV-induced hyperproliferative  
hemicals. The oligonucleotides are useful for increasing p53 activity  
in a cell, reducing the susceptibility to UV-induced dermatitis, allergic  
diseases, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
and reducing susceptibility to skin cancer.

Sequence 5 BP: 2 A: 2 C: 0 G: 1 T: 0 other:

try Match 100.0%; Score 1; DB 20; Length 5;  
at Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

1 g 1  
1  
5 C 5

ULF 26  
11611  
AAZ11611 standard; DNA: 5 BP.

AAZ11611:

16-NOV-1999 (first entry)

DNA enhancer sequence present in an upstream element:  
Plant promoter: TATA motif; transcription start site: upstream element;  
gene expression: oxalate oxidase; plant resistance; pathogen: maize;

Ubi-1 promoter: Syn II core promoter; ss.  
Synthetic.

MO9943838-A1.  
02-SEP-1999.

99WO-US03863.  
23-FEB-1999; 98US-0028819.

24-FEB-1998; 98US-0028819.  
(PION-) PIONEER HI-BRED INT INC.

Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

WPI: 1999-540601/45.

New synthetic promoter functional in plants to provide non-tissue  
specific, constitutive expression, particularly of oxalate oxidase for  
increased resistance to pathogens.

Claim 39: Page 47: 61pp: English.

The invention provides a new synthetic plant promoter that comprises a  
TATA motif; a transcription start site (TSS) and a region between TATA  
and TSS containing at least 64 percent GC content. The synthetic core  
promoter, optionally containing additional upstream elements are used to  
increase expression, provides non-tissue specific, constitutive  
transcription of heterologous genes in any sort of plant, especially the  
gene for oxalate oxidase for increasing plant resistance to pathogens.  
The upstream activating elements can be used to increase transcription  
from any promoter. A combination of the synthetic core promoter with  
synthetic upstream elements can induce expression 10 times greater than  
provided by the maize Ubi-1 promoter. The present sequence element

CC sequence.

XX Sequence 5 BP: 1 A: 1 C: 2 G: 1 T: 0 other:

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

OY 1 g 1  
1  
2 g 2

RESULT 27  
AAZ11611/C  
ID AAZ11611 standard; DNA: 5 BP.

AAZ11611:

16-NOV-1999 (first entry)

DNA enhancer sequence present in an upstream element:  
Plant promoter: TATA motif; transcription start site: upstream element;  
gene expression: oxalate oxidase; plant resistance; pathogen: maize;

Ubi-1 promoter: Syn II core promoter; ss.  
Synthetic.

MO9943838-A1.  
02-SEP-1999.

99WO-US03863.  
23-FEB-1999; 98US-0028819.

24-FEB-1998; 98US-0028819.  
(PION-) PIONEER HI-BRED INT INC.

Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

WPI: 1999-540601/45.

New synthetic promoter functional in plants to provide non-tissue  
specific, constitutive expression, particularly of oxalate oxidase for  
increased resistance to pathogens.

Claim 39: Page 47: 61pp: English.

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TATA motif; a transcription start site (TSS) and a region between TATA  
and TSS containing at least 64 percent GC content. The synthetic core  
promoter, optionally containing additional upstream elements are used to  
increase expression, provides non-tissue specific, constitutive  
transcription of heterologous genes in any sort of plant, especially the  
gene for oxalate oxidase for increasing plant resistance to pathogens.  
The upstream activating elements can be used to increase transcription  
from any promoter. A combination of the synthetic core promoter with  
synthetic upstream elements can induce expression 10 times greater than  
provided by the maize Ubi-1 promoter. The present sequence element  
represents a DNA enhancer OSC-like motif present in an upstream element  
sequence.

Sequence 5 BP: 1 A: 1 C: 2 G: 1 T: 0 other:

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

OY 1 g 1  
1

Db 5 C 5

RESULT 28

AAV72347/C

ID AAV72347 standard; DNA; 5 BP.

XX AAV72347;

XX 28-JUL-1999 (first entry)

DE US5908745 primer #4.

XX DNA sequencing; disease-associated allele; polyacrylamide matrix;  
 KW continuous/contiguous stacking hybridization technique; detection;  
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI; 1999-347002/29.

XX Detecting disease-associated alleles using continuous/contiguous  
 PT stacking hybridization as a diagnostic tool

XX Example 1; Column 9; 16pp; English.

XX This invention describes novel methods for sequencing and analysing DNA  
 CC samples to detect disease-associated alleles, by continuous/contiguous  
 CC stacking hybridization techniques (utilizing universal bases) with  
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may  
 CC be used to detect multiple DNA base mutations which are specific for  
 CC certain diseases. The methods of the invention provide accurate and  
 CC efficient and sensitive methods for diagnosing disease by detecting  
 CC multiple mutation sequences in patient DNA. The method require the  
 CC minimum number of oligonucleotides and few stacking hybridization steps  
 CC than prior art methods. The methods are also efficient enough to  
 CC discriminate between perfect and imperfect duplexes. The methods also  
 CC obviate the need for the fabrication and array placement of large numbers  
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

Db 5 C 5

RESULT 29

AAV72348

ID AAV72348 standard; DNA; 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

XX

DE US5908745 primer #5.

XX DNA sequencing; disease-associated allele; polyacrylamide matrix;  
 KW continuous/contiguous stacking hybridization technique; detection;  
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

XX 16-JAN-1996; 96US-0587332.

XX 16-JAN-1996; 96US-0587332.

XX (UYCH-) UNIV CHICAGO.

XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

XX Parinov SV, Yershov GM;

XX WPI; 1999-347002/29.

XX Detecting disease-associated alleles using continuous/contiguous  
 PT stacking hybridization as a diagnostic tool

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 CC samples to detect disease-associated alleles, by continuous/contiguous  
 CC stacking hybridization techniques (utilizing universal bases) with  
 CC oligonucleotides immobilized on polyacrylamide matrices. The methods may  
 CC be used to detect multiple DNA base mutations which are specific for  
 CC certain diseases. The methods of the invention provide accurate and  
 CC efficient and sensitive methods for diagnosing disease by detecting  
 CC multiple mutation sequences in patient DNA. The method require the  
 CC minimum number of oligonucleotides and few stacking hybridization steps  
 CC than prior art methods. The methods are also efficient enough to  
 CC discriminate between perfect and imperfect duplexes. The methods also  
 CC obviate the need for the fabrication and array placement of large numbers  
 CC of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

Db 2 g 2

RESULT 30

AAV72348/C

ID AAV72348 standard; DNA; 5 BP.

XX AAV72348;

XX 28-JUL-1999 (first entry)

XX US5908745 primer #5.

XX DNA sequencing; disease-associated allele; polyacrylamide matrix;  
 KW continuous/contiguous stacking hybridization technique; detection;  
 KM mutation; diagnosis; primer; ss.

XX Synthetic.

XX US5908745-A.

XX 01-JUN-1999.

```
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
XX
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9, 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;
```

```
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 5 G 5

RESULT 31
AAV72349/c
ID AAV72349 standard; DNA: 5 BP.
XX
XX AAV72349;
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #6.
XX
XX DE
XX
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX PN
XX
XX 01-JUN-1999.
XX
XX PD
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX PF
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX PR
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX PA
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
XX
XX DR
```

```
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9, 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;
```

```
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 5 G 5

RESULT 32
AAV72350/c
ID AAV72350 standard; DNA: 5 BP.
XX
XX AAV72350;
XX
XX 28-JUL-1999 (first entry)
XX
XX US5908745 primer #7.
XX
XX DE
XX
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX
XX OS
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX PN
XX
XX 01-JUN-1999.
XX
XX PD
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX PF
XX
XX 16-JAN-1996; 96US-0587332.
XX
XX PR
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX PA
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
XX Parinov SV, Yershov GM;
XX WPI: 1999-347002/29.
XX
XX DR
XX
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9, 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
```

CC certain diseases. The methods of the invention provide accurate and  
CC efficient and sensitive methods for diagnosing disease by detecting  
CC multiple mutation sequences in patient DNA. The method require the  
CC minimum number of oligonucleotides and few stacking hybridization steps  
CC than prior art methods. The methods are also efficient enough to  
CC discriminate between perfect and imperfect duplexes. The methods also  
CC obviate the need for the fabrication and array placement of large numbers  
CC of immobilized oligomers.

SO Sequence 5 BP: 3 A: 2 C: 0 G: 0 U: 0 other:

Query Match Best Local Similarity 100.0%; Score 1: DB 20: Length 5:

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
DB 5 G 5

RESULT 33

AA56964 ID AAX56964 standard: DNA: 5 BP.

AC AAX56964:

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene: modulator; liposome: primer; antisense; anticancer; inhibition;  
cell growth inhibitor; treatment; cancer; ras protein; ss.

US Synthetic.

PN W09922772-A1.

PD 14-MAY-1999.

PF 28-OCT-1998: 98WO-US22821.

PR 31-OCT-1997: 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

PT Templin MV;

DE WPI: 1999-313181/26.  
Liposome-encapsulated oligonucleotides useful for treating or  
preventing cancers associated with ras gene activation

Example 1: Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 20: Length 5:

Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
DB 2 g 2

RESULT 34

AA56964/c ID AAX56964 standard: DNA: 5 BP.

AC AAX56964:

DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

KW Ras gene: modulator; liposome: primer; antisense; anticancer; inhibition;  
cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

PN W09922772-A1.

PD 14-MAY-1999.

PF 28-OCT-1998: 98WO-US22821.

PR 31-OCT-1997: 97US-0961469.

PA (ISIS-) ISIS PHARM INC.

PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

PT Templin MV;

DE WPI: 1999-313181/26.  
Liposome-encapsulated oligonucleotides useful for treating or  
preventing cancers associated with ras gene activation

Example 1: Page 107; 120pp; English.

CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

SO Sequence 5 BP: 1 A: 2 C: 2 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 20: Length 5:

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
DB 4 G 4

RESULT 35

AA56964 ID AAX21608 standard: DNA: 5 BP.

AC AAX21608:

XX	14-MAY-1999	(first entry)
DT		
XX		
DE	Mutant H-ras specific antisense oligo ISIS #2563.	
XX		
KM	Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;	
KW	diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.	
US		
XX	Synthetic.	
PN	WO9902732-A1.	
XX		
XX	21-JAN-1999.	
PD		
XX		
XX	06-JUL-1998; 98WO-US13966.	
PK		
XX	08-JUL-1997; 97US-0889296.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
PI		
XX	Cowser LM, Manoharan M, Monia BP;	
DR		
XX	WPI: 1999-120932/10.	
XX		
PT	New oligonucleotide targeting human N-ras nucleic acid - is	
PT	capable of inhibiting human N-ras expression, useful for preventing	
PT	or treating conditions arising from the activation of a human N-ras	
PT	oncogene	
XX		
PS	Disclosure; Page 22; 97pp; English.	
XX		
CC	The invention relates to oligonucleotides, which target a nucleic acid	
CC	encoding human N-ras, and are capable of inhibiting human N-ras	
CC	expression. The antisense oligonucleotides form a pharmaceutical	
CC	composition, which is useful for modulating the expression of human	
CC	N-ras, inhibiting the proliferation of cancer cells, and preventing or	
CC	treating conditions arising from the activation of a human N-ras	
CC	oncogene. The oligonucleotides are also useful in diagnostics,	
CC	therapeutics, and as research reagents and kits. The oligonucleotides	
CC	enable the specific modulation of activated human N-ras expression,	
CC	which is associated with tumour formation. Sequences AAX21601-619	
CC	represent antisense oligonucleotides targeted to mutant H-ras.	
XX		
SO	Sequence 5 BP: 1 A; 2 C; 2 G; 0 U; 0 other;	
Query Match	100.0%; Score 1; DB 20; Length 5;	
Best local Similarity	100.0%; Prd. No. 0;	
Matches 1; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 g 1	
	1	
Db	2 g 2	
RESULT 36		
AAX21608/C		
ID AAX21608 standard; DNA; 5 BP.		
XX		
AC AAX21608;		
XX		
DT 14-MAY-1999 (first entry)		
XX		
DE Mutant H-ras specific antisense oligo ISIS #2563.		
XX		
KM Human: N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;		
KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.		
OS Synthetic.		
XX		
XX WO9902732-A1.		
PN		
XX		
XX 21-JAN-1999.		

```
XX PF 06-JUL-1998; 98MO-US13966.
XX XX
PR 08-JUL-1997; 97US-0889296.
XX XX
PA (ISIS-) ISIS PHARM INC.
XX PI Cowser LM, Manoharan M, Montla BP;
XX XX WPI: 1999-120932/10.
DR XX
PT New oligonucleotide targetting human N-ras nucleic acid - is
PT capable of inhibiting human N-ras expression, useful for preventing
PT or treating conditions arising from the activation of a human N-ras
PT oncogene
PS
PS Disclosure: Page 22; 97Pp; English.
XX XX
CC The invention relates to oligonucleotides, which target a nucleic acid
CC encoding human N-ras, and are capable of inhibiting human N-ras
CC expression. The antisense oligonucleotides form a pharmaceutical
CC composition, which is useful for modulating the expression of human
CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
CC treating conditions arising from the activation of a human N-ras
CC oncogene. The oligonucleotides are also useful in diagnostics.
CC Therapeutics, and as research reagents and kits. The oligonucleotides
CC enable the specific modulation of activated human N-ras expression,
CC which is associated with tumour formation. Sequences AAX21601-619
CC represent antisense oligonucleotides targeted to mutant H-ras.
SO
Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match          100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy      1 g 1
        |
Db       4 G 4

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX
AC AAA56981;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human colon cancer cell cDNA sequence #109.
XX
KW Human: arbitrary primer; cDNA synthesis; conlig sequence construction;
KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX
OS Homo sapiens.
XX
PN WO200031299-A2.
XX
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99WO-US27430.
XX
PR 20-NOV-1998; 98US-0196716.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Simpson AUG, Dias Neto E, Brentani RR;
XX
DR WPI: 2000-400100/34.
XX
XX Method for determining open reading frames of the genome of an organism
XX using primers at low stringency conditions, useful in the construction
```



PT of contigs or constructs of sequenced nucleic acid molecules -  
XX  
PS Example 6; Page 47; 113pp; English.  
XX  
CC The present sequence is a cDNA sequence obtained using a method for  
CC determining open reading frames (ORFs) of the genome of an  
CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse  
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
CC incubated under low stringency conditions to yield single stranded  
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
CC than providing nucleotide sequence information from the non-coding  
CC terminal of nucleic acid molecules, the method provides information on  
CC the more interesting and relevant internal portions, such as ORFs. The  
CC method also permits the construction of contigs of sequenced nucleic  
CC acid molecules.  
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 3 g 3  
RESULT 38  
ID AAA56981/c  
XX AAA56981 standard; cDNA; 5 BP.  
AC  
XX AAA56981;  
XX  
DT 14-NOV-2000 (first entry)  
XX  
DE Human colon cancer cell cDNA sequence #109.  
XX  
KW Human: arbitrary primer; cDNA synthesis; contig sequence construction;  
XX open reading frame; ORF; low stringency; cDNA sequencing; ss.  
OS Homo sapiens.  
XX  
PN WO200031299-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 19-NOV-1999; 99WO-US27430.  
XX  
PR 20-NOV-1998; 98US-0196716.  
XX  
PA (LUDM-) LUDWIG INST CANCER RES.  
XX  
PI Simpson AJG, Dias Neto E, Brentani RR;  
XX WPI: 2000-400100/34.  
XX  
DR WPI: 2000-400100/34.  
XX  
PT Method for determining open reading frames of the genome of an organism  
PT using primers at low stringency conditions, useful in the construction  
PT of contigs or constructs of sequenced nucleic acid molecules -  
XX  
XX Example 6; Page 47; 113pp; English.  
XX  
CC The present sequence is a cDNA sequence obtained using a method for  
CC determining open reading frames (ORFs) of the genome of an  
CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
CC with a single, arbitrary primer, Moloney murine leukemia virus reverse  
CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
CC incubated under low stringency conditions to yield single stranded  
CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
CC than providing nucleotide sequence information from the non-coding  
CC terminal of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The  
CC method also permits the construction of contigs of sequenced nucleic  
CC acid molecules.  
SQ Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other:  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
DB 5 G 5  
RESULT 39  
ID AA293601  
XX AA293601 standard; DNA; 5 BP.  
AC  
XX AA293601;  
XX  
DT 24-JUL-2000 (first entry)  
XX  
DE Transcription factor binding site of tobacco gene promoter sequence.  
XX  
KW Regulatory sequence; meristem; genetic engineering;  
XX gene expression; crop protection; transgenic plant; resistance;  
XX tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.  
OS Synthetic.  
XX  
PN Nicotiana acuminata.  
XX  
PD WO200012713-A1.  
XX  
PF 09-MAR-2000.  
XX  
PF 26-AUG-1999; 99WO-AU00692.  
XX  
PR 26-AUG-1998; 98AU-0005498.  
XX  
PA (UYQU ) UNIV QUEBENS LAND.  
XX  
PI Mudge SR, Birch RG;  
XX  
DR WPI: 2000-237875/20.  
XX  
PT Meristem-expressible nucleic acid sequences, useful for producing  
PT transgenic plants with improved characteristics such as resistance to  
PT pathogens  
XX  
PS Example 9; Page 51; 102pp; English.  
XX  
CC Isolated regulatory sequences of plants that are operable in  
CC dividing cells, in particular the meristem cells of plants are useful  
CC in the genetic engineering of plants. The regulatory sequences can  
CC be used to control the expression of foreign genes placed under their  
CC control. Such methods are useful for producing transgenic plants with  
CC altered shape and/or size. The sequences are also useful for  
CC producing transgenic plants capable of rapid regeneration following  
CC harvest or plants having improved resistance to pathogens. This  
CC sequence has been shown to bind a factor involved in the activation  
CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three  
CC times in the meristem regulatory sequence of Tobacco described in  
CC GENSEQ record AA293567.  
XX  
SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other:  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 5 g 5

RESULT 40  
AA293601/C  
ID AA293601 standard; DNA: 5 BP.  
XX  
AC AA293601;

XX 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;  
KW gene expression; crop protection; transgenic plant; resistance;  
KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

XX Synthetic.  
OS Nicotiana acuminata.

XX W0200012713-A1.

XX 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DK WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing  
transgenic plants with improved characteristics such as resistance to  
pathogens

PS Example 9; Page 51; 102pp; English.

CC Isolated regulatory sequences of plants that are operable in  
dividing cells, in particular the meristem cells of plants are useful  
in the genetic engineering of plants. The regulatory sequences can  
be used to control the expression of foreign genes placed under their  
control. Such methods are useful for producing transgenic plants with  
altered shape and/or size. The sequences are also useful for  
producing transgenic plants capable of rapid regeneration following  
harvest or plants having improved resistance to pathogens. This  
sequence has been shown to bind a factor involved in the activation  
of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three  
times in the meristem regulatory sequence of Tobacco described in  
GENESQ record AA293567.

XX Sequence 5 BP: 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 4 G 4

RESULT 41  
AA293602/C  
ID AA293602 standard; DNA: 5 BP.  
XX  
AC AA293602;  
XX

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;  
KW gene expression; crop protection; transgenic plant; resistance;  
KW tobacco; transcription factor; N1R2; nitrate; ss.

XX Synthetic.  
OS Nicotiana acuminata.

XX W0200012713-A1.

XX 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing  
transgenic plants with improved characteristics such as resistance to  
pathogens

PS Example 9; Page 51; 102pp; English.

CC Isolated regulatory sequences of plants that are operable in  
dividing cells, in particular the meristem cells of plants are useful  
in the genetic engineering of plants. The regulatory sequences can  
be used to control the expression of foreign genes placed under their  
control. Such methods are useful for producing transgenic plants with  
altered shape and/or size. The sequences are also useful for  
producing transgenic plants capable of rapid regeneration following  
harvest or plants having improved resistance to pathogens. This  
sequence has been shown to regulate nitrate metabolism in the  
fungus Neurospora crassa. It occurs multiple times in the meristem  
regulatory sequence of Tobacco described in GENESQ record AA293567.

XX Sequence 5 BP: 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 4 G 4

RESULT 42  
AA289330/C  
ID AA289330 standard; DNA: 5 BP.

AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
fat metabolism; ss.

XX Homo sapiens.

XX DE19838837-A1.

PD 02-MAR-2000.

XX 27-AUG-1998; 98DE-1038837.  
PF  
XX  
PR 27-AUG-1998; 98DE-1038837.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
PI Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
PT Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX  
PS Claim 25; Page 12; 38pp; German.  
XX  
CC This invention describes novel recombinant DNA molecules containing  
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
CC cells but not functional in muscle cells or vice versa. The recombinant  
CC DNA molecules are useful for transcription of genes and, with host cells,  
CC used to test for substances that can influence transcription. They can also be  
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
CC metabolism and control of the promoter is useful in combating diseases  
CC with inappropriate fat tissue metabolism. This sequence represents a  
CC fragment of the human UCP-3 promoter which is used to illustrate the  
CC method of the invention.  
SO Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;  
XX  
SO  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 2 C 2  
XX  
RESULT 43  
AAZ89331  
ID AAZ89331 standard; DNA: 5 BP.  
XX  
AC AAZ89331;  
XX  
DT 13-JUN-2000 (first entry)  
XX  
DE Human UCP3 promoter fragment #11.  
XX  
UE UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
KM fat metabolism; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN DE19838837-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 27-AUG-1998; 98DE-1038837.  
XX  
PS 27-AUG-1998; 98DE-1038837.  
PR 27-AUG-1998; 98DE-1038837.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
PI Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
PT Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX

PS Claim 26; Page 12; 38pp; German.  
XX  
XX This invention describes novel recombinant DNA molecules containing  
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
CC cells but not functional in muscle cells or vice versa. The recombinant  
CC DNA molecules are useful for transcription of genes and, with host cells,  
CC used to test for substances that can influence transcription. They can also be  
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
CC metabolism and control of the promoter is useful in combating diseases  
CC with inappropriate fat tissue metabolism. This sequence represents a  
CC fragment of the human UCP-3 promoter which is used to illustrate the  
CC method of the invention.  
SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;  
XX  
SO  
Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 4 g 4  
XX  
RESULT 44  
AAZ89332  
ID AAZ89332 standard; DNA: 5 BP.  
XX  
AC AAZ89332;  
XX  
DT 13-JUN-2000 (first entry)  
XX  
DE Human UCP3 promoter fragment #12.  
XX  
UE UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;  
KM fat metabolism; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN DE19838837-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 27-AUG-1998; 98DE-1038837.  
XX  
PS 27-AUG-1998; 98DE-1038837.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX (NOVO ) NOVO-NORDISK AS.  
PI Esterbauer H, Oberkofler H, Patsch W;  
XX WPI: 2000-272214/24.  
XX  
PT Recombinant fat and muscle tissue specific uncoupling protein 3  
XX promoters useful for identifying UCP3 modulators  
XX  
PS Claim 31; Page 12; 38pp; German.  
XX  
CC This invention describes novel recombinant DNA molecules containing  
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
CC cells but not functional in muscle cells or vice versa. The recombinant  
CC DNA molecules are useful for transcription of genes and, with host cells,  
CC used to test for substances that can influence transcription. They can also be  
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
CC metabolism and control of the promoter is useful in combating diseases  
CC with inappropriate fat tissue metabolism. This sequence represents a  
CC fragment of the human UCP-3 promoter which is used to illustrate the  
CC method of the invention.  
SO Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;  
XX

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 1 1  
1 9 1  
4 9 4  
Search completed: July 15, 2002, 23:10:11  
Job time: 16429 sec

RESULT 4:

AA248433  
ID AA248433 standard; DNA; 5 BP.

AC AA248433;

UT 27-MAR-2000 (first entry)

DE First DNA arm segment.

Microorganism: virus; polymerase chain reaction: food; cosmetic;  
clinical diagnostic; molecular beacon; PCR primer; ss.

OS Synthetic.

PN WO9963112-A2.

PD 09-DEC-1999.

PF 18-MAY-1999; 99WO-US10940.

PR 18-MAY-1998; 98US-0086025.

PR 17-MAY-1999; 99US-0086025.

PA (HUNT-) HUNT WESSON INC.

PI Romick TL, Fraser MS;

DK WPI: 2000-086985/07.

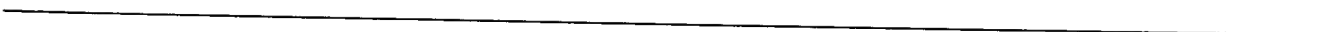
PT Detection of microorganisms and viruses, for use in the food and  
cosmetic industries and for clinical diagnostics

PS Claim 51: Page 40: 63pp: English.

CC The invention provides a novel in vitro method for the detection of  
CC microorganisms and viruses. The method comprises: (1) forming a  
CC polymerase chain reaction (PCR) mixture by combining a predetermined  
CC volume of a sample to be tested for the presence of a nucleic acid  
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer  
CC comprising 5'-GCTAAGCTCTCTAAGC-3', and a second primer comprising  
CC 5'-AGAAGCTCTCTAAGC-3', and PCR reagents; (2) forming a PCR product by  
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,  
CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)  
CC adding a probe containing DNA comprising 5'-GCTGCTCTCTAAGC-3' to  
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with  
CC the nucleic acid sequence, if present, and change the conformation of the  
CC probe; and (4) determining whether or not bacteria are present in the  
CC sample by detecting the conformational change of the probe, a  
CC conformational change indicating the presence of bacteria in the sample.  
CC The methods can be used for the detection of viruses and microorganisms,  
CC including bacteria, yeast, molds and protoista. They can be used in the  
CC food and cosmetic industry and in clinical diagnostics. Using the method  
CC it is not necessary to remove non-hybridized probe from the system.  
SQ Sequence 5 BP: 1 A; 1 C; 2 G; 1 T; 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 9 1



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 : Search time 223.79 Seconds  
(without alignments)  
1.098 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3164\_3164

Perfect score: 191

Scoring table:

OLIGO\_NUC  
Gapop 60.0, Capext 60.0

Searched: 38353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:\*

- 1: /cgn2\_6/plodata/2/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/plodata/2/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/plodata/2/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/plodata/2/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/plodata/2/ina/pCTUS.COMB.seq:\*
- 6: /cgn2\_6/plodata/2/ina/backlist1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	1	2	1	US-08-268-6798-8
2	100.0	1	2	1	US-08-484-192-16
3	100.0	1	2	4	US-08-361-024-3
4	100.0	1	2	4	US-08-361-024-3
5	100.0	1	3	1	US-07-791-213D-46
6	100.0	1	3	1	US-07-791-213D-46
7	100.0	1	3	1	US-07-791-213D-46
8	100.0	1	3	1	US-07-791-213D-62
9	100.0	1	3	1	US-07-791-213D-62
10	100.0	1	3	1	US-08-268-6798-7
11	100.0	1	3	1	US-08-602-036A-2
12	100.0	1	3	1	US-08-602-036A-2
13	100.0	1	3	1	US-08-293-150A-46
14	100.0	1	3	1	US-08-293-150A-46
15	100.0	1	3	1	US-08-293-150A-62
16	100.0	1	3	2	US-08-502-374A-2
17	100.0	1	3	2	US-08-502-374A-2
18	100.0	1	3	2	US-08-502-374A-2
19	100.0	1	3	2	US-08-642-407A-2
20	100.0	1	3	3	US-08-642-407A-2
21	100.0	1	3	3	US-08-873-709-9
22	100.0	1	3	3	US-09-032-365A-36
23	100.0	1	3	4	US-08-793-634B-12
24	100.0	1	3	4	US-08-973-568-55
25	100.0	1	4	1	US-07-755-462-2
26	100.0	1	4	1	US-07-755-462-2
27	100.0	1	4	1	US-08-169-950-6
					Sequence 6, Appl1

28	1	100.0	4	1	US-07-630-288A-7	Sequence 7, Appl1
29	1	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl1
30	1	100.0	4	1	US-07-630-288A-13	Sequence 11, Appl1
31	1	100.0	4	1	US-07-630-288A-13	Sequence 11, Appl1
32	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
33	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl1
34	1	100.0	4	1	US-07-630-288A-34	Sequence 14, Appl1
35	1	100.0	4	1	US-07-630-288A-34	Sequence 14, Appl1
36	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
37	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl1
38	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
39	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
40	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
41	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
42	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
43	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl1
44	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
45	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-268-6798-8  
Sequence 8, Application US/082686798  
Patent No. 5674729  
GENERAL INFORMATION:  
APPLICANT: WIMMER, ECKARD; MOLLA,  
APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.  
TITLE OF INVENTION: DE NOVO CELL-FREE  
TITLE OF INVENTION: SYNTHESIS PICONNAVIRUS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,6798  
FILING DATE: 30-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07\846,914  
FILING DATE: 06-MAR-1992  
CLASSIFICATION: 435  
APPLICATION NUMBER: 07\719,761  
FILING DATE: 24-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C.H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 0887-4095 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.  
US-08-268-679B-8

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 1 G 1

RESULT 2  
US-08-484-192-16  
Sequence 16, Application US/08484192  
Patent No. 5756291  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: ALBRECHT, GLENN  
APPLICANT: LATHAM, JOHN  
APPLICANT: LEUNG, LAWRENCE  
APPLICANT: VERMAAS, ERIC  
APPLICANT: TOOLE, JOHN J.  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
METHODS OF MAKING  
TITLE OF INVENTION: METHODS OF MAKING  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,192  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,387  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 246102002221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc.difference  
LOCATION: replace(1,"")  
OTHER INFORMATION: /note="This is a biotin-17  
OTHER INFORMATION: nucleotide stretch of abasic residues."  
US-08-484-192-16

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 9 1

DB 2 G 2

RESULT 3  
US-08-361-024-3  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 MB  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgoon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 1280-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 9 1  
DB 1 G 1

RESULT 4  
US-08-361-024-3/C  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 Mb  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgoon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 128D-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match  
Best Local Similarity 100.0%; Score 1; DB 4; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
1  
DB 2 g 2

RESULT 5  
US-07-791-213D-46  
Sequence 46, Application US/07/91213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
1  
DB 2 g 2

RESULT 6  
US-07-791-213D-46/c  
Sequence 46, Application US/07/91213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021



INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 G 3

RESULT 7  
US-07-791-213D-62  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 2 G 2

RESULT 8  
US-07-791-213D-62/c  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
Db 3 G 3

RESULT 9  
US-08-268-679B-7  
Sequence 7, Application US/08268679B  
Patent No. 5674729  
GENERAL INFORMATION:  
APPLICANT: WIMMER, Eckard; Molla,  
APPLICANT: AKHTEROZZAMAN; PAUL, ANIKO V.  
TITLE OF INVENTION: DE NOVO CELL-FREE  
SYNTHESIS PICORNAVIRUS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,679B  
FILING DATE: 30-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07\846,914  
FILING DATE: 06-MAR-1992  
CLASSIFICATION: 435  
APPLICATION NUMBER: 07\719,761  
FILING DATE: 24-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C.H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 0887-4095 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE: N.A.  
POSITION IN GENOME: N.A.  
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 2 g 2

RESULT 10  
US-08-602-036A-2  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oegystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 g 1

RESULT 11  
US-08-602-036A-2/c  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oegystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-602-036A-2

Query Match 100.0% Score 1: DB 1: Length 3:  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 G 3

RESULT 12  
US-08-293-150A-46  
Sequence 46, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-46

Query Match 100.0% Score 1: DB 1: Length 3:

Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 G 2

RESULT 13  
US-08-293-150A-46/c  
Sequence 46, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-46

Query Match 100.0% Score 1: DB 1: Length 3:  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 3 G 3

RESULT 14  
US-08-293-150A-62  
Sequence 62, Application US/08293150A  
Patent No. 5792629

GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 9 1  
DB 2 G 2  
RESULT 15  
US-08-293-150A-62/C  
Sequence 62, Application US/08293150A  
Patent No. 5792629  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshiro  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404

CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,150A  
FILING DATE: 19-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/791,213  
FILING DATE: 13-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 9 1  
DB 3 G 3  
RESULT 16  
US-08-502-374A-2  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oeystein  
APPLICANT: Hovig, Elvind  
APPLICANT: Engestraten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,374A  
FILING DATE: 14-Jul-1995

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 1 G 1

RESULT 17  
US-08-502-374A-2/c  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oeystein  
APPLICANT: Hovig, Eivind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,374A  
FILING DATE: 14-Jul-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 3 G 3

RESULT 18  
US-08-642-407A-2  
Sequence 2, Application US/08642407A  
Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Eivind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
1  
Db 1 G 1

RESULT 19  
US-08-642-407A-2/c  
Sequence 2, Application US/08642407A

Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oestlein, Rodstad  
APPLICANT: Hovig, Eivind  
APPLICANT: Engedraeten, Olav  
APPLICANT: MacIandemo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
APTI-SENSE: NO  
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
1  
Db 3 G 3

RESULT 20  
US-08-873-709-9  
Sequence 9, Application US/08873709  
Patent No. 6037126  
GENERAL INFORMATION:  
APPLICANT: Grossman, Abraham  
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND  
TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF  
PROTEIN COMPONENT OF TELOMERASE ENZYME  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abraham Grossman  
STREET: 666 Washington Avenue  
CITY: Pleasantville  
STATE: NY  
COUNTRY: USA  
ZIP: 10570  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873,709  
FILING DATE: 12-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: 0001/002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-747-9108  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
1  
Db 1 G 1

RESULT 21  
US-09-032-365A-36  
Sequence 36, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Nagart, Jaryen  
APPLICANT: No. 6114502en-Trauh, Konrad  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
NEUROSENSORY DEFECTS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESS: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-2CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-032-365A-36

Query Match 100.0% Score 1: DB 3: Length 3:  
Best Local Similarity 100.0% Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
Db 1 G 1

RESULT 22  
US-08-793-634B-12  
Sequence 12, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Kcese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-12

Query Match 100.0% Score 1: DB 4: Length 3:  
Best Local Similarity 100.0% Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
Db 2 G 2

RESULT 23  
US-08-973-568-55  
Sequence 55, Application US/08973568B  
Patent No. 6277634  
GENERAL INFORMATION:  
APPLICANT: McCall, Maxine J.  
APPLICANT: Hendry, Philip  
APPLICANT: Lockett, Trevor  
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF  
FILE REFERENCE: 47203ppctus  
CURRENT APPLICATION NUMBER: US/08/973,568B  
CURRENT FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 55  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Combined DNA/RNA molecule:  
FEATURE: Synthetic Ribozyme or portion thereof  
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and  
US-08-973-568-55

Query Match 100.0% Score 1: DB 4: Length 3:  
Best Local Similarity 100.0% Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 g 1  
Db 1 G 1

RESULT 24  
US-07-755-462-2  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sema, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn1  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 1 G 1

RESULT 25  
US-07-755-462-2/C  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn1  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 4 G 4

RESULT 26  
US-08-169-950-6  
Sequence 6, Application US/08169950  
Patent No. 5366882  
GENERAL INFORMATION:  
APPLICANT: LUNNEN, KEITH D.  
APPLICANT: WILSON, GEOFFREY G.  
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI  
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,950  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1  
DB 1 G 1

RESULT 27  
US-08-169-950-6/C  
Sequence 6, Application US/08169950  
Patent No. 5366882  
GENERAL INFORMATION:  
APPLICANT: LUNNEN, KEITH D.  
APPLICANT: WILSON, GEOFFREY G.  
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI  
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE



NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,950  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 4 G 4

RESULT 28  
US-07-630-288A-7  
Sequence 7, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-7

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 1 G 1

RESULT 29  
US-07-630-288A-11  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1 g 1  
Db 1 g 1

RESULT 30  
US-07-630-288A-11/c  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 13:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1 g 1  
Db 1 g 1

Db 4 G 4

RESULT 31  
US-07-630-288A-13  
Sequence 13, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 13:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1 g 1  
Db 1 g 1

RESULT 32  
US-07-630-288A-14  
Sequence 14, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser

```

: STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
: CITY: Naperville
: STATE: IL
: COUNTRY: USA
: ZIP: 60563
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/630,288A
: FILING DATE: 17-DEC-1990
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/370,218
: FILING DATE: 06-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/252,243
: FILING DATE: 30-SEP-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Glesser, Joanne M.
: REGISTRATION NUMBER: 32,838
: REFERENCE/DOCKET NUMBER: 58190 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (708) 717-2443
: TELEFAX: (708) 717-2430
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
DB 1 G 1

RESULT 33
US-07-630-288A-14/C
: Sequence 14, Application US/07630288A
: Patent No. 5472840
: GENERAL INFORMATION:
: APPLICANT: Stefano, James E.
: TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
: TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Joanne M. Glesser
: STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
: CITY: Naperville
: STATE: IL
: COUNTRY: USA
: ZIP: 60563
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/630,288A
: FILING DATE: 17-DEC-1990
: CLASSIFICATION: 435
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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/370,218
: FILING DATE: 06-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/252,243
: FILING DATE: 30-SEP-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Glesser, Joanne M.
: REGISTRATION NUMBER: 32,838
: REFERENCE/DOCKET NUMBER: 58190 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (708) 717-2443
: TELEFAX: (708) 717-2430
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-07-630-288A-14

Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9 1
DB 4 G 4

RESULT 34
US-07-630-288A-34
: Sequence 34, Application US/07630288A
: Patent No. 5472840
: GENERAL INFORMATION:
: APPLICANT: Stefano, James E.
: TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
: TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Joanne M. Glesser
: STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
: CITY: Naperville
: STATE: IL
: COUNTRY: USA
: ZIP: 60563
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/630,288A
: FILING DATE: 17-DEC-1990
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/370,218
: FILING DATE: 06-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/252,243
: FILING DATE: 30-SEP-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Glesser, Joanne M.
: REGISTRATION NUMBER: 32,838
: REFERENCE/DOCKET NUMBER: 58190 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (708) 717-2443
: TELEFAX: (708) 717-2430
: INFORMATION FOR SEQ ID NO: 34:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 2 G 2

RESULT 35  
US-07-630-288A-34/C  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630.288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 4 G 4

RESULT 36  
US-08-126-594-25  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Algis  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
NUMBER OF INVENTION: CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
Db 3 G 3

RESULT 37  
US-08-126-594-25/C  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Algis  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
NUMBER OF INVENTION: CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP U1  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 G 1  
DB 4 G 4

RESULT 38  
US-08-188-943-1  
Sequence 1, Application US/08188943  
Patent No. 565347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtiss, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 G 1  
DB 3 G 3

RESULT 39  
US-08-188-943-1/C  
Sequence 1, Application US/08188943  
Patent No. 565347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtiss, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1  
1  
Db 4 C 4

## RESULT 40

US-08-188-943-2  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudlbande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1  
1  
Db 1 C 1

## RESULT 41

US-08-188-943-2/C  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudlbande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 g 1  
1  
Db 2 G 2

## RESULT 42

US-08-465-811A-25  
Sequence 25, Application US/08465811A  
Patent No. 5637685  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JW/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 3 g 3

RESULT 43  
US-08-465-811A-25/C  
Sequence 25, Application US/08465811A  
Patent No. 5637685  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JW/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 4 g 4

RESULT 44  
US-08-199-317-2  
Sequence 2, Application US/08199317  
Patent No. 5670316  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calloun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,317  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,791  
FILING DATE: 09-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,462  
FILING DATE: 04-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Stralford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 9150-0004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 g 1  
Db 1 g 1

RESULT 45  
US-08-199-317-2/c  
; Sequence 2, Application US/08199317  
; Patent No. 5670316  
; GENERAL INFORMATION:  
; APPLICANT: Sena, Elissa P.  
; APPLICANT: Calhoun, Cornelia J.  
; APPLICANT: Zarling, David A.  
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
; TITLE OF INVENTION: Formation  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/199,317  
; FILING DATE: 25-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/910,791  
; FILING DATE: 09-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,462  
; FILING DATE: 04-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520,321  
; FILING DATE: 07-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 9150-0004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
; US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 4 G 4

Search completed: July 15, 2002, 23:07:39  
Job time: 22992 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 ; Search time 12941.8 Seconds

(without alignments)  
1.672 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3164\_3164

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Capext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

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2: /cgn2\_6/ptodata/2/pna/US086.COMB.seq.\*  
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42: /cgn2\_6/ptodata/2/pna/US046.COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US045.COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	100.0	2	3	US-07-934-385-14	Sequence 14, Appl
2	100.0	2	5	US-08-107-721-46	Sequence 46, Appl
3	100.0	2	5	US-08-107-721-46	Sequence 46, Appl
4	100.0	2	15	US-09-172-828-15	Sequence 15, Appl
5	100.0	2	16	US-09-284-725-201	Sequence 201, Appl
6	100.0	2	17	US-09-306-333A-32	Sequence 32, Appl
7	100.0	2	17	US-09-387-777-7	Sequence 7, Appl
8	100.0	2	17	US-09-387-777-3	Sequence 3, Appl
9	100.0	2	17	US-09-387-777-5	Sequence 5, Appl
10	100.0	2	17	US-09-387-777-6	Sequence 6, Appl
11	100.0	2	17	US-09-387-777-10	Sequence 10, Appl
12	100.0	2	17	US-09-387-777-11	Sequence 11, Appl
13	100.0	2	17	US-09-387-777-12	Sequence 12, Appl
14	100.0	2	17	US-09-387-777-14	Sequence 14, Appl
15	100.0	2	17	US-09-472-035A-19	Sequence 19, Appl
16	100.0	2	18	US-09-472-035A-20	Sequence 20, Appl
17	100.0	2	24	US-09-634-306B-51869	Sequence 51869, A
18	100.0	2	24	US-09-634-306B-52280	Sequence 52280, A
19	100.0	2	24	US-09-634-306B-52357	Sequence 52357, A
20	100.0	2	24	US-09-634-306B-53003	Sequence 53003, A
21	100.0	2	24	US-09-634-306B-58305	Sequence 58305, A
22	100.0	2	24	US-09-634-306B-175312	Sequence 175312, A
23	100.0	2	24	US-09-634-306B-175337	Sequence 175337, A
24	100.0	2	24	US-09-634-306B-175354	Sequence 175354, A

32 1 100.0 2 24 US-09-634-306B-175401 Sequence 175401,  
33 1 100.0 2 24 US-09-634-306B-175403 Sequence 175403,  
34 1 100.0 2 24 US-09-634-306B-175415 Sequence 175415,  
35 1 100.0 2 24 US-09-634-306B-175419 Sequence 175419,  
36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426,  
37 1 100.0 2 24 US-09-634-306B-175433 Sequence 175433,  
38 1 100.0 2 24 US-09-634-306B-175449 Sequence 175449,  
39 1 100.0 2 24 US-09-634-306B-176848 Sequence 176848,  
40 1 100.0 2 24 US-09-634-306B-176849 Sequence 176849,  
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42 1 100.0 2 24 US-09-634-306B-178420 Sequence 178420,  
43 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,  
44 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,  
45 1 100.0 2 24 US-09-634-306B-178617 Sequence 178617,

## ALIGNMENTS

RESULT 1  
US-07-934-385-14  
Sequence 14, Application US/07934385  
GENERAL INFORMATION:  
APPLICANT: LATHAM, JOHN  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES  
TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES  
NUMBER OF SEQUENCES: 177  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,385  
FILING DATE: 19920821  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 24610-20022.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc\_difference  
LOCATION: replace(1,"")  
OTHER INFORMATION: /note="This position is a  
OTHER INFORMATION: biotin-17 nucleotide stretch of random sequences."  
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 2 G 2

RESULT 2  
US-08-107-721-46  
Sequence 46, Application US/08107721  
GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: LATHAM, JOHN A.  
APPLICANT: MUENCHAU, DARYL D.  
APPLICANT: KRANCZYK, STEVEN  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
TITLE OF INVENTION: METHODS OF MAKING  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GILEAD SCIENCES, INC.  
STREET: 344 LAKEVIEW DRIVE  
CITY: FOSTER CITY  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,721  
FILING DATE: 20-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28216  
REFERENCE/DOCKET NUMBER: 24610-20022.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)574-3000  
TELEFAX: (415)578-9264  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1  
OTHER INFORMATION: /note="This is a biotin-17  
OTHER INFORMATION: nucleotide stretch of abasic residues."  
US-08-107-721-46

Query Match 100.0%; Score 1; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 g 1  
1  
Db 2 G 2

RESULT 3  
US-08-107-721B-46  
Sequence 46, Application US/08107721B  
GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: LATHAM, JOHN A.  
APPLICANT: MUENCHAU, DARYL D.  
APPLICANT: KRANCZYK, STEVEN  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GILEAD SCIENCES, INC.  
STREET: 344 LAKE SIDE DRIVE  
CITY: FOSTER CITY  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94404

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,721B  
FILING DATE: 20-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28216  
REFERENCE/DOCKET INFORMATION:  
TELEPHONE: (415)574-3000  
TELEFAX: (415)578-9264  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: /note="This is a biotin-17  
OTHER INFORMATION: nucleotide stretch of abasic residues."

US-08-107-721B-46

Query Match  
Best Local Similarity 100.0%; Score 1; DB 5; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
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DB 2 G 2

RESULT 4  
US-09-172-828-15  
; Sequence 15, Application US/09172828  
; GENERAL INFORMATION:  
; APPLICANT: Children's Medical Center Corporation  
; APPLICANT: Klagsbrun, Michael  
; APPLICANT: Elenius, Klaus  
; TITLE OF INVENTION: Novel Human EGF Receptors and Use  
; FILE REFERENCE: 47758-PCF  
; CURRENT APPLICATION NUMBER: US/09/172,828  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: mouse  
US-09-172-828-15

Query Match  
Best Local Similarity 100.0%; Score 1; DB 15; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
|  
DB 1 g 1

RESULT 5  
US-09-284-725-201/C  
; Sequence 201, Application US/09284725  
; GENERAL INFORMATION:  
; APPLICANT: Quint, Wilhelmus  
; APPLICANT: Van Doorn, Leendert  
; TITLE OF INVENTION: Probes, methods and kits for detection and  
; FILE REFERENCE: Typing of Helicobacter pylori nucleic acids in biological  
; TITLE OF INVENTION: samples.  
; NUMBER OF SEQUENCES: 280  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP  
STREET: 620 Newport Center Drive, 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/284,725  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP96/870131.8  
FILING DATE: 16-OCT-1996  
APPLICATION NUMBER: PCT/EP97/05614  
FILING DATE: 10-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: INNOG2.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (949) 760-0404  
TELEFAX: (949) 760-9395  
INFORMATION FOR SEQ ID NO: 201:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-09-284-725-201

Query Match  
Best Local Similarity 100.0%; Score 1; DB 16; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
|  
DB 2 G 2

RESULT 6  
US-09-306-333A-32  
; Sequence 32, Application US/09306333A  
; GENERAL INFORMATION:  
; APPLICANT: Academy of Applied Science  
; TITLE OF INVENTION: BRCAL and hMLH1 Gene Primer Sequences and Method for  
; FILE REFERENCE: BRCAL  
; CURRENT APPLICATION NUMBER: US/09/306,333A  
; FILING DATE: 1999-05-06

JUL 16 09:39:30 2002

US-09-375-248-1\_COPY-3164-2002

APPLICATION NUMBER: PCT/IB00/01607  
FILING DATE: 2000-11-06  
R OF SEQ ID NOS: 122  
ARE: Patent In Ver. 2.1  
ID NO: 32  
ACTH: 2  
E: DNA  
ANISM: Homo sapiens  
106-333A-32

Match 100.0% Score 1: DB 17: Length 2:  
Local Similarity 100.0% Pred. No. 0: Indels 0: Gaps 0:  
hes 1: Conservative

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1 1  
2 9 2

US-09-387-777-2/c  
US-09-387-777-2/c  
Sequence 2, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
POLYMERIZATION USING OLIGONUCLEOTIDE  
BLOCKS  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file

Query Match 100.0% Score 1: DB 17: Length 2:  
Best Local Similarity 100.0% Pred. No. 0: Indels 0: Gaps 0:  
Matches 1: Conservative

1 9 1  
1 1  
2 9 2

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION/DOCKET NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-387-777-2

Query Match 100.0% Score 1: DB 17: Length 2:  
Best Local Similarity 100.0% Pred. No. 0: Indels 0: Gaps 0:  
Matches 1: Conservative

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1 1  
2 9 2

RESULT 9  
US-09-387-777-3  
Sequence 3, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
POLYMERIZATION USING OLIGONUCLEOTIDE  
BLOCKS  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file

Query Match 100.0% Score 1: DB 17: Length 2:  
Best Local Similarity 100.0% Pred. No. 0: Indels 0: Gaps 0:  
Matches 1: Conservative

1 9 1  
1 1  
2 9 2

LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-3

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 2 G 2

RESULT 10  
US-09-387-777-5/C  
Sequence 5, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 1 G 1

RESULT 11

US-09-387-777-6/C  
Sequence 6, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
DB 2 G 2

RESULT 12  
US-09-387-777-7  
Sequence 7, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

```

: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-7
:
: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 9 1
: Db 2 G 2
:
: RESULT 13
: US-09-387-777-7/c
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-8
```

```

: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-7
```

```

: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 9 1
: Db 1 G 1
```

```

: RESULT 14
: US-09-387-777-8/c
: Sequence 8, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Klees
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-387-777-8
```

```

: Query Match          100.0%; Score 1; DB 17; Length 2;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 9 1
```

1  
Db 1 G 1

## RESULT 15

US-09-387-777-9

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1

Db 1 G 1

## RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1

Db 1 G 1

## RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

SOFTWARE: Word for Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-10

Query Match  
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
|  
Db 2 c 2

RESULT 18  
US-09-387-777-11  
Sequence 11, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-11

Query Match  
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
|  
Db 1 g 1

RESULT 19  
US-09-387-777-12  
Sequence 12, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-12

Query Match  
Best Local Similarity 100.0%; Score 1: DB 17; Length 2:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 1 g 1  
|  
Db 1 g 1

RESULT 20  
US-09-387-777-14/c  
Sequence 14, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS



NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 G 2

RESULT 21  
US-09-387-777-15  
Sequence 15, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1  
DB 2 G 2

RESULT 22  
US-09-472-035A-19  
Sequence 19, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kashi et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
SOFTWARE: an ASCII file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472,035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-562553  
TELEFAX: 972-3-562554  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-19

Query Match 100.0%: Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 1 G 1

RESULT 23  
US-09-472-035A-20/c  
Sequence 20, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kashi et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890tx  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472.035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedmam, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-20

Query Match 100.0%: Score 1; DB 18; Length 2;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 G 2

RESULT 24

US-09-634-306B-51869/c  
Sequence 51869, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51869  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-51869

Query Match 100.0%: Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 G 2

RESULT 25  
US-09-634-306B-52280/c  
Sequence 52280, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52280  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 2 g 2

## RESULT 26

US-09-634-306B-52357/c  
; Sequence 52357, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52357  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 2 g 2

## RESULT 27

US-09-634-306B-53003/c  
; Sequence 53003, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53003  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-53003

Oy 1 g 1  
1  
Db 2 g 2

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 2 g 2

## RESULT 28

US-09-634-306B-58305/c  
; Sequence 58305, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58305  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 2 g 2

## RESULT 29

US-09-634-306B-175312  
; Sequence 175312, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21

```

: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175312
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175312
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 30
US-09-634-306B-175337
: Sequence 175337, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175337
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175337
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 31
US-09-634-306B-175354
: Sequence 175354, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175354
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175354
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```

RESULT 32
US-09-634-306B-175401
: Sequence 175401, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 175401
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
```

US-09-634-306B-175401

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
|  
Db 1 g 1

RESULT 33  
US-09-634-306B-175403  
; Sequence 175403, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634.306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 175403  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-175403

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
|  
Db 1 g 1

RESULT 34  
US-09-634-306B-175415  
; Sequence 175415, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634.306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 175415  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-175415

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
|  
Db 1 g 1

RESULT 35  
US-09-634-306B-175419  
; Sequence 175419, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634.306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 175419  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-175419

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
|  
Db 1 g 1

RESULT 36  
US-09-634-306B-175426  
; Sequence 175426, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175426
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
|
Db      1 g 1
```

```
RESULT 37
US-09-634-306B-175433
: Sequence 175433, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175433
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
|
```

```

Db      1 g 1
|
RESULT 38
US-09-634-306B-175849
: Sequence 175849, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175849
```

```
Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
|
Db      1 g 1
```

```
RESULT 39
US-09-634-306B-176848
: Sequence 176848, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
```

TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176848

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 40  
US-09-634-306B-176849  
Sequence 176849, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176849  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176849

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 41  
US-09-634-306B-176880  
Sequence 176880, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176880  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176880

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 42  
US-09-634-306B-178420  
Sequence 178420, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 178420  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-178420

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 1 g 1

RESULT 43  
US-09-634-306B-178440  
Sequence 178440, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440

```

```

Query Match      100.0%; Score 1; DB 24; Length 2;
Host Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 g 1
Db      1 g 1

```

```

RESULT 44
US-09-634-306B-178440/C
: Sequence 178440, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178440
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178440

```

```

Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 g 1
Db      2 g 2

```

```

RESULT 45
US-09-634-306B-178617
: Sequence 178617, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178617
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-178617

```

```

Query Match      100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 g 1
Db      2 g 2

```

Search completed: July 16, 2002, 02:50:26  
Job time: 31279 sec



---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 seconds  
(without alignments)  
2.105 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3164\_3164

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_MA\_New :  
1: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq : \*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq : \*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq : \*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq : \*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq : \*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq : \*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	6	US-10-027-632-51869 Sequence 51869, A
C 2	1	100.0	2	6	US-10-027-632-52280 Sequence 52280, A
C 3	1	100.0	2	6	US-10-027-632-52357 Sequence 52357, A
C 4	1	100.0	2	6	US-10-027-632-53003 Sequence 53003, A
C 5	1	100.0	2	6	US-10-027-632-58305 Sequence 58305, A
C 6	1	100.0	2	6	US-10-027-632-175312 Sequence 175312, A
C 7	1	100.0	2	6	US-10-027-632-175337 Sequence 175337, A
C 8	1	100.0	2	6	US-10-027-632-175401 Sequence 175401, A
C 9	1	100.0	2	6	US-10-027-632-175403 Sequence 175403, A
C 10	1	100.0	2	6	US-10-027-632-175415 Sequence 175415, A
C 11	1	100.0	2	6	US-10-027-632-175419 Sequence 175419, A
C 12	1	100.0	2	6	US-10-027-632-175426 Sequence 175426, A
C 13	1	100.0	2	6	US-10-027-632-175433 Sequence 175433, A
C 14	1	100.0	2	6	US-10-027-632-175843 Sequence 175843, A
C 15	1	100.0	2	6	US-10-027-632-175848 Sequence 175848, A
C 16	1	100.0	2	6	US-10-027-632-176849 Sequence 176849, A
C 17	1	100.0	2	6	US-10-027-632-176880 Sequence 176880, A
C 18	1	100.0	2	6	US-10-027-632-178420 Sequence 178420, A
C 19	1	100.0	2	6	US-10-027-632-178440 Sequence 178440, A
C 20	1	100.0	2	6	US-10-027-632-178440 Sequence 178440, A
C 21	1	100.0	2	6	US-10-027-632-178617 Sequence 178617, A
C 22	1	100.0	2	6	US-10-027-632-178640 Sequence 178640, A
C 23	1	100.0	2	6	US-10-027-632-178640 Sequence 178640, A
C 24	1	100.0	3	1	PCT-US02-00351-20 Sequence 20, Appl
C 25	1	100.0	3	6	US-10-027-632-52136 Sequence 52136, A
C 26	1	100.0	3	6	US-10-027-632-52402 Sequence 52402, A

C 27	1	100.0	3	6	US-10-027-632-52403 Sequence 52403, A
C 28	1	100.0	3	6	US-10-027-632-52404 Sequence 52404, A
C 29	1	100.0	3	6	US-10-027-632-52410 Sequence 52410, A
C 30	1	100.0	3	6	US-10-027-632-52417 Sequence 52417, A
C 31	1	100.0	3	6	US-10-027-632-52418 Sequence 52418, A
C 32	1	100.0	3	6	US-10-027-632-52419 Sequence 52419, A
C 33	1	100.0	3	6	US-10-027-632-52425 Sequence 52425, A
C 34	1	100.0	3	6	US-10-027-632-52491 Sequence 52491, A
C 35	1	100.0	3	6	US-10-027-632-52495 Sequence 52495, A
C 36	1	100.0	3	6	US-10-027-632-52496 Sequence 52496, A
C 37	1	100.0	3	6	US-10-027-632-52508 Sequence 52508, A
C 38	1	100.0	3	6	US-10-027-632-52512 Sequence 52512, A
C 39	1	100.0	3	6	US-10-027-632-52513 Sequence 52513, A
C 40	1	100.0	3	6	US-10-027-632-52515 Sequence 52515, A
C 41	1	100.0	3	6	US-10-027-632-52519 Sequence 52519, A
C 42	1	100.0	3	6	US-10-027-632-52563 Sequence 52563, A
C 43	1	100.0	3	6	US-10-027-632-52565 Sequence 52565, A
C 44	1	100.0	3	6	US-10-027-632-52758 Sequence 52758, A
C 45	1	100.0	3	6	US-10-027-632-52761 Sequence 52761, A

## ALIGNMENTS

RESULT 1  
US-10-027-632-51869/c  
Sequence 51869, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827, 129  
CURRENT APPLICATION NUMBER: US/10/027, 632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218, 006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198, 676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193, 483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185, 218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167, 363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156, 358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146, 002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 51869  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-51869

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1  
Db 2 g 2

RESULT 2  
US-10-027-632-52280/c  
Sequence 52280, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827, 129  
CURRENT APPLICATION NUMBER: US/10/027, 632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218, 006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198, 676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193, 483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185, 218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167, 363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156, 358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146, 002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 51869  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-51869

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 g 1
DB 2 g 2
```

```
RESULT 3
US-10-027-632-52357/c
Sequence 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 g 1
```

```
DB 2 g 2
RESULT 4
US-10-027-632-53003/c
Sequence 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 g 1
DB 2 g 2
```

```
RESULT 5
US-10-027-632-58305/c
Sequence 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58305
```

```
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305
```

```
Query Match          100.0%; Score 1; DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 6
US-10-027-632-175312
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312
```

```
Query Match          100.0%; Score 1; DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 7
US-10-027-632-175337
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337
```

```
Query Match          100.0%; Score 1; DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 8
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354
```

```
Query Match          100.0%; Score 1; DB 6; Length 2:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
        |
Db       1 g 1
```

```
RESULT 9
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
        |
Db       1 g 1
```

```

RESULT 10
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY      1 g 1
        |
Db       1 g 1

RESULT 11
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 g 1
        |
Db       1 g 1

RESULT 12
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
```

```
SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175419
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175419
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 13
US-10-027-632-175426
: Sequence 175426, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175426
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 14
US-10-027-632-175433
: Sequence 175433, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
```

```
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175433
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 15
US-10-027-632-175849
: Sequence 175849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175849
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 1 g 1
```

```
RESULT 16
US-10-027-632-176848
: Sequence 176848, Application US/10027632
```

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT FILING DATE: 2002-04-30
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-04-20
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 1999-11-23
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176848
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 17
US-10-027-632-176849
: Sequence 176849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT FILING DATE: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-04-20
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 1999-11-23
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849
```

```
Query Match          100.0%: Score 1; DB 6; Length 2;
```

```

Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 18
US-10-027-632-176880
: Sequence 176880, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT FILING DATE: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-04-20
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 1999-11-23
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176880
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176880
```

```

Query Match          100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 g 1
        |
Db       1 g 1
```

```

RESULT 19
US-10-027-632-178420
: Sequence 178420, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT FILING DATE: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-07-12
: PRIOR FILING DATE: 2000-04-20
: PRIOR FILING DATE: 2000-04-20
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-03-29
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 2000-02-24
: PRIOR FILING DATE: 1999-11-23
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-09-28
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 178420
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-178420
```

```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 20
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 1 g 1
```

```
RESULT 21
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 g 2
```

```
RESULT 22
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
Db 2 g 2
```

RESULT 23



```
US-10-027-632-178640
: Sequence 178640, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 178640
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-178640
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 2 g 2
```

```
RESULT 24
PCT-US02-00351-20/C
: Sequence 20, Application PC/TUS0200351
: GENERAL INFORMATION:
: APPLICANT: Chel, Ilan
: APPLICANT: Vileto, Ada
: TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
: FILE REFERENCE: 02/23682
: CURRENT APPLICATION NUMBER: PCT/US02/00351
: CURRENT FILING DATE: 2002-05-05
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: motif found in the URSS of both ech42 and prb1 genes
PCT-US02-00351-20
```

```
Query Match          100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 3 g 3
```

RESULT 25

```
US-10-027-632-52136
: Sequence 52136, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 52136
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52136
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 g 1
    |
Db 3 g 3
```

```
RESULT 26
US-10-027-632-52402/C
: Sequence 52402, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 52402
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52402
```

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

```
RESULT 27
US-10-027-632-52403/c
; Sequence 52403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52403
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52403
```

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

```
RESULT 28
US-10-027-632-52404/c
; Sequence 52404, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52404
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52404
```

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 2 G 2

```
RESULT 29
US-10-027-632-52410/c
; Sequence 52410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52410
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52410
```

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 3 G 3

```
RESULT 30
US-10-027-632-52417/c
; Sequence 52417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
```

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52417
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52417
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db      2 g 2
```

```

RESULT 31
US-10-027-632-52418/c
; Sequence 52418, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52418
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52418
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db      2 g 2
```

```

RESULT 32
US-10-027-632-52419/c
; Sequence 52419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52419
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52419
```

```

Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 g 1
Db      2 g 2
```

```

RESULT 33
US-10-027-632-52425/c
; Sequence 52425, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52425
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
DB 3 g 3

RESULT 34

US-10-027-632-52491  
; Sequence 52491, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52491  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
DB 2 g 2

RESULT 35

US-10-027-632-52495/c  
; Sequence 52495, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52495  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52495

US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
DB 3 g 3

RESULT 36

US-10-027-632-52496  
; Sequence 52496, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52496  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
DB 2 g 2

RESULT 37

US-10-027-632-52508  
; Sequence 52508, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52508
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52508
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 2 g 2
```

```

RESULT 38
US-10-027-632-52512/c
: Sequence 52512, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52512
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52512
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
```

```

Db 3 G 3
RESULT 39
US-10-027-632-52513
: Sequence 52513, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52513
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52513
```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 2 g 2
```

```

RESULT 40
US-10-027-632-52615
: Sequence 52615, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 52615
: LENGTH: 3
```

TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52615

Query Match  
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 g 2

RESULT 41  
US-10-027-632-52633  
Sequence 52633, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52633  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52633

Query Match  
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 g 2

RESULT 42  
US-10-027-632-52651  
Sequence 52651, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52651  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52651

Query Match  
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 g 2

RESULT 43  
US-10-027-632-52753  
Sequence 52753, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52753  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-52753

Query Match  
Best Local Similarity 100.0%; Score 1: DB 6; Length 3;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
|  
Db 2 g 2

RESULT 44  
US-10-027-632-52758/C  
Sequence 52758, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758
```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 g 1
        |
db       1 G 1
```

```

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761
```

```

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 g 1
        |
db       1 G 1
```

Search completed: July 16, 2002, 02:57:00  
Job time: 24558 sec

---



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:36 ; Search time 7067.1 Seconds

(without alignments)  
1.910 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3164\_3164

Perfect score: 1 g 1

Sequence: 1 g 1

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Capext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: \*  
1: em\_estbta:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpi:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_hnv:\*  
15: em\_gss\_pin:\*  
16: em\_gss\_vrli:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	2	HSN003817
C 2	1	100.0	2	2	HSN007187
C 3	1	100.0	2	2	HSN008709
C 4	1	100.0	2	2	HSN011919
C 5	1	100.0	2	10	B1817789
C 6	1	100.0	2	10	C55081
C 7	1	100.0	2	10	BE351920
C 8	1	100.0	2	12	A2463604
C 9	1	100.0	3	9	AM672605
C 10	1	100.0	3	12	A2438202
C 11	1	100.0	3	12	CNS00KCV
C 12	1	100.0	4	2	BG926576
C 13	1	100.0	4	2	BG926576
C 14	1	100.0	4	2	HSN003901
C 15	1	100.0	4	2	HSN010467
C 16	1	100.0	4	2	HSN010467
C 17	1	100.0	4	9	AM672622

C 18	1	100.0	4	12	CNS004RB	AL054121 Drosophila
C 19	1	100.0	5	2	HSN007310	A1042460 Homo sapi
C 20	1	100.0	5	2	HSN007835	A1042965 Homo sapi
C 21	1	100.0	5	2	HSN011053	A1046203 Homo sapi
C 22	1	100.0	6	2	BG927410	Bg927410 HNC1-1-C7
C 23	1	100.0	6	2	HSN003844	A1039368 Homo sapi
C 24	1	100.0	6	2	HSN004423	A1039947 Homo sapi
C 25	1	100.0	6	2	HSN007683	A1042484 Homo sapi
C 26	1	100.0	6	2	HSN008014	A1042833 Homo sapi
C 27	1	100.0	6	2	HSN010918	A1043164 Homo sapi
C 28	1	100.0	6	2	HSN010918	A1046068 Homo sapi
C 29	1	100.0	6	2	HSN010918	BE726686 894095D11
C 30	1	100.0	6	10	BE726686	BE726686 894095D11
C 31	1	100.0	7	2	BG97546	Bg97546 HOA14-1-H
C 32	1	100.0	7	2	BG97546	Bg97546 HOA14-1-H
C 33	1	100.0	7	2	HSN007412	A1042562 Homo sapi
C 34	1	100.0	7	2	HSN007412	A1042562 Homo sapi
C 35	1	100.0	7	2	HSN007412	A1042562 Homo sapi
C 36	1	100.0	7	2	HSN007502	A1042652 Homo sapi
C 37	1	100.0	7	2	HSN007502	A1042652 Homo sapi
C 38	1	100.0	7	10	C58888	C58888 C58888 Yuj1
C 39	1	100.0	8	2	HSN001420	A1037095 Homo sapi
C 40	1	100.0	8	2	HSN001743	A1037413 Homo sapi
C 41	1	100.0	8	2	HSN004451	A1039975 Homo sapi
C 42	1	100.0	8	2	HSN004451	A1039975 Homo sapi
C 43	1	100.0	8	2	HSN007277	A1042427 Homo sapi
C 44	1	100.0	8	2	HSN007277	A1042427 Homo sapi
C 45	1	100.0	8	2	HSN007323	A1042473 Homo sapi

## ALIGNMENTS

RESULT 1  
ID HSN003817/c standard; RNA; EST; 2 BP.  
XX HSN003817;  
AC AL039341.1  
XX AL039341.1  
SV AL039341.1  
SV AL039341.1  
DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX Homo sapiens mRNA: EST DKFP434F2010\_r1 (from clone DKFP434F2010)  
DE Homo sapiens mRNA: EST DKFP434F2010\_r1 (from clone DKFP434F2010)  
XX EST: expressed sequence tag.  
KH Homo sapiens (human)  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.  
XX [1]  
RN 1-2  
RP 1-2  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klopferplatz 10a D-82152 Martinsried, GERMANY  
XX  
CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No st sequence available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
XX  
FH Key Location/Qualifiers  
FT source 1. 2  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFP434F2010"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host

FT DH10B: sites NotI + SalI"  
 FT /dev-stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 DB 2 G 2

RESULT 2  
 HSM007187/c standard; RNA: EST; 2 BP.  
 ID HSM007187 standard; RNA: EST; 2 BP.  
 AC AL042337;  
 XX AL042337.1  
 SV AL042337.1  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX Homo sapiens mRNA: EST DKFZp43400820\_r1 (from clone DKFZp43400820)  
 DE EST: expressed sequence tag.  
 XX Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 FH [1]  
 FH 1-2  
 RP 1-2  
 RA Ottenwelder B., Obermayer B., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
 RL  
 XX Clone from S. Wiemann, sequenced by Medigenomix within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No si sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key Location/Qualifiers  
 FH source 1..2  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="DKFZp43400820"  
 FT /clone\_1ib="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B: sites NotI + SalI"  
 FT /dev-stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 DB 2 G 2

RESULT 3

HSM008709/c standard; RNA: EST; 2 BP.  
 ID HSM008709 standard; RNA: EST; 2 BP.  
 AC AL043859;  
 XX AL043859.1  
 SV AL043859.1  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX Homo sapiens mRNA: EST DKFZp434B2128\_r1 (from clone DKFZp434B2128)  
 DE EST: expressed sequence tag.  
 XX Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 FH [1]  
 FH 1-2  
 RP 1-2  
 RA Bioecker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
 RL  
 XX Clone from S. Wiemann, sequenced by GBF within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC si sequence also available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key Location/Qualifiers  
 FH source 1..2  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp434B2128"  
 FT /clone\_1ib="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B: sites NotI + SalI"  
 FT /dev-stage="adult"  
 FT /tissue\_type="testis"  
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 SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 DB 2 G 2

RESULT 4  
 HSM011919/c standard; RNA: EST; 2 BP.  
 ID HSM011919 standard; RNA: EST; 2 BP.  
 AC AL047069;  
 XX AL047069.1  
 SV AL047069.1  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX Homo sapiens mRNA: EST DKFZp586P0517\_r1 (from clone DKFZp586P0517)  
 DE EST: expressed sequence tag.  
 XX Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

XX  (1)
KN  Kocher K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.:
RP  1-2
RT  :
KL  Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX  MIRS, Am Klopferspitz 18a D-8152 Martinsried, GERMANY

CC  Clone from S. Wiemann, sequenced by BMF2 within the CDNA
CC  sequencing consortium of the German Genome Project
CC  No sl sequence available
CC  This clone is available at the RZPD in Berlin
CC  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC  Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de
XX
XX  Key      Location/Qualifiers
XX  F11
XX  F11  source      1..2
XX  FT      /db_xref="taxon:9606"
XX  FT      /organism="Homo sapiens"
XX  FT      /clone_lib="DKFZP586P0517"
XX  FT      /clone_lib="586 (synonym: hntel). Vector pSport1: host
XX  FT      DH10B: sites NotI + SalI/MluI"
XX  FT      /dev_stage="adult"
XX  FT      /tissue_type="uterus"
XX  SO  Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 g 1
    1
Db  2 G 2

RESULT 5
B1817789/c      2 bp  mRNA  linear  EST 04-OCT-2001
LOCUS      B1817789
DEFINITION  G3-G22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
              to putative ribosomal protein S2, mRNA sequence.
ACCESSION  B1817789
VERSION    B1817789.1 GI:15951401
KEYWORDS   EST.
SOURCE     axolotl.
ORGANISM   Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomidae;
            Ambystoma.
REFERENCE  1 (bases 1 to 2)
            Voss,S.R., King,D., Maness,N., Smith,J.J., Kondel,M., Bryant,S.V.,
            Gardner,D.M. and Parichy,D.M.
            Unpublished sequence tags from an axolotl limb regeneration library
            Contact: Voss SR
            Department of Biology
            Colorado State University
            Fort Collins, CO 80523, USA
            Tel: 970 491 4869
            Fax: 970 491 0649
            Email: svoss@lamar.colostate.edu
            Single pass sequence from 5' end. Low quality sequence was trimmed
            from the ends (FHRD error rate ~ 5%). Trace file available:
            svoss@lamar.colostate.edu.
            Location/Qualifiers
            1..2
            /organism="Ambystoma mexicanum"
            /db_xref="taxon:8296"
            /clone_lib="Axolotl Lambda Zap Library"
            /tissue_type="Regenerating forelimb"
            /dev_stage="Medium-bud blastema"

FEATURES
source

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BASE COUNT      0 a      1 c      0 g      1 t
ORIGIN

Query Match      100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 g 1
    1
Db  1 G 1

RESULT 6
C55081/c      2 bp  mRNA  linear  EST 16-SEP-1997
LOCUS      C55081
DEFINITION  C55081 Yui Kohara unpublished cDNA Caenorhabditis elegans cDNA
              clone yk350c9 3', mRNA sequence.
ACCESSION  C55081
VERSION    C55081.1 GI:2399682
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans.
            Caenorhabditis elegans.
ORGANISM   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Pelodierinae; Caenorhabditis.
            1 (bases 1 to 2)
            Kohara,Y., Mochizuki,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            ,M., Miyata,A. and Nishigaki,A.
            Expression map of the C.elegans genome
            Unpublished (1996)
            Contact: Yui Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
            Location/Qualifiers
            1..2
            /organism="Caenorhabditis elegans"
            /strain="CB1489 him-8(e1489)"
            /db_xref="taxon:6239"
            /clone_lib="yk350c9"
            /clone_lib="Yui Kohara unpublished cDNA"
            /sex="hermaphrodite, male"
            /tissue_type="whole animal"
            /dev_stage="varied"

BASE COUNT      1 a      1 c      0 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 g 1
    1
Db  2 G 2

RESULT 7
BE351920      2 bp  mRNA  linear  EST 18-JUL-2000
LOCUS      BE351920
DEFINITION  894053D07 y1 C. reinhardtii CC-1690, normalized, Lambda zap II
              Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION  BE351920
VERSION    BE351920.1 GI:9263773
KEYWORDS   EST.
SOURCE     Chlamydomonas reinhardtii.
            Chlamydomonas reinhardtii.
ORGANISM   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
            1 (bases 1 to 2)

```

## AUTHORS

## TITLE

Crossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,  
Mederbolt, J.P., Sillfow, C., Stern, D. and Surzycki, R.  
Analysis of the Chlamydomonas reinhardtii Genome: A Model,  
Unicellular System for Analyzing Gene Function and Regulation in  
Vascular Plants: project phase 2  
Unpublished (2000)  
Contact: Elizabeth H. Harris  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000, USA  
Tel: 919 613 8164  
Fax: 919 613 8177  
Email: chlamyduke.edu

## FEATURES

## source

1..2  
/organism="Chlamydomonas reinhardtii"  
/strain="CC-1690 wild type mt+ 21gr"  
/db.xref="taxon:3055"  
/clone.lib="C. reinhardtii CC-1690, normalized, lambda zap  
11"

/note="Vector: pBluescript II SK-; Site\_1: EcoRI; Site\_2:  
XhoI; This library, constructed by John Davies and Jeffrey  
Mederbolt, combines cDNAs from CC-1690 cells grown to  
mid-log phase in TAP (acetate-containing) medium in the  
light, TAP medium in the dark, HS (minimal) medium in  
ambient levels of CO<sub>2</sub> and HS medium bubbled with 5% CO<sub>2</sub>.  
Polya mRNA was purified from each sample, pooled and cDNA  
synthesized. The cDNA was directionally cloned into lambda  
zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.  
pBluescript II SK- plasmids were excised from the lambda  
zap clones by superinfection with Exsistist (Stratagene)  
phage. The library was normalized using method 4 described  
in Bonaldi et al (1996) Genome Research 6: 791-806."

BASE COUNT 0 a 0 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 1 g 1

## RESULT 8

AZ463604 2 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0272J05R Mouse 10kb plasmid UUCGM library Mus musculus genomic  
DEFINITION clone UUCGM0272J05 R. DNA sequence.

ACCESSION AZ463604  
VERSION AZ463604.1 GI:10621729  
KEYWORDS GSS.

SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 2)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss R.

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0272 row: 3 column: 05  
Seq primer: CACACAGCAACACGATACACC  
Class: plasmid ends  
High quality sequence stop: 451.  
Location/Qualifiers

## FEATURES

## source

1..2  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db.xref="taxon:10090"  
/clone.lib="UUCGM0272J05"  
/clone.lib="Mouse 10kb plasmid UUCGM library"  
/sex="Male"

/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (911473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 1 g 1

## RESULT 9

AM672605 3 bp mRNA linear EST 26-SEP-2001  
LOCUS 2XA Explanted metanephric mesenchyme induced to differentiate into  
DEFINITION epithelial structures of the nephron ex vivo. Rattus norvegicus  
cDNA similar to: gb|AF022811.1|AF022811 Mus musculus  
cornichon mRNA, mRNA sequence.

ACCESSION AM672605  
VERSION AM672605.1 GI:7541085  
KEYWORDS EST.

## SOURCE

## ORGANISM

Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

## AUTHORS

## TITLE

1 (bases 1 to 3)  
Plisov, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Pliova, T.M.,  
Higginbotham, K.G., Karavanova, I., Lerman, M. and Perantoni, A.O.  
Mesenchymal-epithelial transition in the developing metanephric  
kidney: gene expression study by differential display  
Genes 27 (1), 22-31 (2000)

## JOURNAL

## MEDLINE

## COMMENT

Contact: Plisov S.Y.  
Laboratory of Comparative Carcinogenesis  
National Cancer Institute  
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242  
 Fax: 301 846 4956  
 Email: plisov@mail.ncicrf.gov  
 PCR Primers  
 FORWARD: ctccagctccctc  
 BACKWARD: ttaagcttcttcttc  
 Insert Length: 350 Std Error: 0.00  
 Seq primer: SP6  
 High quality sequence stop: 261.  
 Location/Qualifiers  
 1..3  
 source

/organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_lib="Explanted melanephric mesenchyme induced to  
 differentiate into epithelial structures of the nephron ex  
 vivo."  
 /tissue\_type="Melanephric mesenchyme"  
 /cell\_type="Mesenchymal/Epithelial"  
 /dev\_stage="J3 dpc-16dpc"  
 /lab\_host="JM109"  
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega);  
 Restriction Enzymes: 1: ApaI, AatII, SphI, NcoI, BstXI,  
 NotI, SacII, and EcoRI; SpeI, EcoRI, NotI, BstXI, PstI,  
 SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment  
 PCR-amplified in mRNA differential display analysis;  
 cloned in pGEM-Teasy (Promega); its expression is  
 developmentally regulated during mesenchymal-epithelial  
 conversion in the melanephric kidney."  
 BASE COUNT  
 ORIGIN  
 1 a 0 c 2 g 0 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 9; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
 |  
 Db 1 G 1

RESULT 10  
 A2438202/c 3 bp DNA linear GSS 03-OCT-2000  
 LOCUS  
 DEFINITION  
 clone UGCCIM0228108 F. DNA sequence.  
 ACCESSION  
 A2438202  
 VERSION  
 A2438202.1 GI:10562215  
 KEYWORDS  
 GSS.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus

REFERENCE  
 AUTHORS  
 1 (bases 1 to 3)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0228 row: 1 Column: 08  
 Seq primer: CGTCTAAGACGACGCCACT  
 Class: plasmid ends

FEATURES  
 source  
 High quality sequence stop: 302.  
 Location/Qualifiers  
 1..3

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_lib="UGCCIM0228108"  
 /clone\_lib="Mouse 10kb plasmid UGCCIM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance.  
 BASE COUNT  
 ORIGIN  
 1 a 1 c 0 g 1 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 12; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
 |  
 Db 1 G 1

RESULT 11  
 CNS00KCV 3 bp DNA linear GSS 03-JUN-1999  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster genome survey sequence TET3 end of BAC:  
 BACR17D19 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly) genomic survey sequence.  
 ACCESSION  
 AL077515  
 VERSION  
 AL077515.1 GI:4956992  
 KEYWORDS  
 GSS.  
 SOURCE  
 fruit fly.  
 ORGANISM  
 Drosophila melanogaster

REFERENCE  
 AUTHORS  
 1 (bases 1 to 3)  
 Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:  
 Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:  
 Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.  
 TITLE  
 Direct Submission  
 JOURNAL  
 COMMENT  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw<sup>sp</sup>, the same strain used for the BDGP's

PI and EST Libraries: A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/trosophila\\_bac.htm](http://bacpac.med.buffalo.edu/trosophila_bac.htm).

## FEATURES

source  
1..3  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPC1-98"  
/clone="BACR17D19"  
/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1 c 1  
Db

## RESULT 12

BC926576 standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10-R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

XX EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

KA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritic Cartilage 9(7):641-653(2001).

RL Contact: Sanjay Kumar

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsk.com

CC Seq primer: T7.

XX Key Location/Qualifiers

PH source

FT 1..4

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional

FT /organism="Homo sapiens"

FT /clone\_lib="HNC (Human Normal Cartilage)"

FT /tissue\_type="Cartilage"

FT /lab\_host="E.coli DH10 B"

XX Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

SO

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1 c 1  
Db

## RESULT 13

BC926576/c standard; RNA; EST; 4 BP.

AC BC926576;

SV BC926576.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HNC56-1-A10-R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

XX EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

KA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritic Cartilage 9(7):641-653(2001).

RL Contact: Sanjay Kumar

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsk.com

CC Seq primer: T7.

XX Key Location/Qualifiers

PH source

FT 1..4

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional

FT /organism="Homo sapiens"

FT /clone\_lib="HNC (Human Normal Cartilage)"

FT /tissue\_type="Cartilage"

FT /lab\_host="E.coli DH10 B"

FT

SO Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Oy 1 g 1

Db 3 G 3

RESULT 14

HSM003901 standard; RNA; EST; 4 BP.

AL039425;

AL039425.1

12-MAR-1999 (Rel. 59, Created)

12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZp434L0810\_s1 (from clone DKFZp434L0810)

EST; expressed sequence tag.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

Clone from S. Wiemann, sequenced by Qiagen within the CDNA

sequencing consortium of the German Genome Project

This clone is available at the RZPD in Berlin

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key

Location/Qualifiers

source

1..4

/db\_xref="taxon:9606"

/organism="Homo sapiens"

/clone\_id="DKFZp434L0810"

/clone\_lib="434 (synonym: htes3). Vector pSport1; host

DH10B; sites NotI + SalI"

/dev\_stage="adult"

/tissue\_type="testis"

Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 2; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 G 1

DB 4 G 4

RESULT 15

HSM010467

ID HSM010467 standard; RNA; EST; 4 BP.

AL045617;

AL045617.1

12-MAR-1999 (Rel. 59, Created)

12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZp4340245\_r1 (from clone DKFZp4340245)

KW EST; expressed sequence tag.

XX

Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

Clone from S. Wiemann, sequenced by Qiagen within the CDNA

sequencing consortium of the German Genome Project

This clone is available at the RZPD in Berlin

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key

Location/Qualifiers

source

1..4

/db\_xref="taxon:9606"

/organism="Homo sapiens"

/clone\_id="DKFZp4340245"

/clone\_lib="434 (synonym: htes3). Vector pSport1; host

DH10B; sites NotI + SalI"

/dev\_stage="adult"

/tissue\_type="testis"

Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 2; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 G 1

DB 4 G 4

RESULT 16

HSM010467/C

ID HSM010467 standard; RNA; EST; 4 BP.

AL045617;

AL045617.1

12-MAR-1999 (Rel. 59, Created)

12-MAR-1999 (Rel. 59, Last updated, Version 1)

Homo sapiens mRNA; EST DKFZp4340245\_r1 (from clone DKFZp4340245)

EST; expressed sequence tag.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

MIPS, Am Klopsterspitz 18a D-82152 Martinsried, GERMANY

Clone from S. Wiemann, sequenced by Qiagen within the CDNA

sequencing consortium of the German Genome Project

This clone is available at the RZPD in Berlin

```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
PI
PI source 1..4
PI /db_xref="taxon:9606"
PI /organism="Homo sapiens"
PI /clone_id="DKFZp4340245"
PI /clone_11b="434 (synonym: htes3). Vector pSport1; host
PI DH10B; sites NotI + SalI"
PI /dev_stage="adult"
PI /tissue_type="testis"
XX
SQ Sequence 4 BP: 0 A; 2 C; 1 G; 1 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 4;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 g 2

RESULT 17
LOCUS AM672622 4 bp mRNA linear EST 26-SEP-2001
DEFINITION 73c Explanted metanephric mesenchyme induced to differentiate into
cytithelial structures of the nephron ex vivo. Rattus norvegicus
CDNA similar to: embjAL049970.1|HSM800317 Homo sapiens
mRNA: cDNA DKFZp564B102 (from clone DKFZp564B102);, mRNA sequence.
AM672622
AM672622.1 GI:7541102
EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 4)
Pilisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Pilisova,T.M.,
Hilgibocham,K.G., Karavanova,I., Lerman,M. and Perantoni,A.O.,
Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
Genesis 27 (1), 22-31 (2000)
20321327
COMMENT Contact: Pilisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg 538, Room 205, Frederick, MD 21702, USA
Tel: 301 846 1242
Fax: 301 846 4956
Email: pilisov@mail.ncicrf.gov
PCR Primers
FORWARD: ctgagcttcgcgc
BACKWARD: ttaagctttttttt
Insert length: 262 Std Error: 0.00
Seq primer: SP6
High quality sequence stop: 262
POLY-A=yes.

FEATURES
source Location/Qualifiers
1..4
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_11b="Explanted metanephric mesenchyme induced to
differentiate into epithelial structures of the nephron ex
vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"

```

```

/note="Organ: kidney; Vector: pGEM-Teasy (Promega).;
Restriction Enzymes: I, ApaI, AatII, SphI, NcoI, BstXI,
NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI,
SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
PCR-amplified in mRNA differential display analysis;
cloned in pGEM-Teasy (Promega); Its expression is
developmentally regulated during mesenchymal-epithelial
conversion in the metanephric kidney."

BASE COUNT
ORIGIN 1 a 0 c 3 g 0 t

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 9; Length 4;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
Db 1 g 1

```

```

RESULT 18
LOCUS CNS004RB 4 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL054121
AL054121.1 GI:4931932
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 4)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES
source Location/Qualifiers
1..4
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_11b="RPCI-98"
/clone="BACR10A06"
/note="end : TET3"

```

```

BASE COUNT
ORIGIN 1 a 1 c 0 g 2 t

```

```

Query Match
Best Local Similarity 100.0%; Score 1; DB 12; Length 4;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1

```



```

Db      4 C 4

RESULT 19
HSM007310
ID      HSM007310 standard; RNA; EST: 5 BP.
XX
XX      AL042460:
XX
XX      AL042460.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434E1821_r1 (from clone DKFZp434E1821)
XX
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the cDNA
XX      sequencing consortium of the German Genome Project
XX      No sl sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH
XX      FT      source
XX      FT      1..5
XX      FT      /db_xref="taxon:9606"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFZp434E1821"
XX      FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /rissue_type="testis"
XX
XX      SQ      Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other:

Query Match      100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 9 1
        |
DB      1 G 1

RESULT 20
HSM007835/C
ID      HSM007835 standard; RNA; EST: 5 BP.
XX
XX      AL042985:
XX
XX      AL042985.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434N1522_r1 (from clone DKFZp434N1522)
XX
XX      EST: expressed sequence tag.

```

```

XX      XX      Homo sapiens (human)
XX      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      RN      [1]
XX      RP      1-5
XX      RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      RL      MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
XX      CC      sequencing consortium of the German Genome Project
XX      CC      No sl sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      FH      Key      Location/Qualifiers
XX      FT      source
XX      FT      1..5
XX      FT      /db_xref="taxon:9606"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFZp434N1522"
XX      FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /rissue_type="testis"
XX
XX      SQ      Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other:

Query Match      100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 9 1
        |
DB      5 G 5

RESULT 21
HSM011053
ID      HSM011053 standard; RNA; EST: 5 BP.
XX
XX      AL046203:
XX
XX      AL046203.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434D137_r1 (from clone DKFZp434D137)
XX
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      RN      [1]
XX      RP      1-5
XX      RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
XX      RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      RL      MIPs, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      CC      Clone from S. Wiemann, sequenced by BMF within the cDNA
XX      CC      sequencing consortium of the German Genome Project
XX      CC      No sl sequence available
XX      CC      This clone is available at the RZPD in Berlin
XX      CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_lib="434 (synonym: hies3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other:

```

```

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
Db 1 G 1

```

```

RFSUIT 22
BG927410/C standard; RNA; EST: 6 BP.
ID HC927410
XX
AC HC927410;
XX
SV HC927410.1
XX
DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DH HNC1-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
KW EST.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
XX [1]
XX 1-6
XX MEDLINE: 21482651.
XX PUBMED: 11597177.
XX Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
XX Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
XX "Identification and initial characterization of 5000 expressed sequenced
XX RT tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA
XX libraries";
XX Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX Contact: Sanjay Kumar
XX UW2109
XX GlaxoSmithKline
XX 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
XX Tel: 610-270-7245
XX Fax: 610-270-5598
XX Email: sanjay_kumar_1@sk.com
XX Seq primer: T7.
XX
FH Key Location/Qualifiers
FH source 1..6
FH /db_xref="taxon:9606"
FH /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FH Directional"
FH /organism="Homo sapiens"
FH /clone_lib="HNC (Human Normal Cartilage)"
FH /tissue_type="cartilage"

```

```

FT /lab_host="E.coli DH10 B"
SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other:

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
Db 6 G 6

```

```

RESULT 23
HSM003844 standard; RNA; EST: 6 BP.
ID HSM003844
XX
AC AL039368;
XX
SV AL039368.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
KW EST: expressed sequence tag.
XX
XX Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX CC No sl sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH Key Location/Qualifiers
FH source 1..6
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone="DKFZp434I0110"
FH /clone_lib="434 (synonym: hies3). Vector pSPORT1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other:

```

```

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 g 1
Db 1 G 1

```

```

RESULT 24
HSM004423 standard; RNA; EST: 6 BP.
ID HSM004423

```

```

XX AC AL039947;
XX SV AL039947.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX KW EST: expressed sequence tag.
XX US Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX FN [1]
XX RP 1-6
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No sl sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_id="DKFZp434J0112"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 25
HSM007334 standard; RNA; EST; 6 BP.
XX AC AL042484;
XX SV AL042484.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX KW EST: expressed sequence tag.
XX US Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX FN [1]

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No sl sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_id="DKFZp434F0321"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 1; DB 2; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 G 1

RESULT 26
HSM007683/c
ID HSM007683 standard; RNA; EST; 6 BP.
XX AC AL042833;
XX SV AL042833.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX KW EST: expressed sequence tag.
XX US Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX FN [1]
XX RP 1-6
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No sl sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key
XX FH Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"

```

```

FT      /organism="Homo sapiens"
FT      /clone_id="DKFZp434G1622"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites Ncli + SalI"
FT      /dev_stage="adult"
FT      /issue_type="testis"
XX
SU      Sequence 6 BP: 2 A; 2 C; 0 G; 2 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      6 G 6

```

```

RESULT 27
HSM008014/C
11 HSM008014 standard; RNA; EST; 6 BP.
XX
AC AL043164;
XX
SV AL043164.1
XX
12-MAR-1999 (Rel. 59, Created)
12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434F1123_s1 (from clone DKFZp434F1123)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
KA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
KT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
KL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434F1123"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites Ncli + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
XX
SQ Sequence 6 BP: 1 A; 2 C; 0 G; 3 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      5 G 5

```

```

RESULT 28
HSM010918
ID HSM010918 standard; RNA; EST; 6 BP.
XX
AC AL046068;
XX
SV AL046068.1
XX
12-MAR-1999 (Rel. 59, Created)
12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-6
RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by DKFZ within the CDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434F1672"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites Ncli + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
XX
SQ Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      1 G 1

```

```

RESULT 29
HSM010918/C
ID HSM010918 standard; RNA; EST; 6 BP.
XX
AC AL046068;
XX
SV AL046068.1
XX
12-MAR-1999 (Rel. 59, Created)
12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
XX
KM EST; expressed sequence tag.
XX

```

```

II*
/ote="vector: pbluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
Mederholt, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pbluescript II SK- plasmids were excised from the lambda
zap clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806.*

```

		100.0%;	Score 1;	DB 10;	Length 6;	
Query Match			Pred. No. 0;			
Best Local Similarity		100.0%;				
Matches	1;	Conservative	0;	Mismatches	0;	Gaps 0
QY	1 g 1					
Dd	1 G 1					

RESULT 31				
BE726686/C				
LOCUS	BE726686	6 bp	mRNA	linear
DEFINITION	894095D11.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II			
ACCESSION	Chlamydomonas reinhardtii cDNA, mRNA sequence.			
	BE726686			

VERSION BE/2608b.1 GI:10128110  
 KEYWORDS EST.  
 SOURCE Chlamydomonas reinhardtii.  
 ORGANISM Chlamydomonas reinhardtii  
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 Chlamydomonadaceae; Chlamydomonas.  
 1 (bases 1 to 6)

NOTIONS	TITLE	JOURNAL COMMENT
Gerschlager, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McMichael, J. P., Sillflow, C., Stern, D., and Surzycyl, R.	Analyses of the <i>Chlamydomonas reinhardtii</i> Genome: A Model, Unellular System for Analyzing Gene Function and Regulation in Vascular Plants: project phase 2	Unpublished (2000)
		Contact: Charles Hauser

DCMB, Box 91000  
Duke University  
Durham, NC 27708-1000  
Tel.: 919 613 8159  
Fax: 919 613 8177  
Email: [chauser@duke.edu](mailto:chauser@duke.edu).

SOURCE

1. .6  
/organism="Chlamydomonas reinhardtii"  
/strain="CC-1690 wild type mt+ 21gr"  
/db\_xref="taxon:3055"  
/clone\_1lb="C. reinhardtii CC-1690, normalized, lambda zap  
IT"

/note="Vector: pBluescript II SK-; site.1: EcoRI; site.2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1650 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO<sub>2</sub> and HS medium bubbled with 5% CO<sub>2</sub>. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene). In the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exsistit (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 0 a 1 c 5 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
1  
Db 2 G 2

RESULT 32

ID BG897546 standard; RNA; EST: 7 BP.

XX BG897546;

XX BG897546.1

SV BG897546.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA, mRNA

XX sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

XX 1-7

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

SA Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

libraries";

KL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

XX UW2109

XX GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsf.com

CC Seq primer: T7.

XX Key Location/Qualifiers

XX source

XX 1..7

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone\_lib="HOA (Human Osteoarthritic Cartilage)"

FT /tissue\_type="cartilage"

FT /lab\_host="E.coli DH10 B"

XX SO

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 2; Length 7;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

1

Db 6 G 6

RESULT 33

ID BG897546/C standard; RNA; EST: 7 BP.

XX BG897546;

XX BG897546.1

SV BG897546.1

DT 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA, mRNA

XX sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

XX 1-7

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

SA Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

libraries";

KL Osteoarthritic Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

XX UW2109

XX GlaxoSmithKline

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CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsf.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source

XX 1..7

FT /db\_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

FT Directional"

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FT /clone\_lib="HOA (Human Osteoarthritic Cartilage)"

FT /tissue\_type="cartilage"

FT /lab\_host="E.coli DH10 B"

XX SO

Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 2; Length 7;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1

1

Db 7 G 7

RESULT 34

HS0007412

ID HSM007412 standard; RNA; EST: 7 BP.

XX AL042562;

XX AL042562.1

SV AL042562.1

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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-7
KA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH
FI Source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
FT
SO Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST: 7 BP.
XX
AC AL042562;
XX
SV AL042562.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
DE Homo sapiens mRNA; EST DKFZp434J1721_r1 (from clone DKFZp434J1721)
XX EST: expressed sequence tag.
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-7
KA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH
FI Source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT
SO Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

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```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH
FI Source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT
SO Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST: 7 BP.
XX
AC AL042652;
XX
SV AL042652.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
DE Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX EST: expressed sequence tag.
KM Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-7
KA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH
FI Source
FT 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT
SO Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

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FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 7 BP: 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 2 G 2

RESULT 37  
 HSM007502/c  
 ID HSM007502 standard; RNA: EST; 7 BP.  
 AC AL042652;  
 XX AL042652.1  
 SV  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA: EST DKFZp434N1921\_r1 (from clone DKFZp434N1921)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP 1-7  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC No st sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key Location/Qualifiers  
 FT source 1..7  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="DKFZp434N1921"  
 FT DH10B; sites NOTI + SalI  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 7 BP: 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 1 G 1

RESULT 38  
 C58888

LOCUS C58888 7 bp mRNA linear EST 22-SEP-1997  
 DEFINITION C58888 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA  
 accession clone yk383a7 3', mRNA sequence.  
 C58888  
 ACCESSION C58888.1 GI:2417593  
 VERSION EST.  
 KEYWORDS Caenorhabditis elegans.  
 SOURCE Caenorhabditis elegans.  
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 ; Rhabditidae; Peliorderinae; Caenorhabditis.  
 REFERENCE 1 (bases 1 to 7)  
 Kohara,Y., Mochizuki,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
 M., Miyata,A. and Nishigaki,A.  
 Expression map of the C.elegans genome  
 Unpublished (1996)  
 COMMENT Contact: Yuji Kohara  
 National Institute of Genetics  
 Yata 1111, Mishima, Shizuoka 411, Japan  
 Tel: 81-559-81-6854  
 Fax: 81-559-81-6855  
 Email: ykohara@lab.nig.ac.jp.

FEATURES  
 source Location/Qualifiers  
 1..7  
 /organism="Caenorhabditis elegans"  
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 /db\_xref="taxon:6239"  
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 /clone\_lib="Yuji Kohara unpublished cDNA"  
 /sex="hermaphrodite, male"  
 /tissue\_type="whole animal"  
 /dev\_stage="varied"  
 BASE COUNT 2 a 0 c 1 g 3 t 1 others  
 ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1  
 Db 7 G 7

RESULT 39  
 HSM001420/c  
 ID HSM001420 standard; RNA: EST; 8 BP.  
 AC AL037095;  
 XX AL037095.1  
 SV  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA: EST DKFZp564L2064\_r1 (from clone DKFZp564L2064)  
 XX  
 KW EST; expressed sequence tag.  
 XX

OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP 1-8  
 RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA  
 CC sequencing consortium of the German Genome Project



```
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FH source
FH 1..8
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone="DKFZp564L071"
FH /clone_1lb="564 (synonym: hibr2). Vector pAMP1: host
FH X1-2blue: sites NotI + SalI"
FH /dev_stage="fetal"
FH /tissue_type="brain"
XX
SU Sequence 8 BP: 2 A; 3 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
DB 7 G 7

RESULT 40
HSM001743/c
ID HSM001741 standard; RNA; EST; 8 BP.
XX
XX AL037413;
XX
XX AL037413.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp564L071_s1 (from clone DKFZp564L071)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
XX [1]
XX RN 1-8
XX RP Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
XX RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by GBF within the CDNA
XX sequencing consortium of the German Genome Project
XX
XX No s1 sequence available
XX
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source
XX 1..8
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp564L071"
XX /clone_1lb="564 (synonym: hibr2). Vector pAMP1: host
XX X1-2blue: sites NotI + SalI"
XX /dev_stage="fetal"
XX /tissue_type="brain"
XX
SU Sequence 8 BP: 1 A; 7 C; 0 G; 0 T; 0 other;
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Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
DB 7 G 7

RESULT 41
HSM004451
ID HSM004451 standard; RNA; EST; 8 BP.
XX
XX AL039975;
XX
XX AL039975.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
XX [1]
XX RN 1-8
XX RP Duysterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX sequencing consortium of the German Genome Project
XX
XX No s1 sequence available
XX
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX
XX source
XX 1..8
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZp434K0712"
XX /clone_1lb="434 (synonym: htes3). Vector pSport1: host
XX DH10B: sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
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SU Sequence 8 BP: 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 9 1
DB 1 G 1

RESULT 42
HSM004451/c
ID HSM004451 standard; RNA; EST; 8 BP.
XX
XX AL039975;
XX
```

```
SV      AL039975.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      1-8
XX      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Olagen within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No sl sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..8
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone="DKFZp434K0712"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other:
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XX      Query Match      100.0%; Score 1; DB 2; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 g 1
DB      8 C 8

RESULT 43
HSM007277 standard; RNA; EST; 8 BP.
XX
XX      AL042427;
XX
XX      AL042427.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      1-8
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No sl sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..8
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone="DKFZp434C2421"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other:
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RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No sl sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX
XX      source      1..8
XX                  /db_xref="taxon:9606"
XX                  /organism="Homo sapiens"
XX                  /clone="DKFZp434C2421"
XX                  /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX                  DH10B; sites NotI + SalI"
XX                  /dev_stage="adult"
XX                  /tissue_type="testis"
XX
XX      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other:
XX
XX      Query Match      100.0%; Score 1; DB 2; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 g 1
DB      1 C 1

RESULT 44
HSM007277/c standard; RNA; EST; 8 BP.
XX
XX      AL042427;
XX
XX      AL042427.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
XX      EST: expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      1-8
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No sl sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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XX                  /organism="Homo sapiens"
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XX      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other:
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Search completed: July 15, 2002, 20:07:36  
 Job time: 14494 sec

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SO Sequence 8 BP: 2 A; 2 C; 2 G; 2 T; 0 other;

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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1  
 DB 8 G 8

## RESULT 45

HSM007323  
 ID HSM007323 standard; RNA; EST; 8 BP.

AC AL042473;

SV AL042473.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434F0121\_r1 (from clone DKFZp434F0121)

XX EST: expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX

RN

RP 1-8

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC NO 81 sequence available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

Key Location/Qualifiers

FT source

FT 1..8

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434F0121"

FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

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SO Sequence 8 BP: 2 A; 2 C; 2 G; 2 T; 0 other;

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100.0%; Score 1; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1

DB 1 G 1

Tue Jul 16 09:39:30 2002

us-09-375-248-1\_copy\_3164\_3164.oli.rst

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:07 ; Search time 9532.94 Seconds

(without alignments)

2.195 Million cell updates/sec

Title: us-09-375-248-1\_COPY-3360\_3360

Perfect score: 1 c 1

Sequence: 1 c 1

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_da:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C	2	100.0	2	6	AX092442	Sequence
C	3	100.0	2	6	AX092443	Sequence
C	4	100.0	2	6	AX092444	Sequence
C	5	100.0	2	6	AX092445	Sequence
C	6	100.0	2	6	AX092446	Sequence
C	7	100.0	2	6	AX092447	Sequence
C	8	100.0	2	6	AX092448	Sequence
C	9	100.0	2	6	AX092449	Sequence
C	10	100.0	2	6	AX092450	Sequence
C	11	100.0	2	6	AX092451	Sequence
C	12	100.0	2	6	AX092452	Sequence
C	13	100.0	2	6	AX092453	Sequence
C	14	100.0	2	6	AX092454	Sequence
C	15	100.0	2	6	AX092455	Sequence
C	16	100.0	2	6	AX092456	Sequence
C	17	100.0	2	6	AX092457	Sequence
C	18	100.0	2	6	AX092458	Sequence
C	19	100.0	2	6	AX092459	Sequence
C	20	100.0	2	6	AX092460	Sequence
C	21	100.0	2	6	AX092461	Sequence
C	22	100.0	2	6	AX092462	Sequence
C	23	100.0	2	6	AX092463	Sequence
C	24	100.0	2	6	AX092464	Sequence
C	25	100.0	2	6	AX092465	Sequence
C	26	100.0	2	6	AX092466	Sequence
C	27	100.0	2	6	AX092467	Sequence
C	28	100.0	2	6	AX092468	Sequence
C	29	100.0	2	6	AX092469	Sequence
C	30	100.0	2	6	AX092470	Sequence
C	31	100.0	2	6	AX092471	Sequence
C	32	100.0	2	6	AX092472	Sequence
C	33	100.0	2	6	AX092473	Sequence
C	34	100.0	2	6	AX092474	Sequence
C	35	100.0	2	6	AX092475	Sequence

#### ALIGNMENTS

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DEFINITION	Sequence 2 from Patent WO0116366.					
ACCESSION	AX092441					
VERSION	AX092441.1	GI:13444536				
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 2)					
AUTHORS	Kless,H.					
TITLE	Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks					
JOURNAL	Patent: WO 0116366-A 2 08-MAR-2001;					
	YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar					
	(IL)					

#### FEATURES

Source

BASE COUNT 1 a 1 c 0 g 0 t

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 C 2

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DEFINITION Sequence 3 from Patent WO0116366.  
ACCESSION AX092442  
VERSION AX092442.1 GI:13444537  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 3 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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source Location/Qualifiers  
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DEFINITION Sequence 5 from Patent WO0116366.  
ACCESSION AX092444  
VERSION AX092444.1 GI:13444539  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 5 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
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/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t  
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OY 1 C 1  
DB 1 C 1

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LOCUS AX092445 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 6 from Patent WO0116366.  
ACCESSION AX092445  
VERSION AX092445.1 GI:13444540  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 6 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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BASE COUNT 0 a 2 c 0 g 0 t  
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OY 1 C 1  
DB 1 C 1

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LOCUS AX092446 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 7 from Patent WO0116366.  
ACCESSION AX092446  
VERSION AX092446.1 GI:13444541  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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Db 1 c 1

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ACCESSION AX092446  
VERSION AX092446.1 GI:13444541  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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Db 2 c 2

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DEFINITION Sequence 8 from Patent WO0116366.  
ACCESSION AX092447  
VERSION AX092447.1 GI:13444542  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1

Db 1 c 1

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DEFINITION Sequence 9 from Patent WO0116366.  
ACCESSION AX092448  
VERSION AX092448.1 GI:13444543  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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BASE COUNT 1 a 0 c 1 g 0 t  
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Best Local Similarity 100.0%; Pred. No. 0;  
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OY 1 c 1  
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RESULT 9  
LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 10 from Patent WO0116366.  
ACCESSION AX092449  
VERSION AX092449.1 GI:13444544  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;  
VEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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BASE COUNT 0 a 1 c 1 g 0 t  
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Best Local Similarity 100.0%; Pred. No. 0;  
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OY 1 c 1  
Db 2 c 2

RESULT 10  
AX092449/c 2 bp DNA PAT 21-MAR-2001  
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DEFINITION Sequence 10 from Patent WO0116366.  
ACCESSION AX092449  
VERSION AX092449.1 GI:13444544  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 c 1

RESULT 11  
AX092450/c 2 bp DNA PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 11 from Patent WO0116366.  
ACCESSION AX092450  
VERSION AX092450.1 GI:13444545  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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Best Local Similarity 100.0%; Pred. No. 0;  
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OY 1 c 1  
DB 2 c 2

RESULT 12  
AX092451/c 2 bp DNA PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 12 from Patent WO0116366.  
ACCESSION AX092451  
VERSION AX092451.1 GI:13444546  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source Location/Qualifiers  
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/note="synthetic oligonucleotide;"  
BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
DB 2 c 2

DEFINITION Sequence 12 from Patent WO0116366.  
ACCESSION AX092451  
VERSION AX092451.1 GI:13444546  
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ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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BASE COUNT 0 a 0 c 1 g 1 t  
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Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
DB 1 c 1

RESULT 13  
AX092453  
LOCUS  
DEFINITION Sequence 14 from Patent WO0116366.  
ACCESSION AX092453  
VERSION AX092453.1 GI:13444548  
KEYWORDS  
SOURCE  
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OY 1 c 1  
DB 1 c 1

RESULT 14  
AX092454/c 2 bp DNA PAT 21-MAR-2001  
LOCUS  
DEFINITION Sequence 15 from Patent WO0116366.  
ACCESSION AX092454  
VERSION AX092454.1 GI:13444549

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
DB 2 c 2



KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

unclassified.  
1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 15 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

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BASE COUNT  
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Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
Db 2 c 2

RESULT 15  
AX092528  
LOCUS AX092528 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 89 from Patent WO0116366.  
ACCESSION AX092528  
VERSION AX092528.1 GI:13444623  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 89 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
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BASE COUNT  
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Query Match  
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
Db 1 c 1

RESULT 16  
AX092529  
LOCUS AX092529 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 90 from Patent WO0116366.  
ACCESSION AX092529  
VERSION AX092529.1 GI:13444624  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

unclassified.  
1 (bases 1 to 2)  
Kless, H.  
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 90 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
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Location/Qualifiers  
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BASE COUNT  
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Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
Db 2 c 2

RESULT 17  
AX092530/c  
LOCUS AX092530 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 91 from Patent WO0116366.  
ACCESSION AX092530  
VERSION AX092530.1 GI:13444625  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
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Location/Qualifiers  
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BASE COUNT  
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Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
Db 2 c 2

RESULT 18  
AX092538  
LOCUS AX092538 2 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 99 from Patent WO0116366.  
ACCESSION AX092538  
VERSION AX092538.1 GI:13444633  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 016366-A 99-08-MAR-2001;  
VPDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) : Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..2 /organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 1 c 1

RESULT 19  
LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 50 from Patent WO0144465.  
ACCESSION AX175286  
VERSION AX175286.1 GI:14598654  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 2)  
AUTHORS Phillips,N.C. and Fillon,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)

FEATURES  
source Location/Qualifiers  
1..2 /organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 1 c 1

RESULT 20  
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 51 from Patent WO0144465.  
ACCESSION AX175287  
VERSION AX175287.1 GI:14598655  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 2)  
AUTHORS Phillips,N.C. and Fillon,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)

FEATURES  
source Location/Qualifiers  
1..2 /organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 2 c 2

RESULT 21  
LOCUS BD009609 2 bp DNA linear PAT 31-JAN-2002  
DEFINITION Probes, methods and kits for detection and typing of Helicobacter pylori, nucleic acids in biological samples.  
ACCESSION BD009609  
VERSION BD009609.1 GI:18637982  
KEYWORDS JP 2001502536-A/201.  
SOURCE unidentified.  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2)  
AUTHORS Quint,W. and Doorn,L.J.V.  
TITLE Probes, methods and kits for detection and typing of Helicobacter pylori, nucleic acids in biological samples  
JOURNAL Patent: JP 2001502536-A 201 27-FEB-2001;  
INNOGENETICS NV,DDL BV

COMMENT OS Unidentified  
PN JP 2001502536-A/201  
PD 27-FEB-2001  
PF 10-OCT-1997 JP 1998518004  
PR 16-OCT-1996 EP 96870131.8  
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN  
PC C12Q1/68,C07K14/205,C12N15/11  
CC  
FH Key  
FT source Location/Qualifiers

FEATURES  
source Location/Qualifiers  
1..2 /organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 0 a 1 c 0 g 0 t 1 others  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 2 c 2

RESULT 22  
LOCUS CNS01C99 2 bp mRNA linear PLN 02-SEP-1999  
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.  
ACCESSION AL115237  
VERSION AL115237.1 GI:5829856  
KEYWORDS cDNA library; nitrogen deprivation.  
SOURCE Botryotinia fuckeliana.  
ORGANISM Botryotinia fuckeliana.

REFERENCE 1 (bases 1 to 2)  
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.  
Bliton,F., Levis,C., Fortini,D., Pradler,J.M. and Brygoo,Y.

TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,  
78026 Versailles, France  
REFERENCE 2 (bases 1 to 2)  
AUTHORS Genoscope.  
JOURNAL Direct Submission  
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage ;  
CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT The cDNA library to be analyzed within the framework of this  
project was created using a Botrytis cinerea strain which was grown  
under conditions of nitrogen deprivation, which is the normal  
situation for B. cinerea during its development on its host plant.  
The library was produced in an oriented direction, in the pBSII  
vector.

FEATURES  
source location/Qualifiers  
1..2  
/organism="Botryocinia fuckelliana"  
/strain="T4"  
/db\_xref="taxon:40559"  
/note="Genoscope sequence ID : W04F091"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
1  
1 c 1

Db 1 c 1

RESULT 23  
AC079635/c 3 bp DNA linear HTG 14-AUG-2001  
LOCUS AC079635  
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC079635.3 GI:14647267  
VERSION AC079635.3  
KEYWORDS HTG: HTGS\_PHASE0.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
McCombie, W.R., Baker, J.P., Baheti, A., Yang, C., Balija, V.,  
Dechka, N.N., de la Bastide, M., Kuhl, R., King, L., Kirchoff, K.A.,  
Miller, B., Mascimendo, L.U., O'Shaughnessy, A.L., Preston, R.R.,  
Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L.,  
Vil, M.D. and Zlatavern, T.  
JOURNAL Mouse Genomic Sequence  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 3)  
JOURNAL McCombie, W.R.  
TITLE Direct Submission  
COMMENT Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing  
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring  
Harbor, NY 11724, USA  
On Jul 10, 2001 this sequence version replaced gi:14595773.  
\* NOTE: This record contains 1 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
3: contig of 3 bp in length.  
This entry has been temporarily removed. An update for RP23-152L20

will be submitted as soon as it becomes available.  
Location/Qualifiers  
1..3  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="RP23-152L20"

BASE COUNT 1 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
1  
1 c 1

Db 3 c 3

RESULT 25  
A97991  
LOCUS A97991  
DEFINITION Sequence 21 from Patent W09914366.  
ACCESSION A97991  
VERSION A97991.1 GI:6781229  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified

RESULT 24  
CHNCAMC5/c 3 bp DNA linear VRT 17-JUL-2000  
LOCUS CHNCAMC5  
DEFINITION Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.  
ACCESSION M23994 J04140  
VERSION M23994.1 GI:212442  
KEYWORDS  
SEGMENT 5 of 6  
SOURCE chicken.  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Prediger, E.A., Hoffman, S., Edelman, G.M. and Cunningham, B.A.  
TITLE Four exons encode a 93-base-pair insert in three neural cell  
adhesion molecule mRNAs specific for chicken heart and skeletal  
muscle  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)  
MEDLINE 89071747  
PUBMED 3200847  
COMMENT Exon 12D represents a very small exon.  
LOCATION/Qualifiers  
1..3  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pEC101B"  
/tissue\_type="cardiac muscle"  
/dev\_stage="day 10 embryo"  
1..3  
/gene="NACM"  
/number=12

BASE COUNT 2 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 5; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1  
1  
1 c 1

Db 3 c 3

unclassified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willieme,M.J. and Van,D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 1 c 1

RESULT 26  
A97991/c  
LOCUS A97991 Sequence 21 from Patent WO9914366. 3 bp DNA linear PAT 26-JAN-2000  
DEFINITION A97991  
ACCESSION A97991  
VERSION A97991.1 GI:6781229  
KEYWORDS  
SOURCE  
ORGANISM  
unclassified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Pongers-Willieme,M.J. and Van,D.J.  
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES  
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;  
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 0 a 1 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 1 c 1

RESULT 27  
AX092457  
LOCUS AX092457 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 18 from Patent WO0116366.  
ACCESSION AX092457  
VERSION AX092457.1 GI:13444552  
KEYWORDS  
SOURCE  
ORGANISM  
unclassified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)  
FEATURES  
source Location/Qualifiers

source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 1 c 1

RESULT 28  
AX092458/c  
LOCUS AX092458 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 19 from Patent WO0116366.  
ACCESSION AX092458  
VERSION AX092458.1 GI:13444553  
KEYWORDS  
SOURCE  
ORGANISM  
unclassified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 1 c 1

RESULT 29  
AX092460  
LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 21 from Patent WO0116366.  
ACCESSION AX092460  
VERSION AX092460.1 GI:13444555  
KEYWORDS  
SOURCE  
ORGANISM  
unclassified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar  
(IL)  
FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
1  
Db 2 c 2

## RESULT 30

AX092461 AX092461 3 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 22 from Patent W00116366.  
DEFINITION AX092461  
ACCESSION AX092461  
VERSION AX092461.1 GI:13444556  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 3)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 22 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source Location/Qualifiers

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
1  
Db 2 c 2

## RESULT 31

AX092462 AX092462 3 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 23 from Patent W00116366.  
DEFINITION AX092462  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 3)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source Location/Qualifiers

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
1  
Db 2 c 2

## RESULT 32

AX092462 AX092462 3 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 23 from Patent W00116366.  
DEFINITION AX092462  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 3)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source Location/Qualifiers

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
1  
Db 3 c 3

## RESULT 33

AX092463 AX092463 3 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 24 from Patent W00116366.  
DEFINITION AX092463  
ACCESSION AX092463  
VERSION AX092463.1 GI:13444558  
KEYWORDS  
SOURCE

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 3)  
Kless,H.  
Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 24 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source Location/Qualifiers

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t  
ORIGIN  
Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 2 C 2

RESULT 34  
AX092464/C  
LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 25 from Patent WO0116366.  
ACCESSION AX092464  
VERSION AX092464.1 GI:13444559  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 25 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 2 a 0 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 2 C 2

RESULT 35  
AX092465  
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 3 C 3

RESULT 36  
AX092465/C  
LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 26 from Patent WO0116366.  
ACCESSION AX092465  
VERSION AX092465.1 GI:13444560  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 26 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 1 c 1 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 2 C 2

RESULT 37  
AX092466/C  
LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 27 from Patent WO0116366.  
ACCESSION AX092466  
VERSION AX092466.1 GI:13444561  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 27 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"  
BASE COUNT 1 a 0 c 2 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 3 C 3

RESULT 38  
AX092467/c  
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 28 from Patent WO0116366.  
ACCESSION AX092467  
VERSION AX092467.1 GI:13444562  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"  
BASE COUNT 1 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 39  
AX092469  
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 30 from Patent WO0116366.  
ACCESSION AX092469  
VERSION AX092469.1 GI:13444564  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"  
BASE COUNT 1 a 1 c 0 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 40

AX092470/c  
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 31 from Patent WO0116366.  
ACCESSION AX092470  
VERSION AX092470.1 GI:13444565  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"  
BASE COUNT 1 a 0 c 1 g 1 t  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 41  
AX092472  
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 33 from Patent WO0116366.  
ACCESSION AX092472  
VERSION AX092472.1 GI:13444567  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide:"  
BASE COUNT 2 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 42  
AX092473  
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 34 from Patent WO0116366.

ACCESSION AX092473  
VERSION AX092473.1 GI:13444568  
KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using

JOURNAL oligonucleotide triphosphates building blocks

Patent: WO 0116366-A 34 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers

1..3

/organism="unidentified"

/db\_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 1 c 1

RESULT 43

AX092474

LOCUS AX092474 3 bp DNA

DEFINITION Sequence 35 from Patent WO0116366. linear PAT 21-MAR-2001

ACCESSION AX092474

VERSION AX092474.1 GI:13444569

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using

JOURNAL oligonucleotide triphosphates building blocks

Patent: WO 0116366-A 35 03-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers

1..3

/organism="unidentified"

/db\_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 1 c 1

RESULT 44

AX092474

LOCUS AX092474 3 bp DNA

DEFINITION Sequence 35 from Patent WO0116366. linear PAT 21-MAR-2001

ACCESSION AX092474

VERSION AX092474.1 GI:13444569

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using

JOURNAL oligonucleotide triphosphates building blocks

Patent: WO 0116366-A 35 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers

1..3

/organism="unidentified"

/db\_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 3 c 3

RESULT 45

AX092475

LOCUS AX092475 3 bp DNA

DEFINITION Sequence 36 from Patent WO0116366. linear PAT 21-MAR-2001

ACCESSION AX092475

VERSION AX092475.1 GI:13444570

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)

AUTHORS Kless, H.

TITLE Template-dependent nucleic acid polymerization using

JOURNAL oligonucleotide triphosphates building blocks

Patent: WO 0116366-A 36 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers

1..3

/organism="unidentified"

/db\_xref="taxon:32644"

/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 1 c 1

Search completed: July 15, 2002, 23:28:08  
Job time: 24541 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:10 ; Search time 932.4 Seconds

(Without alignment)  
1.841 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3360\_3360

Perfect score: 1 c 1

Scoring table: OLIGO\_NUC  
Capopt 60.0 , Capext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1	100.0	3	17	AAT33326			CAPL trinucleotide
2	1	100.0	3	17	AAT33326			CAPL trinucleotide
3	1	100.0	3	17	AAAG4655			Human TUB gene pro
4	1	100.0	3	22	AAAL20244			Human breast cance
5	1	100.0	4	16	AAO81664			bFGF binding oligo
6	1	100.0	4	16	AAO81664			bFGF binding oligo
7	1	100.0	4	16	AAO81665			bFGF binding oligo
8	1	100.0	4	16	AAO81665			bFGF binding oligo
9	1	100.0	4	18	AAAT86385			Probe for target n

C	10	1	100.0	4	18	AAT86385	Probe for target n
C	11	1	100.0	4	18	AAT77252	Immunostimulatory
C	12	1	100.0	4	18	AAT77252	Immunostimulatory
C	13	1	100.0	4	22	AAAL17191	Human breast cance
C	14	1	100.0	4	22	AAAL17191	Human breast cance
C	15	1	100.0	4	22	AAAL24357	Human breast cance
C	16	1	100.0	4	22	AAAF61450	Cyclin binding ham
C	17	1	100.0	5	10	AAAN93676	Synthetic probe fo
C	18	1	100.0	5	15	AAQ68752	CHA255 heavy chain
C	19	1	100.0	5	16	AAO81667	bFGF binding oligo
C	20	1	100.0	5	17	AAAT12043	Cleavable replicab
C	21	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	22	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	23	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	24	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
C	25	1	100.0	5	20	AAAT20695	Fungal telomeric n
C	26	1	100.0	5	20	AAAT20695	Oligonucleotide se
C	27	1	100.0	5	20	AAAT21611	Oligonucleotide se
C	28	1	100.0	5	20	AAAT21611	DNA enhancer seque
C	29	1	100.0	5	20	AAV72347	DNA enhancer seque
C	30	1	100.0	5	20	AAV72348	US508745 primer #
C	31	1	100.0	5	20	AAV72348	US508745 primer #
C	32	1	100.0	5	20	AAV72349	US508745 primer #
C	33	1	100.0	5	20	AAV72350	US508745 primer #
C	34	1	100.0	5	20	AAV72350	US508745 primer #
C	35	1	100.0	5	20	AAV72350	Ras gene modulat
C	36	1	100.0	5	20	AAV72350	Ras gene modulat
C	37	1	100.0	5	20	AAV72350	Mutant H-ras speci
C	38	1	100.0	5	21	AAV72350	Human colon cancer
C	39	1	100.0	5	21	AAV72350	Human colon cancer
C	40	1	100.0	5	21	AAV72350	Transcription fact
C	41	1	100.0	5	21	AAV72350	Transcription fact
C	42	1	100.0	5	21	AAV72350	Human UCP3 promote
C	43	1	100.0	5	21	AAV72350	Human UCP3 promote
C	44	1	100.0	5	21	AAV72350	Human UCP3 promote
C	45	1	100.0	5	21	AAV72350	First DNA arm segm

#### ALIGNMENTS

RESULT	1
ID	AAT33326 standard; RNA; 3 BP.
AC	AAT33326;
XX	
XX	12-NOV-1996 (first entry)
DT	
DE	CAPL trinucleotide.
XX	
XX	CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
KW	osteosarcoma; therapy; ss.
XX	
OS	Synthetic.
XX	
PM	MO9625499-AL.
XX	
PD	22-AUG-1996.
XX	
XX	16-FEB-1996; 96WO-0502108.
XX	
PR	17-FEB-1995; 95US-0391375.
XX	
PA	(HYBR-) HYBRIDON INC.
PA	(NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX	
PI	Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandemo GJ;
XX	Von Hofe E;
XX	WPI: 1996-393400/39.
DR	
XX	Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

PT useful to inhibit metastatic cancer, partic. osteosarcoma  
 XX  
 PS Claim 2: Page 56; 70pp; English.  
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
 CC expression may include the trinucleotide GUC (AAT33326, given in 5',  
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
 CC other antisense oligonucleotides (AAT33327-36) complementary to  
 CC specific regions of the CAPL gene (see also AAT33345), as well as  
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
 CC patient as a means of inhibiting metastatic cancer.  
 XX  
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 OY 1 c 1  
 Db 1 c 1

RESULT 2  
 AAT33326/c  
 ID AAT33326 standard; RNA; 3 BP.  
 XX  
 AC AAT33326;  
 XX  
 DT 12-NOV-1996 (first entry)  
 XX  
 DE CAPL trinucleotide.  
 XX  
 KW CAPL: antisense oligonucleotide; ribozyme; cancer; metastasis;  
 KM osteosarcoma; therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9625499-A1.  
 XX  
 PD 22-AUG-1996.  
 XX  
 PF 16-FEB-1996; 96WO-US02108.  
 XX  
 PR 17-FEB-1995; 95US-0391375.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PA (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.  
 XX  
 PI Agrawal S, Enggebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;  
 PI Von Hofe E;  
 XX  
 DR WPI: 1996-393400/39.  
 XX  
 PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -  
 PT useful to inhibit metastatic cancer, partic. osteosarcoma  
 XX  
 PS Claim 2: Page 56; 70pp; English.  
 XX  
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
 CC expression may include the trinucleotide GUC (AAT33326, given in 5',  
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
 CC other antisense oligonucleotides (AAT33327-36) complementary to  
 CC specific regions of the CAPL gene (see also AAT33345), as well as  
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
 CC patient as a means of inhibiting metastatic cancer.  
 XX  
 SO Sequence 3 BP: 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 OY 1 c 1  
 Db 3 C 3

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 ID AAA94655 standard; DNA; 3 BP.  
 XX  
 AC AAA94655;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human TUB gene probe #2.  
 XX  
 KW Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;  
 KM TUB; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6114502-A.  
 XX  
 PD 05-SEP-2000.  
 XX  
 PF 27-FEB-1998; 98US-0032365.  
 XX  
 PR 22-AUG-1996; 96US-0701380.  
 PR 04-SEP-1996; 96US-0706282.  
 PR 10-APR-1996; 96US-0630592.  
 PR 17-SEP-1996; 96US-0714991.  
 PR 30-APR-1997; 97US-0850218.  
 PR 01-AUG-1997; 97US-0904699.  
 PR 17-SEP-1997; 97US-0932306.  
 XX  
 PA (AXYS-) AXYS PHARM INC.  
 XX  
 PI North M, Nishina P, Noben-Trauth K, Nagert J;  
 XX  
 DR WPI: 2000-586483/55.  
 XX  
 PT Mammalian proteins expressed in retina and brain, useful for producing  
 PT antibodies and for diagnosing neurosensory defects including cochlear  
 PT degeneration, peripheral retinal degeneration and cone-rod retinal  
 PT dystrophy -  
 XX  
 PS Disclosure; Columns 81-82; 61pp; English.  
 XX  
 CC The present invention relates to human and murine cDNAs from a  
 CC neurosensory defect associated gene family. The novel cDNAs are mouse  
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB  
 CC form 6 (see AAA94632), human TUB form I (see AAA94633), human TULP1 (see  
 CC AAA94633), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and  
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as  
 CC immunogens to raise antibodies that specifically identify TUB/TULP  
 CC expressing cells and in drug screening assays directed at neurosensory  
 CC defects. The novel proteins encoded by the present sequence can be used  
 CC for the treatment of neurosensory degenerative conditions e.g. retinal  
 CC dystrophies. The present sequence is a probe used to isolate the novel  
 CC genes of the present invention.  
 XX  
 SO Sequence 3 BP: 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 OY 1 c 1  
 Db 3 C 3

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ID AAL20244
XX AAL20244 standard: cDNA: 3 BP.
AC AAL20244:
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 12701.
DE
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX
XX 19-JUL-2001.
PD
XX
XX 10-JAN-2001: 2001WO-US00798.
PF
XX 14-JAN-2000: 2000US-0176077.
PR 14-MAR-2000: 2000US-0189167.
PR 24-MAR-2000: 2000US-0192099.
PR 29-MAR-2000: 2000US-0193480.
PR 15-MAY-2000: 2000US-0205230.
PR 09-JUN-2000: 2000US-0211315.
PR 25-JUL-2000: 2000US-0220534.
XX
XX (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI
XX
XX WPI: 2001-451856/48.
DR
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX
XX Claim 1: Page 2245; 3695PP; English.
PS
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing, treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 3 BP: 1 A; 1 C; 0 G; 1 T; 0 other;
SQ

Query Match 100.0%; Score 1: DB 22; Length 3:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 2 c 2

RESULT 5
ID AAO81664 standard: RNA: 4 BP.
XX
XX AAO81664:
AC
XX
XX 29-SEP-1995 (first entry)
DT
XX
XX bFGF binding oligomer core sequence #1.
DE
XX
XX Basic; fibroblast growth factor; bFGF; stem-loop structure;
KM bubble structure; pseudoknot; receptor; heparin; competition;
XX
```

```
KM inhibition; enhance; neovascularisation; solid tumour; cancer;
KM metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
OS
XX WO9500528-A.
PN
XX
XX 05-JAN-1995.
PD
XX
XX 17-JUN-1994: 94WO-US06884.
PF
XX
XX 18-JUN-1993: 93US-0079677.
PR 07-JAN-1994: 94US-0179491.
PR
XX
XX (PHAR-) PHARMAGENICS INC.
PA
XX
XX Beutel BA, Joesten ME;
PI
XX
XX WPI: 1995-051992/07.
DR
XX
XX New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
XX Claim 3: Page 25; 44pp; English.
PS
XX
XX The sequences given in AAO81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAO81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
XX Sequence 4 BP: 0 A; 1 C; 2 G; 1 U; 0 other;
SQ

Query Match 100.0%; Score 1: DB 16; Length 4:
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1
DB 4 c 4

RESULT 6
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XX
XX AAO81664 standard: RNA: 4 BP.
AC
XX
XX 29-SEP-1995 (first entry)
DT
XX
XX bFGF binding oligomer core sequence #1.
DE
XX
XX Basic; fibroblast growth factor; bFGF; stem-loop structure;
KM bubble structure; pseudoknot; receptor; heparin; competition;
KM inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
OS
XX
XX WO9500528-A.
PN
XX
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PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994: 94WO-US06884.  
 XX  
 PR 18-JUN-1993: 93US-0079677.  
 PR 07-JAN-1994: 94US-0179491.  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DK WPI: 1995-051992/07.  
 XX  
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 4 BP: 0 A: 1 C: 2 G: 1 U: 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 16; Length 4;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 c 1  
 Db 3 c 3

RESULT 7  
 AA081665  
 ID AA081665 standard; RNA: 4 BP.  
 AC  
 AC AA081665;  
 DT 29-SEP-1995 (first entry)  
 DE  
 DE bFGF binding oligomer core sequence #2.  
 XX  
 KW Basic; fibroblast growth factor: bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 OS Synthetic.  
 XX  
 PN WO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994: 94WO-US06884.  
 XX  
 PR 18-JUN-1993: 93US-0079677.  
 PR 07-JAN-1994: 94US-0179491.  
 XX

PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 4 BP: 0 A: 2 C: 1 G: 1 U: 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 16; Length 4;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 c 1  
 Db 1 c 1

RESULT 8  
 AA081665/C  
 ID AA081665 standard; RNA: 4 BP.  
 AC  
 AC AA081665;  
 DT 29-SEP-1995 (first entry)  
 DE  
 DE bFGF binding oligomer core sequence #2.  
 XX  
 KW Basic; fibroblast growth factor: bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 OS Synthetic.  
 XX  
 PN WO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994: 94WO-US06884.  
 XX  
 PR 18-JUN-1993: 93US-0079677.  
 PR 07-JAN-1994: 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth

f factor - modulating, esp. inhibiting, its activity, useful in  
f treating cancer, preventing metastasis, and diagnosis.

S Claim 3; Page 25; 44pp; English.

CC The sequences given in AA081642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC with its receptor and heparin. Particularly, they inhibit  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.

CC Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 3 C 3

RESULT 9

AA0816385  
ID AA0816385 standard; DNA; 4 BP.

XX AA0816385;

DT 23-APR-1998 (first entry)

XX Probe for target nucleic acid sequence P0.

XX Point mutation detection; nucleic acid sequence analysis; probe;

XX viral disease diagnosis; genetic disease diagnosis; ss.

XX Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /note= "C-5' phosphate"

XX MO9738131-A1.

XX 16-OCT-1997.

XX 11-APR-1996; 96MO-RU00087.

XX 11-APR-1996; 96MO-RU00087.

XX (DYMSHITS G M.

XX (IVANOV IVANOVA E M.

XX (KRIVK KRIVENKO A A.

XX (KULIK KULIKOVA V F.

XX (LOKH LOKHOV S G.

XX (PYSH PYSHNY D V.

XX DYMSHITS GM, IVANOVA EM, KRIVENKO AA, KULIKOVA VF;  
XX LOKHOV SG, PYSHNY DV;  
XX WPI: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of  
PT hybridised short probe to flanking target-complementary sequences  
XX Example; Page 4; 15pp; Russian.

CC This sequence represents a probe for the target sequence P0 (shown in  
CC AA0816376). This sequence was used to test the method of the invention.  
CC The method of the invention is for detecting a nucleic acid sequence to  
CC be analysed, and comprises hybridisation of an oligonucleotide probe  
CC complementary to the sequence to be analysed and bearing a reporter  
CC group, the novelty is that detection of a sequence is based on the  
CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
CC flanking oligonucleotide sequences (or their derivatives bearing  
CC polycyclic aromatic groups). The method is especially useful for  
CC detecting point mutations. Diagnosis of viral, genetic and other  
CC diseases is also mentioned.

CC Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 1 C 1

RESULT 10

AA0816385/C  
ID AA0816385 standard; DNA; 4 BP.

XX AA0816385;

DT 23-APR-1998 (first entry)

XX Probe for target nucleic acid sequence P0.

XX Point mutation detection; nucleic acid sequence analysis; probe;

XX viral disease diagnosis; genetic disease diagnosis; ss.

XX Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /note= "C-5' phosphate"

XX MO9738131-A1.

XX 16-OCT-1997.

XX 11-APR-1996; 96MO-RU00087.

XX 11-APR-1996; 96MO-RU00087.

XX (DYMSHITS G M.

XX (IVANOV IVANOVA E M.

XX (KRIVK KRIVENKO A A.

XX (KULIK KULIKOVA V F.

XX (LOKH LOKHOV S G.

XX (PYSH PYSHNY D V.

XX DYMSHITS GM, IVANOVA EM, KRIVENKO AA, KULIKOVA VF;  
XX LOKHOV SG, PYSHNY DV;  
XX WPI: 1997-512737/47.

PT Detection of target nucleic acid sequence - based on ligation of  
PT hybridised short probe to flanking target-complementary sequences  
XX Example; Page 4; 15pp; Russian.

XX This sequence represents a probe for the target sequence P0 (shown in  
CC AAT86376). This sequence was used to test the method of the invention.  
CC The method of the invention is for detecting a nucleic acid sequence to  
CC be analysed, and comprises hybridisation of an oligonucleotide probe to  
CC complementary to the sequence to be analysed and bearing a reporter  
CC group, the novelty is that detection of a sequence is based on the  
CC ligation of a short oligonucleotide (with a length of 4-6 units) with  
CC flanking oligonucleotide sequences (or their derivatives bearing  
CC polycyclic aromatic groups). The method is especially useful for  
CC detecting point mutations. Diagnosis of viral, genetic and other  
CC diseases is also mentioned.

SO Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
Db 3 C 3

## RESULT 11

AAT77252  
ID AAT77252 standard; DNA: 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

KW Immunostimulatory polynucleotide: ISP: palindrome; vaccine;  
KW immune response; antigen; naked gene expression vector; IGE;  
KW antibody; immunotherapy; ss.

OS Synthetic.

PN WO9728259-A1.

PD 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC ) UNIV CALIFORNIA.

PI Carson DA, Raz E;

WIPI: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic  
PT polynucleotide - useful for selectively enhancing the TH1 immune  
PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide  
CC (ISP) comprised of at least one strand of a palindrome, which includes  
CC at least one dinucleotide consisting of adjacent, unmodified cytosine  
CC and guanine residues. ISP's could be used in vaccination methods  
CC for enhancing the immune response of a host to an antigen. Administration  
CC of naked gene expression vectors which encode antigens or their  
CC immunostimulatory fragments suppresses IGE antibody production  
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.  
XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 2 C 2

## RESULT 12

AAT77252/C  
ID AAT77252 standard; DNA: 4 BP.

AC AAT77252;

DT 18-MAR-1998 (first entry)

DE Immunostimulatory polynucleotide 11.

KW Immunostimulatory polynucleotide: ISP: palindrome; vaccine;  
KW immune response; antigen; naked gene expression vector; IGE;  
KW antibody; immunotherapy; ss.

OS Synthetic.

PN WO9728259-A1.

PD 07-AUG-1997.

PF 28-JAN-1997; 97WO-US01277.

PR 30-JAN-1996; 96US-0593554.

PA (REGC ) UNIV CALIFORNIA.

PI Carson DA, Raz E;

WIPI: 1997-402613/37.

PT Recombinant vector containing immunostimulatory palindromic  
PT polynucleotide - useful for selectively enhancing the TH1 immune  
PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide  
CC (ISP) comprised of at least one strand of a palindrome, which includes  
CC at least one dinucleotide consisting of adjacent, unmodified cytosine  
CC and guanine residues. ISP's could be used in vaccination methods  
CC for enhancing the immune response of a host to an antigen. Administration  
CC of naked gene expression vectors which encode antigens or their  
CC immunostimulatory fragments suppresses IGE antibody production  
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.  
XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 3 C 3

## RESULT 13

AAL17191  
ID AAL17191 standard; CDNA: 4 BP.

AC AAL17191;

DT 07-DEC-2001 (first entry)

```

XX Human breast cancer expressed polynucleotide 9648.
DE
XX
XX Human: breast cancer; cell marker: cytosstatic; ss.
KW
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US00798.
PF
XX 14-JAN-2000; 2000US-0176077.
PA 14-MAR-2000; 2000US-0189167.
XX 24-MAR-2000; 2000US-0192099.
PI 29-MAR-2000; 2000US-0193480.
XX 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
XX 25-JUL-2000; 2000US-0220534.
PP (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI: 2001-451856/48.
XX New peptide useful as a marker for the diagnosis of breast cancer .
PT Claim 1; Page 1720; 3695pp; English.
PS
XX The invention relates to human breast cancer expressed polynucleotides
CC (AL07544-AL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 c 1
DB 3 c 3
RESULT 14
ID AL17191/C
XX AL17191 standard; CDNA; 4 BP.
AC AL17191;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 9648.
XX
XX Human: breast cancer; cell marker: cytosstatic; ss.
OS Homo sapiens.
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US00798.
PX

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PR      14-JAN-2000; 2000US-0176077.
PR      14-MAR-2000; 2000US-0189167.
PR      24-MAR-2000; 2000US-0192099.
PR      29-MAR-2000; 2000US-0193480.
PR      15-MAY-2000; 2000US-0205230.
PR      09-JUN-2000; 2000US-0211315.
PR      25-JUL-2000; 2000US-0220534.
XX
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI      Lillie J, Xu Y, Wang Y, Steinmann K;
XX      WPI; 2001-451856/48.
XX
DR      WPI; 2001-451856/48.
XX
XX
PT      New peptide useful as a marker for the diagnosis of breast cancer -
PS      Claim 1: Page 1720; 3695pp; English.
XX
XX      The invention relates to human breast cancer expressed polynucleotides
CC      (AAL07544-AAL26789) and methods of assessing whether a patient is
CC      afflicted with breast cancer by examining the correlation between the
CC      expression of certain markers and the cancerous state of breast cells.
CC      The polynucleotides and encoded polypeptides are potential markers for
CC      detecting, diagnosing, monitoring, characterising treating and
CC      potentially preventing breast cancer. The polynucleotides and encoded
CC      polypeptides are also useful for isolating compounds with cytostatic
CC      activity.
XX
SO      Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match          100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred No. 0;
Matches    1; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      1 C 1
        |
DB      1 C 1

RESULT 15
AAL24357
ID      AAL24357 standard; cDNA; 4 BP.
XX
AC      AAL24357;
XX
DT      07-DEC-2001 (first entry)
XX
DE      Human breast cancer expressed polynucleotide 16814.
XX
XX      Human; breast cancer; cell marker; cytosstatic; ss.
XX
XX      Homo sapiens.
XX
PN      WO200151628-A2.
PD      19-JUL-2001.
XX
PF      10-JAN-2001; 2001WO-US00798.
XX
PR      14-JAN-2000; 2000US-0176077.
PR      14-MAR-2000; 2000US-0189167.
PR      24-MAR-2000; 2000US-0192099.
PR      29-MAR-2000; 2000US-0193480.
PR      15-MAY-2000; 2000US-0205230.
PR      09-JUN-2000; 2000US-0211315.
PR      25-JUL-2000; 2000US-0220534.
XX
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI      Lillie J, Xu Y, Wang Y, Steinmann K;
XX      WPI; 2001-451856/48.
XX
```





KW tumour; cancer; colorectal; breast; metal chelate; hapten; ss.  
XX  
XX Synthetic.

OS  
XX  
PN A09350602-A.

XX  
PD 26-MAY-1994.

XX  
PF 10-NOV-1993; 93AU-0050602.

XX  
PR 12-NOV-1992; 92US-0975230.

XX  
PA (HYBR-) HYBRTECH INC.

XX  
PI Ahweller PM, Moore MD;

XX  
DR WPI: 1994-209063/26.

XX  
UK P-PSDB: AAR54150.

XX  
PT Polypeptide used in imaging and treatment of carcinomas and  
PT tumours - comprising subunit antibody CDR having binding affinity  
PT for metal chelate of EDTA or DETA or analogues

XX  
PS Claim 25: Fig 3A; 61pp; English.

XX  
XX The sequences given in A0068747-57 encode the wild type and mutagenised  
CC versions of the complementarity determining region 1 (CDR1) of the  
CC antibody designated CHA255. CHA255 is a murine monoclonal antibody  
CC (Mab) which is capable of binding complexes. Mutagenesis of these  
CC CDRs causes the production of polypeptides with a particularly  
CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3  
CC of the heavy chain, and CDR2 and -3 of the light chain were targeted  
CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255  
CC heavy chain, five of seven residues of light chain CDR and six of  
CC nine light chain CDR residues were specifically targeted for  
CC codon-based mutagenesis. The mutagenised Mab's can be used in  
CC compositions for in vivo imaging of malignant tissues or tumours. They  
CC are also useful for the treatment of malignant tissues or tumours eg.  
CC colorectal or breast cancer. Both methods involve the use of  
CC radionuclides which bind to metal chelates or haptens which are  
CC specifically delivered to the target site by a targeting molecule. CDR  
CC derived peptides may be used to construct bi-functional antibodies  
CC having dual specificities, or as donor or recipients of CDR sequences.

XX  
SQ Sequence 5 BP: 0 A; 0 G; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
I  
DB 1 c 1

RESULT 19

AA081667  
ID A081667 standard; RNA: 5 BP.

XX  
AC A081667;

XX  
DT 29-SEP-1995 (first entry)

XX  
DE bFGF binding oligomer core sequence #4.

XX  
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;

KW bubble structure; pseudoknot; receptor; heparin; competition;

KW inhibition; enhance; neovascularisation; solid tumour; cancer;

XX  
XX metastasis; diagnosis; gene therapy; ss.  
XX Synthetic.

PN W09500528-A.

XX  
PD 05-JAN-1995.

XX  
PF 17-JUN-1994; 94WO-US06884.

XX  
PR 18-JUN-1993; 93US-0079677.

XX  
PR 07-JAN-1994; 94US-0179491.

XX  
PA (PHAR-) PHARMAGENICS INC.

XX  
PI Beutel BA, Joesten ME;

XX  
DR WPI: 1995-051992/07.

XX  
PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
PT factor - modulating, esp. inhibiting, its activity, useful in  
PT treating cancer, preventing metastasis, and diagnosis.

XX  
PS Claim 3; Page 25; 44pp; English.

XX  
XX The sequences given in A081642-95 are oligonucleotides which modulate  
CC the activity of basic fibroblast growth factor (bFGF) by binding  
CC to the bFGF protein. Most esp. the sequences given in A081664-67  
CC represent core sequences of which at least one is present in each of  
CC the binding oligos. These oligonucleotides may form a single  
CC strand, double strand, a stem-loop structure, a bubble structure, a  
CC pseudoknot or a closed, circular structure. bFGF binds to high  
CC affinity receptor and low affinity heparin-like molecules on the  
CC cell surface. These oligonucleotides bind to bFGF in competition  
CC with its receptor and heparin. These oligonucleotides may inhibit  
CC or enhance the activity of bFGF. Particularly, they inhibit  
CC neovascularisation so they can be used to suppress growth of solid  
CC tumours and to reduce the risk of metastasis. They can be used as  
CC diagnostic reagents to determine the presence of thrombin, or used in  
CC gene therapy.

XX  
SQ Sequence 5 BP: 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
I  
DB 4 c 4

RESULT 20

AAT12043  
ID AAT12043 standard; RNA: 5 BP.

XX  
AC AAT12043;

XX  
DT 17-JUL-1996 (first entry)

XX  
DE Cleavable replicable-inhibiting sequence.

XX  
KW Ribozyme; hairpin; hammerhead; probe; MDV-1; midvariant-1;

KW replication; cleavage; ss.

XX  
OS Synthetic.

XX  
PN US5472840-A.

XX  
XX 05-DEC-1995.

XX  
PF 30-SEP-1988; 88US-0252243.

XX  
PR 17-DEC-1990; 90US-0630288.

XX  
PR 30-SEP-1988; 88US-0252243.

XX  
PR 22-JUN-1989; 89US-0370218.



AC AAT96299;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Fungal telomeric nucleic acid sequence.  
 XX  
 KM Detection: eukaryotic pathogen; telomeric nucleic acid sequence;  
 KM telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 XX malarial infection; malaria; ss.  
 OS Saccharomyces cerevisiae.  
 XX  
 PN US5695932-A.  
 PD 09-DEC-1997.  
 XX  
 PF 13-MAY-1993; 93US-0060952.  
 XX  
 PR 13-MAY-1993; 93US-0060952.  
 PR 13-MAY-1992; 92US-0882438.  
 PR 24-MAR-1993; 93US-0038766.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;  
 DR WPI: 1998-041292/04.  
 XX  
 DT Detection of eukaryotic pathogens, especially fungal or Plasmidium  
 PT spp. - by detecting telomerase activity  
 PT  
 XX  
 PS Claim 5: Columns 81-82; 82pp; English.  
 XX  
 CC The present sequence can be used in a novel method for detecting a  
 CC eukaryotic pathogen in a patient. The method comprises obtaining a  
 CC sample of somatic tissue or cells from the patient, determining if  
 CC telomerase activity is present and correlating this with the  
 CC presence of the pathogen. The method is useful for diagnosis of  
 CC fungal infections, especially a fungus of the genus Candida,  
 CC Kluyveromyces, Saccharomyces, Sporobolix, Coccidioides,  
 CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,  
 CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially  
 CC Plasmidium vivax, P. ovale, P. malariae or P. falciparum.  
 CC  
 XX  
 SQ Sequence 5 BP: 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 19; Length 5;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
 I  
 Db 5 C 5

RESULT 24  
 AA210695/C  
 ID AA210695 standard; DNA: 5 BP.  
 XX  
 AC AA210695;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide sequence that increases p53 activity in a cell.  
 XX  
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KM skin cancer; ss.  
 XX  
 OS Synthetic.

XX  
 PN GB2336157-A.  
 XX  
 PD 13-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99GB-0006758.  
 XX  
 PR 26-MAR-1998; 98US-0048927.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrist BA, Yaar M, Eller M;  
 DR WPI: 1999-543520/46.  
 XX  
 PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX  
 PS Claim 11: Page 30; 44pp; English.  
 XX  
 CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.  
 CC  
 XX  
 SQ Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 20; Length 5;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
 I  
 Db 5 C 5

RESULT 25  
 AA210696  
 ID AA210696 standard; DNA: 5 BP.  
 XX  
 AC AA210696;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide sequence that increases p53 activity in a cell.  
 XX  
 KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KM skin cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2336157-A.  
 XX  
 PD 13-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99GB-0006758.  
 XX  
 PR 26-MAR-1998; 98US-0048927.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrist BA, Yaar M, Eller M;  
 DR WPI: 1999-543520/46.  
 XX  
 PT DNA fragments useful for increasing p53 activity in a cell and reducing

PT susceptibility to UV-induced hyperproliferative diseases -  
XX  
PS Claim 11: Page 30; 44pp; English.  
XX  
CC AA10692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.  
XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
|  
Db 1 c 1

RESULT 26  
AA211611  
ID AA211611 standard; DNA: 5 BP.  
XX

AC AA211611:

DT 16-NOV-1999 (first entry)

DE DNA enhancer sequence present in an upstream element.

KM Plant promoter: TATA motif; transcription start site; upstream element;  
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;  
KW Ubi-1 promoter; Syn II core promoter; ss.

XX Synthetic.

XX MO9943838-A1.

XX 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.

XX 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.

XX Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;

XX WPI; 1999-540601/45.

PT New synthetic promoter functional in plants to provide non-tissue  
PT specific, constitutive expression, particularly of oxalate oxidase for  
PT increased resistance to pathogens -

PS Claim 39; Page 47; 61pp; English.

CC The invention provides a new synthetic plant promoter that comprises a  
CC TATA motif; a transcription start site (TSS) and a region between TATA  
CC and TSS containing at least 64 percent GC content. The synthetic core  
CC promoter, optionally containing additional upstream elements are used to  
CC increase expression, provides non-tissue specific, constitutive  
CC transcription of heterologous genes in any sort of plant, especially the  
CC gene for oxalate oxidase for increasing plant resistance to pathogens.  
CC The upstream activating elements can be used to increase transcription  
CC from any promoter. A combination of the synthetic core promoter with  
CC synthetic upstream elements can induce expression 10 times greater than  
CC that provided by the maize Ubi-1 promoter. The present sequence  
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.

XX  
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
|  
Db 5 c 5

RESULT 27  
AA211611/C  
ID AA211611 standard; DNA: 5 BP.  
XX

AC AA211611:

DT 16-NOV-1999 (first entry)

DE DNA enhancer sequence present in an upstream element.

KM Plant promoter: TATA motif; transcription start site; upstream element;  
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;  
KW Ubi-1 promoter; Syn II core promoter; ss.

XX Synthetic.

XX MO9943838-A1.

XX 02-SEP-1999.

XX 23-FEB-1999; 99WO-US03863.

XX 24-FEB-1998; 98US-0028819.

XX (PION-) PIONEER HI-BRED INT INC.

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XX WPI; 1999-540601/45.

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PT specific, constitutive expression, particularly of oxalate oxidase for  
PT increased resistance to pathogens -

PS Claim 39; Page 47; 61pp; English.

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CC and TSS containing at least 64 percent GC content. The synthetic core  
CC promoter, optionally containing additional upstream elements are used to  
CC increase expression, provides non-tissue specific, constitutive  
CC transcription of heterologous genes in any sort of plant, especially the  
CC gene for oxalate oxidase for increasing plant resistance to pathogens.  
CC The upstream activating elements can be used to increase transcription  
CC from any promoter. A combination of the synthetic core promoter with  
CC synthetic upstream elements can induce expression 10 times greater than  
CC that provided by the maize Ubi-1 promoter. The present sequence  
CC represents a DNA enhancer OSC-like motif present in an upstream element  
CC sequence.

SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
|

DB 4 C 4

## RESULT 28

AAV72347  
ID AAV72347 standard; DNA: 5 BP.

AC AAV72347:

DT 28-JUL-1999 (first entry)

DE US5908745 primer #4.

KW DNA sequencing: disease-associated allele; polyacrylamide matrix;  
contiguous/contiguous stacking hybridization technique; detection;  
mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

PA (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Partinov SV, Yershov GM;

DR WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous  
stacking hybridization as a diagnostic tool

PS Example 1: Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA  
samples to detect disease-associated alleles, by continuous/contiguous  
stacking hybridization techniques (utilizing universal bases) with  
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may  
be used to detect multiple DNA base mutations which are specific for  
CC certain diseases. The methods of the invention provide accurate and  
efficient and sensitive methods for diagnosing disease by detecting  
CC multiple mutation sequences in patient DNA. The method require the  
minimum number of oligonucleotides and few stacking hybridization steps  
than prior art methods. The methods are also efficient enough to  
CC discriminate between perfect and imperfect duplexes. The methods also  
obviate the need for the fabrication and array placement of large numbers  
of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

DB 1 C 1

## RESULT 29

AAV72348  
ID AAV72348 standard; DNA: 5 BP.

AC AAV72348;

DT 28-JUL-1999 (first entry)

XX

DE US5908745 primer #5.

KW DNA sequencing: disease-associated allele; polyacrylamide matrix;  
contiguous/contiguous stacking hybridization technique; detection;  
mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

PF 16-JAN-1996; 96US-0587332.

PR 16-JAN-1996; 96US-0587332.

PA (UYCH-) UNIV CHICAGO.

PI Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;

PI Partinov SV, Yershov GM;

DR WPI: 1999-347002/29.

PT Detecting disease-associated alleles using continuous/contiguous  
stacking hybridization as a diagnostic tool

PS Example 1: Column 9; 16pp; English.

CC This invention describes novel methods for sequencing and analysing DNA  
samples to detect disease-associated alleles, by continuous/contiguous  
stacking hybridization techniques (utilizing universal bases) with  
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may  
be used to detect multiple DNA base mutations which are specific for  
CC certain diseases. The methods of the invention provide accurate and  
efficient and sensitive methods for diagnosing disease by detecting  
CC multiple mutation sequences in patient DNA. The method require the  
minimum number of oligonucleotides and few stacking hybridization steps  
than prior art methods. The methods are also efficient enough to  
CC discriminate between perfect and imperfect duplexes. The methods also  
obviate the need for the fabrication and array placement of large numbers  
of immobilized oligomers.

SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

DB 1 C 1

## RESULT 30

AAV72348/c  
ID AAV72348 standard; DNA: 5 BP.

AC AAV72348;

DT 28-JUL-1999 (first entry)

DE US5908745 primer #5.

KW DNA sequencing: disease-associated allele; polyacrylamide matrix;  
contiguous/contiguous stacking hybridization technique; detection;  
mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

PD 01-JUN-1999.

```
XX 16-JAN-1996: 96US-0587332.
PF 16-JAN-1996: 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
PA Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
PI Parinov SV, Yershov GM:
XX WPI: 1999-347002/29.
DK
XX
XX Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other:
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 20; Length 5;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 c 1
Db 2 c 2
```

```
RESULT 31
AAV72349
ID AAV72349 standard; DNA: 5 BP.
XX
XX AAV72349:
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX US5908745 primer #6.
DE
XX
XX DNA sequencing: disease-associated allele: polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
KM mutation; diagnosis; primer: ss.
XX
XX Synthetic.
OS
XX
XX US5908745-A.
PN
XX
XX 01-JUN-1999.
PD
XX
XX 16-JAN-1996: 96US-0587332.
PF
XX
XX 16-JAN-1996: 96US-0587332.
PR
XX
XX (UYCH-) UNIV CHICAGO.
PA
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
PI Parinov SV, Yershov GM:
XX WPI: 1999-347002/29.
DR
```

```
XX Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other:
```

```
Query Match
Best Local Similarity 100.0%; Score 1: DB 20; Length 5;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 c 1
Db 1 c 1
```

```
RESULT 32
AAV72350
ID AAV72350 standard; DNA: 5 BP.
XX
XX AAV72350:
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX US5908745 primer #7.
DE
XX
XX DNA sequencing: disease-associated allele: polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
KM mutation; diagnosis; primer: ss.
XX
XX Synthetic.
OS
XX
XX US5908745-A.
PN
XX
XX 01-JUN-1999.
PD
XX
XX 16-JAN-1996: 96US-0587332.
PF
XX
XX 16-JAN-1996: 96US-0587332.
PR
XX
XX (UYCH-) UNIV CHICAGO.
PA
XX
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD:
PI Parinov SV, Yershov GM:
XX WPI: 1999-347002/29.
DR
XX
XX Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp; English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods
CC be used to detect multiple DNA base mutations which are specific for
```

CC certain diseases. The methods of the invention provide accurate and  
CC efficient and sensitive methods for diagnosing disease by detecting  
CC multiple mutation sequences in patient DNA. The method requires the  
CC minimum number of oligonucleotides and few stacking hybridization steps  
CC than prior art methods. The methods are also efficient enough to  
CC discriminate between perfect and imperfect duplexes. The methods also  
CC obviate the need for the fabrication and array placement of large numbers  
CC of immobilized oligomers.

XX  
SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1  
Db 4 C 4

## RESULT 33

AA556964  
ID AAX56964 standard; DNA; 5 BP.

XX  
AC AAX56964;

XX  
UT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX  
KM Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;  
XX cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

XX  
PN WO922772-A1.

XX  
PD 14-MAY-1999.

XX  
PF 28-OCT-1998; 98WO-US22821.

XX  
PR 31-OCT-1997; 97US-0961469.

XX  
PA (ISIS-) ISIS PHARM INC.

XX  
PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

XX  
DR Templin MV;

XX  
WPI: 1999-313181/26.

XX  
PT Liposome-encapsulated oligonucleotides useful for treating or  
XX preventing cancers associated with ras gene activation  
XX  
PS Example 1: Page 107; 120pp; English.

XX  
CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

XX  
SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1  
Db 1 C 1

## RESULT 34

AA556964/C  
ID AAX56964 standard; DNA; 5 BP.

XX  
AC AAX56964;

XX  
DT 16-JUL-1999 (first entry)

DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX  
KM Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;  
XX cell growth inhibitor; treatment; cancer; ras protein; ss.

OS Synthetic.

XX  
PN WO922772-A1.

XX  
PD 14-MAY-1999.

XX  
PF 28-OCT-1998; 98WO-US22821.

XX  
PR 31-OCT-1997; 97US-0961469.

XX  
PA (ISIS-) ISIS PHARM INC.

XX  
PI Geary RS, Hardee GE, Howard R, Levin A, Mehra RC;

XX  
DT Templin MV;

XX  
WPI: 1999-313181/26.

XX  
PT Liposome-encapsulated oligonucleotides useful for treating or  
XX preventing cancers associated with ras gene activation  
XX  
PS Example 1: Page 107; 120pp; English.

XX  
CC This invention describes novel compositions comprising oligonucleotides  
CC (AAX56957-X57017), entrapped within liposomes, that hybridize  
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type  
CC ras protein. The products of the invention have anticancer activity and  
CC specifically bring about the antisense inhibition of ras genes or mRNA.  
CC The products of the invention are used to modulate expression of a ras  
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell  
CC growth and especially to treat or prevent cancers associated with  
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the  
CC rate at which it is cleared from the blood when compared with  
CC non-encapsulated material, and the oligonucleotides become distributed to  
CC practically all parts of the body.

XX  
SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1  
Db 5 C 5

## RESULT 35

AA556964/C  
ID AAX21608 standard; DNA; 5 BP.

XX  
AC AAX21608;



```

XX PF 06-JUL-1998; 98WO-USI3966.
XX XX 08-JUL-1997; 97US-0889296.
PR XX (ISIS-) ISIS PHARM INC.
PA XX Cowsert LM, Manoharan M, Monia BP;
PI XX WPI; 1999-120932/10.
DR XX
XX PT New oligonucleotide targeting human N-ras nucleic acid - is
PT capable of inhibiting human N-ras expression, useful for preventing
PT or treating conditions arising from the activation of a human N-ras
PT oncogene
XX PS Disclosure; Page 22; 97pp; English.
XX CC The invention relates to oligonucleotides, which target a nucleic acid
CC encoding human N-ras, and are capable of inhibiting human N-ras
CC expression. The antisense oligonucleotides form a pharmaceutical
CC composition, which is useful for modulating the expression of human
CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
CC treating conditions arising from the activation of a human N-ras
CC oncogene. The oligonucleotides are also useful in diagnostics,
CC therapeutics, and as research reagents and kits. The oligonucleotides
CC enable the specific modulation of activated human N-ras expression,
CC which is associated with tumour formation. Sequences AAX21601-619
XX represent antisense oligonucleotides targeted to mutant H-ras.
SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB S C S

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX AC AAA56981;
XX DT 14-NOV-2000 (first entry)
XX DE Human colon cancer cell cDNA sequence #109.
XX KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
XX open reading frame; ORF; low stringency; cDNA sequencing; ss.
OS Homo sapiens.
XX PN WO200031299-A2.
XX PD 02-JUN-2000.
XX PF 19-NOV-1999; 99WO-US27430.
PR 20-NOV-1998; 98US-0196716.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Simpson AJG, Dias Neto E, Brentani RR;
XX DR WPI; 2000-400100/34.
PT Method for determining open reading frames of the genome of an organism
PT using primers at low stringency conditions, useful in the construction

```

PT of contigs or constructs of sequenced nucleic acid molecules -  
 XX  
 PS Example 6; Page 47: 113pp; English.  
 XX

CC The present sequence is a cDNA sequence obtained using a method for  
 CC determining open reading frames (ORFs) of the genome of an  
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
 CC with a single, arbitrary primer. Moloney murine leukaemia virus reverse  
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
 CC incubated under low stringency conditions to yield single stranded  
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
 CC than providing nucleotide sequence information from the non-coding  
 CC termini of nucleic acid molecules, the method provides information on  
 CC the more interesting and relevant internal portions, such as ORFs. The  
 CC method also permits the construction of contigs of sequenced nucleic  
 CC acid molecules.

SO Sequence 5 BP: 0 A: 3 C: 1 G: 1 T: 0 other:

Query Match 100.0%; Score 1: DB 21: Length 5:  
 Best Local Similarity 100.0%; Pred. No. 0:  
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 OY 1 c 1  
 Db 1 c 1

RESULT 38  
 ID AA556981/C  
 XX AA556981 standard; cDNA: 5 BP.  
 AC  
 XX AA556981:

DT 14-NOV-2000 (first entry)

DE Human colon cancer cell cDNA sequence #109.

KW Human: arbitrary primer; cDNA synthesis; contig sequence construction;  
 XX open reading frame; ORF; low stringency; cDNA sequencing; ss.

OS Homo sapiens.

PN WO200031299-A2.

PD 02-JUN-2000.

PF 19-NOV-1999: 99MO-US27430.

PR 20-NOV-1998: 98US-0196716.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Simpson AJG, Dias Neto E, Brentani RR;

WP1: 2000-400100/34.

PT Method for determining open reading frames of the genome of an organism  
 PT using primers at low stringency conditions, useful in the construction  
 PT of contigs or constructs of sequenced nucleic acid molecules -  
 XX  
 PS Example 6; Page 47: 113pp; English.

CC The present sequence is a cDNA sequence obtained using a method for  
 CC determining open reading frames (ORFs) of the genome of an  
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed  
 CC with a single, arbitrary primer. Moloney murine leukaemia virus reverse  
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was  
 CC incubated under low stringency conditions to yield single stranded  
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather  
 CC than providing nucleotide sequence information from the non-coding  
 CC termini of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The  
 CC method also permits the construction of contigs of sequenced nucleic  
 CC acid molecules.

SO Sequence 5 BP: 0 A: 3 C: 1 G: 1 T: 0 other:

Query Match 100.0%; Score 1: DB 21: Length 5:  
 Best Local Similarity 100.0%; Pred. No. 0:  
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 OY 1 c 1  
 Db 3 C 3

RESULT 39  
 ID AA293601  
 XX AA293601 standard; DNA: 5 BP.  
 AC  
 XX AA293601:

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;  
 KW gene expression; crop protection; transgenic plant; resistance;  
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.

OS Nicotiana glauca.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999: 99MO-AU00692.

PR 26-AUG-1998: 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

WP1: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing  
 PT transgenic plants with improved characteristics such as resistance to  
 PT pathogens  
 XX  
 PS Example 9; Page 51: 102pp; English.

CC Isolated regulatory sequences of plants that are operable in  
 CC dividing cells, in particular the meristem cells of plants are useful  
 CC in the genetic engineering of plants. The regulatory sequences can  
 CC be used to control the expression of foreign genes placed under their  
 CC control. Such methods are useful for producing transgenic plants with  
 CC altered shape and/or size. The sequences are also useful for  
 CC producing transgenic plants capable of rapid regeneration following  
 CC harvest or plants having improved resistance to pathogens. This  
 CC sequence has been shown to bind a factor involved in the activation  
 CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three  
 CC times in the meristem regulatory sequence of tobacco described in  
 CC GENESEQ record AA293567.

SO Sequence 5 BP: 1 A: 3 C: 1 G: 0 U: 0 other:

Query Match 100.0%; Score 1: DB 21: Length 5:  
 Best Local Similarity 100.0%; Pred. No. 0:  
 Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 c 1  
Db 1 c 1

## RESULT 40

AA293601/c  
ID AA293601 standard; DNA: 5 BP.

AC AA293601;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

XX tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

OS Synthetic.

OS Nicotiana acuminata.

PN W0200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DK WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing

PT transgenic plants with improved characteristics such as resistance to

PT pathogens

PS Example 9: Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in

CC dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to bind a factor involved in the activation

CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three

CC times in the meristem regulatory sequence of Tobacco described in

CC GENES0 record AA293567.

XX Sequence 5 BP: 1 A; 3 C; 1 G; 0 U; 0 other;

SO

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 5 c 5

RESULT 41

AA293602

ID AA293602 standard; DNA: 5 BP.

AC AA293602;

XX

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KW gene expression; crop protection; transgenic plant; resistance;

XX tobacco; transcription factor; NIT2; nitrate; ss.

OS Synthetic.

OS Nicotiana acuminata.

PN W0200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYOU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing

PT transgenic plants with improved characteristics such as resistance to

PT pathogens

PS Example 9: Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in

CC dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to regulate nitrate metabolism in the

CC fungus Neurospora crassa. It occurs multiple times in the meristem

CC regulatory sequence of Tobacco described in GENES0 record AA293567.

XX Sequence 5 BP: 1 A; 1 C; 0 G; 3 T; 0 other;

SO

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1

Db 4 c 4

RESULT 42

AA289330

ID AA289330 standard; DNA: 5 BP.

AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

XX fat metabolism; ss.

OS Homo sapiens.

PN DE19838837-A1.

PD 02-MAR-2000.



Query Match 100.0%; Score 1; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
 Db 5 C 5

db 2 C 2

Search completed: July 15, 2002, 23:10:11  
 Job time: 18429 sec

## RESULT: 45

AA248433  
 ID AA248433 standard; DNA: 5 BP.

AC AA248433;

DT 27-MAR-2000 (first entry)

DE First DNA arm segment.

KW Microorganism; virus; polymerase chain reaction; food; cosmetic;  
 clinical diagnostic; molecular beacon; PCR primer; ss.

OS Synthetic.

PN WO9963112-A2.

PD 09-DEC-1999.

PF 18-MAY-1999; 99WO-US10940.

PR 18-MAY-1998; 98US-0086025.  
 PR 17-MAY-1999; 99US-0086025.

PA (HUNT-) HUNT WESSON INC.

PI Romick TL, Fraser MS;

WPI: 2000-086985/07.

DR Detection of microorganisms and viruses, for use in the food and  
 PT cosmetic industries and for clinical diagnostics

PS Claim 51: Page 40; 63pp; English.

XX The invention provides a novel in vitro method for the detection of  
 CC microorganisms and viruses. The method comprises: (1) forming a  
 CC polymerase chain reaction (PCR) mixture by combining a predetermined  
 CC volume of a sample to be tested for the presence of a nucleic acid  
 CC sequence comprising 5'-TAGAACC-3', known amounts of a first primer  
 CC comprising 5'-GCTAAGTCCCAAGT-3', and a second primer comprising  
 CC 5'-AGAACCTCTCCACC-3', and PCR reagents; (2) forming a PCR product by  
 CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,  
 CC to replicate and attain 0.25-1000nmg nucleotide product/ml mixture; (3)  
 CC adding a probe containing DNA comprising 5'-GGTGGCTCTTCAACCACC-3' to  
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with  
 CC the nucleic acid sequence, if present, and change the conformation of the  
 CC probe; and (4) determining whether or not bacteria are present in the  
 CC sample by detecting the conformational change of the probe, a  
 CC conformational change indicating the presence of bacteria in the sample.  
 CC The methods can be used for the detection of viruses and microorganisms,  
 CC including bacteria, yeast, molds and protozoa. They can be used in the  
 CC food and cosmetic industry and in clinical diagnostics. Using the method  
 CC it is not necessary to remove non-hybridized probe from the system.  
 SO Sequence 5 BP: 1 A: 1 C: 2 G: 1 T: 0 other:

Query Match 100.0%; Score 1; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds

(without alignments)  
1.098 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3360\_3360

Perfect score: 1 c 1

Sequence: 1 c 1

Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents\_NA:\*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCRT05.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1	100.0	2	1 US-08-268-6798-8	Sequence 8, Appl1
C 2	1	100.0	2	1 US-08-484-192-16	Sequence 16, Appl1
C 3	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl1
C 4	1	100.0	2	4 US-08-361-024-3	Sequence 3, Appl1
C 5	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl1
C 6	1	100.0	3	1 US-07-791-213D-46	Sequence 46, Appl1
C 7	1	100.0	3	1 US-07-791-213D-62	Sequence 62, Appl1
C 8	1	100.0	3	1 US-07-791-213D-62	Sequence 62, Appl1
C 9	1	100.0	3	1 US-08-268-6798-7	Sequence 7, Appl1
C 10	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl1
C 11	1	100.0	3	1 US-08-602-036A-2	Sequence 2, Appl1
C 12	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl1
C 13	1	100.0	3	1 US-08-293-150A-46	Sequence 46, Appl1
C 14	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl1
C 15	1	100.0	3	1 US-08-293-150A-62	Sequence 62, Appl1
C 16	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl1
C 17	1	100.0	3	2 US-08-502-374A-2	Sequence 2, Appl1
C 18	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl1
C 19	1	100.0	3	2 US-08-642-407A-2	Sequence 2, Appl1
C 20	1	100.0	3	3 US-08-873-709-9	Sequence 9, Appl1
C 21	1	100.0	3	3 US-08-873-709-9	Sequence 9, Appl1
C 22	1	100.0	3	3 US-09-032-365A-36	Sequence 36, Appl1
C 23	1	100.0	3	4 US-08-793-634B-12	Sequence 12, Appl1
C 24	1	100.0	4	1 US-08-973-568-55	Sequence 55, Appl1
C 25	1	100.0	4	1 US-07-755-462-2	Sequence 2, Appl1
C 26	1	100.0	4	1 US-07-755-462-2	Sequence 2, Appl1
C 27	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl1
C 27	1	100.0	4	1 US-08-169-950-6	Sequence 6, Appl1

C 28	1	100.0	4	1 US-07-630-288A-7	Sequence 7, Appl1
C 29	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl1
C 30	1	100.0	4	1 US-07-630-288A-11	Sequence 11, Appl1
C 31	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl1
C 32	1	100.0	4	1 US-07-630-288A-13	Sequence 13, Appl1
C 33	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl1
C 34	1	100.0	4	1 US-07-630-288A-14	Sequence 14, Appl1
C 35	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl1
C 36	1	100.0	4	1 US-07-630-288A-34	Sequence 34, Appl1
C 37	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl1
C 38	1	100.0	4	1 US-08-126-594-25	Sequence 25, Appl1
C 39	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl1
C 40	1	100.0	4	1 US-08-188-943-1	Sequence 1, Appl1
C 41	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl1
C 42	1	100.0	4	1 US-08-188-943-2	Sequence 2, Appl1
C 43	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl1
C 44	1	100.0	4	1 US-08-465-811A-25	Sequence 25, Appl1
C 45	1	100.0	4	1 US-08-199-317-2	Sequence 2, Appl1
C 45	1	100.0	4	1 US-08-199-317-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-268-6798-8/c  
: Sequence 8, Application US/08268679B  
: Patent No. 5674729  
: GENERAL INFORMATION:  
: APPLICANT: WIMMER, ECKARD; MOLLA,  
: APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.  
: TITLE OF INVENTION: DE NOVO CELL-FREE  
: TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
: STREET: 345 PARK AVE.  
: CITY: NEW YORK  
: STATE: NEW YORK  
: COUNTRY: USA  
: ZIP: 10154  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: FLOPPY DISK  
: COMPUTER: IBM PC COMPATIBLE  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: WORD PERFECT # 5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/268,679B  
: FILING DATE: 30-JUN-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/846,914  
: FILING DATE: 06-MAR-1992  
: CLASSIFICATION: 435  
: APPLICATION NUMBER: 07/19,761  
: FILING DATE: 24-JUN-1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: MARIA C. H. LIN  
: REGISTRATION NUMBER: 29,323  
: REFERENCE/DOCKET NUMBER: 0887-4095 US2  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 758-4800  
: TELEFAX: (212) 751-6849  
: TELEX: 421792  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 2  
: TYPE: NUCLEIC ACID  
: STRANDEDNESS: SINGLE  
: TOPOLOGY: UNKNOWN  
: MOLECULE TYPE:  
: DESCRIPTION: OLIGONUCLEOTIDE  
: HYPOTHEetical: NO  
: ANTI-SENSE: YES  
: ORIGINAL SOURCE: N.A.

POSITION IN GENOME: N.A.  
US-08-268-6798-8

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 C 2

RESULT 2  
US-08-484-192-16/c  
Sequence 16, Application US/08484192  
Patent No. 5756291  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: ALBRECHT, GLENN  
APPLICANT: LATHAM, JOHN  
APPLICANT: LEUNG, LAWRENCE  
APPLICANT: VERMAAS, ERIC  
APPLICANT: TOOLE, JOHN J.  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
TITLE OF INVENTION: METHODS OF MAKING  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,192  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,387  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 246102002221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ. ID NO.: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: misc-difference  
LOCATION: replace(1, "")  
OTHER INFORMATION: /note= "This is a biotin-17  
US-08-484-192-16  
OTHER INFORMATION: nucleotide stretch of abasic residues."

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1

Db 2 C 2

RESULT 3  
US-08-361-024-3  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 Mb  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgoon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 128D-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ. ID NO.: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 C 2

RESULT 4  
US-08-361-024-3/c  
Sequence 3, Application US/08361024  
Patent No. 6207368  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
TITLE OF INVENTION: Method, Reagent and Kit  
TITLE OF INVENTION: for Detection and  
TITLE OF INVENTION: Amplification of  
TITLE OF INVENTION: Nucleic Acid Sequence



NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 Mb  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,024  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,059  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Burgoon, Richard P.  
REGISTRATION NUMBER: 34,787  
REFERENCE/DOCKET NUMBER: 128D-126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 773-7610  
TELEFAX: (714) 773-7936  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
US-08-361-024-3

Query Match  
Best Local Similarity 100.0%; Score 1; DB 4; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 1 C 1

RESULT 5  
US-07-791-213D-46  
Sequence 46, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 3 C 3

RESULT 6  
US-07-791-213D-46/C  
Sequence 46, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021

;; INFORMATION FOR SEQ ID NO: 46:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 C 2

RESULT 7  
US-07-791-213D-62  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1

Db 3 C 3

RESULT 8  
US-07-791-213D-62/c  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TITLE OF INVENTION: TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 C 2

RESULT 9  
US-08-268-679B-7/c  
Sequence 7, Application US/08268679B  
Patent No. 5674729  
GENERAL INFORMATION:  
APPLICANT: WIMMER, ECKARD; MULLA,  
APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.  
TITLE OF INVENTION: DE NOVO CELL-FREE  
TITLE OF INVENTION: SYNTHESIS PICO RNA VIRUS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,679B  
FILING DATE: 30-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07\846,914  
FILING DATE: 06-MAR-1992  
CLASSIFICATION: 435  
APPLICATION NUMBER: 07\719,761  
FILING DATE: 24-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C.H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 0887-4095 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE: N.A.  
POSITION IN GENOME: N.A.  
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 10  
US-08-602-036A-2  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Podstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: Linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|  
Db 3 C 3

RESULT 11  
US-08-602-036A-2/c  
Sequence 2, Application US/08602036A  
Patent No. 5789248  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Podstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandsmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,036A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
Db 3 C 3

RESULT 17  
US-08-502-374A-2/C  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oeystein  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,374A  
FILING DATE: 14-Jul-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
Db 1 C 1

RESULT 18  
US-08-642-407A-2  
Sequence 2, Application US/08642407A  
Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Elvind  
APPLICANT: Engebraaten, Olav  
APPLICANT: Maelandmo, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 3 C 3

RESULT 19  
US-08-642-407A-2/C  
Sequence 2, Application US/08642407A

Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oeystein, Fodstad  
APPLICANT: Hovig, Eivind  
APPLICANT: Engebraten, Olav  
APPLICANT: Maelandmo, Gunnild H.  
TITLE OF INVENTION: CARL SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 20  
US-08-873-709-9/c  
Sequence 9, Application US/08873709  
Patent No. 6037126  
GENERAL INFORMATION:  
APPLICANT: Grossman, Abraham  
TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND  
APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF  
TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abraham Grossman  
STREET: 666 Washington Avenue  
CITY: Pleasantville  
STATE: NY  
COUNTRY: USA  
ZIP: 10570  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873,709  
FILING DATE: 12-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: 0001/002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-747-9108  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 3 C 3

RESULT 21  
US-09-032-365A-36/c  
Sequence 36, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Naggart, Juergen  
APPLICANT: No. 6114502en-Trauth, Konrad  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
TITLE OF INVENTION: NEUROSENSORY DEFECTS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-2C1P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-032-365A-36

Query Match 100.0%: Score 1; DB 3; Length 3;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 3 c 3

RESULT 22  
US-08-793-634B-12/C  
Sequence 12, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khen, Rafiqul J.  
APPLICANT: Larkin, Phillip J.  
APPLICANT: Taylor, William C.  
APPLICANT: Marshall, Jerry S.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-12

Query Match 100.0%: Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 2 c 2

RESULT 23  
US-08-973-568-55/C  
Sequence 55, Application US/08973568B  
Patent No. 6277634  
GENERAL INFORMATION:  
APPLICANT: McCall, Maxine J.  
APPLICANT: Hendry, Phillip  
APPLICANT: Lockett, Trevor  
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF  
FILE REFERENCE: 47203bpcus  
CURRENT APPLICATION NUMBER: US/08/973,568B  
CURRENT FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 55  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
FEATURE: Synthetic Ribozyme or portion thereof  
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and  
US-08-973-568-55

Query Match 100.0%: Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%: Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 c 1  
Db 1 c 1

RESULT 24  
US-07-755-462-2  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sene, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 4 C 4

RESULT 25  
US-07-755-462-2/c  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755.462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 1 C 1

RESULT 26  
US-08-169-950-6  
Sequence 6, Application US/08169950  
Patent No. 5366882  
GENERAL INFORMATION:  
APPLICANT: LUNNEN, KEITH D.  
APPLICANT: WILSON, GEOFFREY G.  
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI  
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,950  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 3 C 3

RESULT 27  
US-08-169-950-6/c  
Sequence 6, Application US/08169950  
Patent No. 5366882  
GENERAL INFORMATION:  
APPLICANT: LUNNEN, KEITH D.  
APPLICANT: WILSON, GEOFFREY G.  
TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI  
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DAVID G. COMLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,950  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 43959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-169-950-6

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 2 C 2

RESULT 28  
US-07-630-288A-7/C  
Sequence 7, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-7

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 29  
US-07-630-288A-11  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid



STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 4 C 4

RESULT 30  
US-07-630-288A-11/C  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 4 C 4

Db 1 C 1

RESULT 31  
US-07-630-288A-13/C  
Sequence 13, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 4 C 4

RESULT 32  
US-07-630-288A-14  
Sequence 14, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-14

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 3 C 3

RESULT 33  
US-07-630-288A-14/C  
Sequence 14, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF SEQUENCES: 49  
CURRENT APPLICATION DATA:  
ADDRESS: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-14

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 4;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 2 C 2

RESULT 34  
US-07-630-288A-34  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF SEQUENCES: 49  
CURRENT APPLICATION DATA:  
ADDRESS: Joanne M. Gieser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Gieser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 4 C 4

RESULT 35  
US-07-630-288A-34/C  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 2 C 2

RESULT 36  
US-08-126-594-25  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Estratiadis, Algis  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
TITLE OF INVENTION: CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 37  
US-08-126-594-25/C  
Sequence 25, Application US/08126594  
Patent No. 5482845  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Estratiadis, Algis  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
TITLE OF INVENTION: CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,594  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 3 C 3

RESULT 38  
US-08-188-943-1  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudbande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 4 C 4

RESULT 39  
US-08-188-943-1/C  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudbande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 C 1  
1  
Db 3 C 3

## RESULT 40

US-08-188-943-2  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1: DB 1: Length 4:  
Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 C 1  
1  
Db 2 C 2

## RESULT 41

US-08-188-943-2/C  
Sequence 2, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-2

Query Match 100.0%; Score 1: DB 1: Length 4:  
Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 C 1  
1  
Db 1 C 1

RESULT 42  
US-08-465-811A-25  
Sequence 25, Application US/08465811A  
Patent No. 5637685  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Efstratiadis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 1 C 1

RESULT 43  
US-08-465-811A-25/C  
Sequence 25, Application US/08465811A  
Patent No. 5637685  
GENERAL INFORMATION:  
APPLICANT: Soares, M. Bento  
APPLICANT: Estratidis, Argiris  
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF  
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, c/o Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,811A  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 42840/JPM/AKC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 3 C 3

RESULT 44  
US-08-199-317-2  
Sequence 2, Application US/08199317  
Patent No. 5670316  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double D-loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,317  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,791  
FILING DATE: 09-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,462  
FILING DATE: 04-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 9150-0004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for Dpn I  
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 4 C 4

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RESULT 45
US-08-199-317-2/C
: Sequence 2: Application US/08199317
: Patent No. 5670316
:
: GENERAL INFORMATION:
: APPLICANT: Sena, Elissa P.
: APPLICANT: Calhoun, Cornelia J.
: APPLICANT: Zarling, David A.
: TITLE OF INVENTION: Diagnostic Applications of Double D-loop
: TITLE OF INVENTION: Formation
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave., Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/199,317
: FILING DATE: 25-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/910,791
: FILING DATE: 09-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/755,462
: FILING DATE: 04-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/520,321
: FILING DATE: 07-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Stratford, Carol A.
: REGISTRATION NUMBER: 34,444
: REFERENCE/DOCKET NUMBER: 9150-0004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-324-0880
: TELEFAX: 415-324-0960
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Cleavage site for Dpn I
:
: US-08-199-317-2

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Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 C 1
DB 1 C 1

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Search completed: July 15, 2002, 23:07:38  
Job time: 22991 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:25 : Search time 12941.8 Seconds

(without alignments)  
1.672 Million cell updates/sec

Title: US-09-375-248-1-COPY\_3360\_3360  
Perfect score: 1 c 1  
Sequence: 1 c 1

Scoring table:

OLIGO-NUC  
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

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2: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*

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34: /cgn2\_6/ptodata/2/pna/US118\_COMB.seq:\*

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38: /cgn2\_6/ptodata/2/pna/US122\_COMB.seq:\*

39: /cgn2\_6/ptodata/2/pna/US123\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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45:	100.0	1	2	5	US-08-107-721-46
46:	100.0	1	2	5	US-08-107-721B-46
47:	100.0	1	2	15	US-09-172-828-15
48:	100.0	1	2	16	US-09-284-725-201
49:	100.0	1	2	17	US-09-306-333A-32
50:	100.0	1	2	17	US-09-387-777-3
51:	100.0	1	2	17	US-09-387-777-6
52:	100.0	1	2	17	US-09-387-777-7
53:	100.0	1	2	17	US-09-387-777-8
54:	100.0	1	2	17	US-09-387-777-9
55:	100.0	1	2	17	US-09-387-777-10
56:	100.0	1	2	17	US-09-387-777-11
57:	100.0	1	2	17	US-09-387-777-12
58:	100.0	1	2	17	US-09-387-777-13
59:	100.0	1	2	17	US-09-387-777-14
60:	100.0	1	2	17	US-09-387-777-15
61:	100.0	1	2	17	US-09-387-777-16
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63:	100.0	1	2	17	US-09-387-777-18
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65:	100.0	1	2	17	US-09-387-777-20
66:	100.0	1	2	17	US-09-387-777-21
67:	100.0	1	2	17	US-09-387-777-22
68:	100.0	1	2	17	US-09-387-777-23
69:	100.0	1	2	17	US-09-387-777-24
70:	100.0	1	2	17	US-09-387-777-25
71:	100.0	1	2	17	US-09-387-777-26
72:	100.0	1	2	17	US-09-387-777-27
73:	100.0	1	2	17	US-09-387-777-28
74:	100.0	1	2	17	US-09-387-777-29
75:	100.0	1	2	17	US-09-387-777-30



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C 33 1 100.0 2 24 US-09-634-306B-175403 Sequence 175403.  
C 34 1 100.0 2 24 US-09-634-306B-175415 Sequence 175415.  
C 35 1 100.0 2 24 US-09-634-306B-175419 Sequence 175419.  
C 36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426.  
C 37 1 100.0 2 24 US-09-634-306B-175433 Sequence 175433.  
C 38 1 100.0 2 24 US-09-634-306B-175449 Sequence 175449.  
C 39 1 100.0 2 24 US-09-634-306B-175848 Sequence 175848.  
C 40 1 100.0 2 24 US-09-634-306B-176849 Sequence 176849.  
C 41 1 100.0 2 24 US-09-634-306B-176880 Sequence 176880.  
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C 43 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440.  
C 44 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440.  
C 45 1 100.0 2 24 US-09-634-306B-178617 Sequence 178617.

## ALIGNMENTS

RESULT 1  
US-07-934-385-14/C  
; Sequence 14, Application US/07934385  
; GENERAL INFORMATION:  
; APPLICANT: LATHAM, JOHN  
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES  
; TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES  
; NUMBER OF SEQUENCES: 177  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,385  
; FILING DATE: 19920821  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRACEY, NANCY J.  
; REGISTRATION NUMBER: 28,216  
; REFERENCE/DOCKET NUMBER: 24610-20022-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: misc,difference  
; LOCATION: replace(1,"")  
; OTHER INFORMATION: /note="This position is a  
; OTHER INFORMATION: biotin-17 nucleotide stretch of random sequences."  
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 c 2

RESULT 2  
US-08-107-721-46/C  
; Sequence 46, Application US/08107721  
; GENERAL INFORMATION:  
; APPLICANT: TOOLE, JOHN J.  
; APPLICANT: GRIFFIN, LINDA C.  
; APPLICANT: BOCK, LOUIS C.  
; APPLICANT: LATHAM, JOHN A.  
; APPLICANT: MUENCHAU, DARYL D.  
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
; TITLE OF INVENTION: METHODS OF MAKING  
; NUMBER OF SEQUENCES: 109  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GILEAD SCIENCES, INC.  
; STREET: 344 LAKEVIEW DRIVE  
; CITY: FOSTER CITY  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,721  
; FILING DATE: 20-AUG-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRACEY, NANCY J.  
; REGISTRATION NUMBER: 28216  
; REFERENCE/DOCKET NUMBER: 24610-20022-20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)574-3000  
; TELEFAX: (415)578-9264  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: misc,feature  
; LOCATION: 1  
; OTHER INFORMATION: /note="This is a biotin-17  
; OTHER INFORMATION: nucleotide stretch of abasic residues."  
US-08-107-721-46

Query Match 100.0%; Score 1; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 c 2

RESULT 3  
US-08-107-721B-46/C  
; Sequence 46, Application US/08107721B  
; GENERAL INFORMATION:  
; APPLICANT: TOOLE, JOHN J.  
; APPLICANT: GRIFFIN, LINDA C.  
; APPLICANT: BOCK, LOUIS C.  
; APPLICANT: LATHAM, JOHN A.  
; APPLICANT: MUENCHAU, DARYL D.  
; APPLICANT: KRANCZYK, STEVEN  
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
; TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GILEAD SCIENCES, INC.  
STREET: 344 LAKEVIEW DRIVE  
CITY: FOSTER CITY  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94404

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,721B  
FILING DATE: 20-AUG-1993  
CLASSIFICATION: 415  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28216  
REFERENCE/DOCKET NUMBER: 24610-20022.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)574-3000  
TELEFAX: (415)574-9264  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: /note="This is a biotin-17  
OTHER INFORMATION: nucleotide stretch of abasic residues."  
US-08-107-721B-46

Query Match 100.0%; Score 1; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 2 c 2

## RESULT 4

US-09-172-828-15/c  
Sequence 15; Application US/09172828  
GENERAL INFORMATION:  
APPLICANT: Children's Medical Center Corporation  
APPLICANT: Klagsbrun, Michael  
APPLICANT: Elenius, Klaus  
TITLE OF INVENTION: Novel Human EGF Receptors and Use  
FILE REFERENCE: 47758-PCT  
CURRENT APPLICATION NUMBER: US/09/172,828  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 15  
LENGTH: 2  
TYPE: DNA  
ORGANISM: mouse  
US-09-172-828-15

Query Match 100.0%; Score 1; DB 15; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 1 c 1

## RESULT 5

US-09-284-725-201  
Sequence 201; Application US/09284725  
GENERAL INFORMATION:  
APPLICANT: Quint, Wilhelmus  
APPLICANT: Van Doorn, Leenderl  
TITLE OF INVENTION: Probes, methods and kits for detection and  
TITLE OF INVENTION: Typing of Helicobacter pylori nucleic acids in biological  
TITLE OF INVENTION: samples.  
NUMBER OF SEQUENCES: 280  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP  
STREET: 620 Newport Center Drive, 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/284,725  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP96/870131.8  
FILING DATE: 16-OCT-1996  
APPLICATION NUMBER: PCT/EP97/05614  
FILING DATE: 10-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: INNOG2.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (949) 760-0404  
TELEFAX: (949) 760-9395  
INFORMATION FOR SEQ ID NO: 201:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-284-725-201

Query Match 100.0%; Score 1; DB 16; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
Db 2 c 2

## RESULT 6

US-09-306-333A-32  
Sequence 32; Application US/09306333A  
GENERAL INFORMATION:  
APPLICANT: Academy of Applied Science  
TITLE OF INVENTION: BRCAL and hMLH1 Gene Primer Sequences and Method for  
TITLE OF INVENTION: Testing  
FILE REFERENCE: BRCAL  
CURRENT APPLICATION NUMBER: US/09/306,333A  
CURRENT FILING DATE: 1999-05-06

PRIOR APPLICATION NUMBER: PCT/1B00/01607  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-333A-32

Query Match 100.0% Score 1: DB 17; Length 2;  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 1 c 1

RESULT 7  
US-09-306-333A-32/C  
Sequence 32, Application US/09306333A  
GENERAL INFORMATION:  
APPLICANT: Academy of Applied Science  
TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for  
FILE REFERENCE: BRCA1  
CURRENT APPLICATION NUMBER: US/09/306.333A  
CURRENT FILING DATE: 1999-05-06  
PRIOR APPLICATION NUMBER: PCT/1B00/01607  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-333A-32

Query Match 100.0% Score 1: DB 17; Length 2;  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 c 2

RESULT 8  
US-09-387-777-2  
Sequence 2, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kiess  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman C/O Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead-Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-2

Query Match 100.0% Score 1: DB 17; Length 2;  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 c 1  
Db 2 c 2

RESULT 9  
US-09-387-777-3/C  
Sequence 3, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kiess  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman C/O Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead-Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-1

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 2 C 2

RESULT 10  
US-09-387-777-5  
Sequence 5, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimole-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ. ID NO.: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-5

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 1 C 1

RESULT 11

US-09-387-777-6  
Sequence 6, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimole-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
SOFTWARE: Word for Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:

INFORMATION FOR SEQ. ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-6

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
DB 1 C 1

RESULT 12  
US-09-387-777-7  
Sequence 7, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Klees

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

```
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match      100.0%  Score 1: DB 17; Length 2;
Best local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 C 1
Db 1 C 1

RESULT 13
US-09-387-777-7/C
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-8

Query Match      100.0%  Score 1: DB 17; Length 2;
Best local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;
```

```
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match      100.0%  Score 1: DB 17; Length 2;
Best local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 C 1
Db 2 C 2

RESULT 14
US-09-387-777-8
: Sequence 8, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-8

Query Match      100.0%  Score 1: DB 17; Length 2;
Best local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 C 1
```

Db 1 C 1

## RESULT 15

US-09-387-777-9/c

Sequence 9, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

OPERATING SYSTEM: Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-9

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 1 C 1

RESULT 16

US-09-387-777-10

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

OPERATING SYSTEM: Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 1 C 1

RESULT 17

US-09-387-777-10/c

Sequence 10, Application US/09387777

GENERAL INFORMATION:

APPLICANT: Hadar Kless

TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID

TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE

TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead\* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

OPERATING SYSTEM: Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

SOFTWARE: to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/387,777

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 34/40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-562553

TELEFAX: 972-3-562554

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-387-777-10

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1

Db 2 C 2

```

:
: ATTORNEY/AGENT INFORMATION:
:   NAME: Friedmann, Mark M.
:   REGISTRATION NUMBER: 33,883
:   REFERENCE/DOCKET NUMBER: 34/40
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 972-3-5625553
:     TELEFAX: 972-3-5625554
:   TELEX:
:
: INFORMATION FOR SEQ ID NO: 10:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 2
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
: US-09-387-777-10
:
:
: Query Match      100.0%; Score 1: DB 17; Length 2:
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;
:
: QY      1 C 1
:         1
:         1 C 1
:
: DB
:
:
: RESULT 18
: US-09-387-777-11/C
:   Sequence 11, Application US/09387777
:   GENERAL INFORMATION:
:     APPLICANT: Hadar Kless
:     TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
:     TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
:     NUMBER OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
:     NUMBER OF SEQUENCES: 88
:     CORRESPONDENCE ADDRESS:
:       ADDRESSEE: Mark M. Friedmann c/o Anthony Castorina
:       STREET: 2001 Jefferson Davis Highway, Suite 207
:       CITY: Arlington
:       STATE: Virginia
:       COUNTRY: United States of America
:       ZIP: 22202
:     COMPUTER READABLE FORM:
:       MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
:       COMPUTER: Twinhead* Slimnote-890TX
:       OPERATING SYSTEM: MS DOS version 6.2,
:       SOFTWARE: Word for Windows version 3.11
:       CURRENT APPLICATION DATA:
:         APPLICATION NUMBER: US/09/387,777
:         FILING DATE:
:         CLASSIFICATION:
:         PRIOR APPLICATION DATA:
:         APPLICATION NUMBER:
:         FILING DATE:
:         ATTORNEY/AGENT INFORMATION:
:           NAME: Friedmann, Mark M.
:           REGISTRATION NUMBER: 33,883
:           REFERENCE/DOCKET NUMBER: 34/40
:           TELECOMMUNICATION INFORMATION:
:             TELEPHONE: 972-3-5625553
:             TELEFAX: 972-3-5625554
:             TELEX:
:
: INFORMATION FOR SEQ ID NO: 11:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 2
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
: US-09-387-777-11
```

```

:
: Query Match      100.0%; Score 1: DB 17; Length 2:
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1: Conservative 0; Mismatches 0; Indels 0; Caps 0;
:
: QY      1 C 1
:         1
:         2 C 2
:
: DB
:
:
: RESULT 19
: US-09-387-777-12/C
:   Sequence 12, Application US/09387777
:   GENERAL INFORMATION:
:     APPLICANT: Hadar Kless
:     TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
:     TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
:     NUMBER OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
:     NUMBER OF SEQUENCES: 88
:     CORRESPONDENCE ADDRESS:
:       ADDRESSEE: Mark M. Friedmann c/o Anthony Castorina
:       STREET: 2001 Jefferson Davis Highway, Suite 207
:       CITY: Arlington
:       STATE: Virginia
:       COUNTRY: United States of America
:       ZIP: 22202
:     COMPUTER READABLE FORM:
:       MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
:       COMPUTER: Twinhead* Slimnote-890TX
:       OPERATING SYSTEM: MS DOS version 6.2,
:       SOFTWARE: Word for Windows version 3.11
:       CURRENT APPLICATION DATA:
:         APPLICATION NUMBER: US/09/387,777
:         FILING DATE:
:         CLASSIFICATION:
:         PRIOR APPLICATION DATA:
:         APPLICATION NUMBER:
:         FILING DATE:
:         ATTORNEY/AGENT INFORMATION:
:           NAME: Friedmann, Mark M.
:           REGISTRATION NUMBER: 33,883
:           REFERENCE/DOCKET NUMBER: 34/40
:           TELECOMMUNICATION INFORMATION:
:             TELEPHONE: 972-3-5625553
:             TELEFAX: 972-3-5625554
:             TELEX:
:
: INFORMATION FOR SEQ ID NO: 12:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 2
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
: US-09-387-777-12
:
:
: RESULT 20
: US-09-387-777-14
:   Sequence 14, Application US/09387777
:   GENERAL INFORMATION:
:     APPLICANT: Hadar Kless
:     TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
:     TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
:     NUMBER OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
:     NUMBER OF SEQUENCES: 88
:     CORRESPONDENCE ADDRESS:
:       ADDRESSEE: Mark M. Friedmann c/o Anthony Castorina
:       STREET: 2001 Jefferson Davis Highway, Suite 207
:       CITY: Arlington
:       STATE: Virginia
:       COUNTRY: United States of America
:       ZIP: 22202
:     COMPUTER READABLE FORM:
:       MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
:       COMPUTER: Twinhead* Slimnote-890TX
:       OPERATING SYSTEM: MS DOS version 6.2,
:       SOFTWARE: Word for Windows version 3.11
:       CURRENT APPLICATION DATA:
:         APPLICATION NUMBER: US/09/387,777
:         FILING DATE:
:         CLASSIFICATION:
:         PRIOR APPLICATION DATA:
:         APPLICATION NUMBER:
:         FILING DATE:
:         ATTORNEY/AGENT INFORMATION:
:           NAME: Friedmann, Mark M.
:           REGISTRATION NUMBER: 33,883
:           REFERENCE/DOCKET NUMBER: 34/40
:           TELECOMMUNICATION INFORMATION:
:             TELEPHONE: 972-3-5625553
:             TELEFAX: 972-3-5625554
:             TELEX:
:
: INFORMATION FOR SEQ ID NO: 14:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 2
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
: US-09-387-777-14
```

NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 2 C 2

RESULT 21  
US-09-387-777-15/C  
Sequence 15, Application US/09387777  
GENERAL INFORMATION:  
APPLICANT: Hadar Kless  
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID  
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE  
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,777

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 34/40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
Db 2 C 2

RESULT 22  
US-09-472-035A-19/C  
Sequence 19, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kashi et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead\* Slimnote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472,035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2



TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-19

Query Match  
Best Local Similarity 100.0%; Score 1; DB 18; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
pb 1 C 1

RESULT 23  
US-09-472-035A-20  
Sequence 20, Application US/09472035A  
GENERAL INFORMATION:  
APPLICANT: Yechezkel Kashi et al.  
TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND  
TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS  
TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR  
NUMBER OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING  
CORRESPONDENCE ADDRESS: 42  
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina  
STREET: 2001 Jefferson Davis Highway, Suite 207  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
COMPUTER: Twinhead Slimote-890TX  
OPERATING SYSTEM: MS DOS version 6.2,  
OPERATING SYSTEM: Windows version 3.11  
SOFTWARE: Word for Windows version 2.0 converted to  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/472,035A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedman, Mark M.  
REGISTRATION NUMBER: 33,883  
REFERENCE/DOCKET NUMBER: 74/77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 972-3-5625553  
TELEFAX: 972-3-5625554  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-472-035A-20

Query Match  
Best Local Similarity 100.0%; Score 1; DB 18; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
Db 2 C 2  
RESULT 24

US-09-634-306B-51869  
Sequence 51869, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827,129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51869  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-51869

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 C 1  
Db 2 C 2

RESULT 25  
US-09-634-306B-52280  
Sequence 52280, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827,129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52280  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
db 2 c 2

RESULT 26  
US-09-634-306B-52357  
; Sequence 52357, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 52357  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
db 2 c 2

RESULT 27  
US-09-634-306B-53003  
; Sequence 53003, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 53003  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-53003

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
db 1 c 1

RESULT 28  
US-09-634-306B-58305  
; Sequence 58305, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 58305  
; LENGTH: 2  
; TYPE: DNA  
; ORGANISM: Human  
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 c 1  
db 1 c 1

RESULT 29  
US-09-634-306B-175312/c  
; Sequence 175312, Application US/09634306B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/634,306B  
; PRIOR FILING DATE: 2002-02-21

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
RESULT 30
US-09-634-306B-175337/c
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
RESULT 31
US-09-634-306B-175354/c
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
RESULT 32
US-09-634-306B-175401/c
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
```

US-09-634-306B-175401

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 33

US-09-634-306B-175403/c

Sequence 175403, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/09/634,306B

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175403

LENGTH: 2

TYPE: DNA

ORGANISM: Human

US-09-634-306B-175403

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 34

US-09-634-306B-175415/c

Sequence 175415, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/09/634,306B

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175415

LENGTH: 2

TYPE: DNA

ORGANISM: Human

US-09-634-306B-175415

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 35

US-09-634-306B-175419/c

Sequence 175419, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/09/634,306B

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175419

LENGTH: 2

TYPE: DNA

ORGANISM: Human

US-09-634-306B-175419

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 36

US-09-634-306B-175426/c

Sequence 175426, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
RESULT 37
US-09-634-306B-175433/c
: Sequence 175433, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
Db 1 c 1
US-09-634-306B-175849/c
: Sequence 175849, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-09-634-306B-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 c 2
```

```
RESULT 39
US-09-634-306B-176848/c
: Sequence 176848, Application US/09634306B
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/09/634,306B
: CURRENT FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176848
: LENGTH: 2
```

TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176848

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 40  
US-09-634-306B-176849/c  
Sequence 176849, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176849  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176849

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 41  
US-09-634-306B-176880/c  
Sequence 176880, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176880  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-176880

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 42  
US-09-634-306B-178420/c  
Sequence 178420, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634.306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 178420  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-178420

Query Match  
Best Local Similarity 100.0%; Score 1; DB 24; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 43  
US-09-634-306B-178440  
Sequence 178440, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-106B-178440
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 2 c 2
```

```

RESULT 44
US-09-634-306B-178440/C
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 1 c 1
Db 1 c 1
```

```

RESULT 45
US-09-634-306B-178617/C
; Sequence 178617, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178617
```

```

Query Match          100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 c 1
Db 2 c 2
```

Search completed: July 16, 2002, 02:50:26  
Job time: 31279 sec

\_\_\_\_\_





PT useful to inhibit metastatic cancer, partic. osteosarcoma  
XX  
PS Claim 2: Page 56; 70pp; English.

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene  
CC expression may include the trinucleotide GUC (AAT33326, given in 5'  
CC to 3' direction) found in codon 14 of CAPL mRNA. These and  
CC other antisense oligonucleotides (AAT33327-36) complementary to  
CC specific regions of the CAPL gene (see also AAT33345), as well as  
CC CAPL-specific ribozymes (AAT33337-40) can be administered to a  
CC patient as a means of inhibiting metastatic cancer.

XX  
SQ Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
:  
Db 2 u 2

## RESULT 2

AL20244  
ID AAL20244 standard; cDNA; 3 BP.

AC AAL20244;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 12701.

XX Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN WO200151628-A2.

XX  
PD 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Xu Y, Wang Y, Steimann K;

PI WPI: 2001-451856/48.

DR New peptide useful as a marker for the diagnosis of breast cancer -

XX Claim 1: Page 2245; 3695pp; English.

PS The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.

SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
:  
Db 3 t 3

## RESULT 3

AL20244/C  
ID AAL20244 standard; cDNA; 3 BP.

AC AAL20244;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 12701.

XX Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN WO200151628-A2.

XX  
PD 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Xu Y, Wang Y, Steimann K;

PI WPI: 2001-451856/48.

DR New peptide useful as a marker for the diagnosis of breast cancer -

XX Claim 1: Page 2245; 3695pp; English.

PS The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.

SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
:  
Db 1 t 1

## RESULT 4

AA081664

ID AA081664 standard; RNA; 4 BP.  
 XX  
 AC AA081664;  
 XX  
 DT 29-SEP-1995 (first entry)  
 XX  
 DE bFGF binding oligomer core sequence #1.  
 XX  
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 XX  
 CS Synthetic.  
 XX  
 PN MO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994; 94WO-US06884.  
 XX  
 PR 18-JUN-1993; 93US-0079677.  
 PR 07-JAN-1994; 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity; useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 ;  
 Db 2 u 2

RESULT 5  
 ID AA081665 standard; RNA; 4 BP.  
 XX  
 AC AA081665;  
 XX  
 DT 29-SEP-1995 (first entry)  
 XX  
 DE bFGF binding oligomer core sequence #2.

XX  
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994; 94WO-US06884.  
 XX  
 PR 18-JUN-1993; 93US-0079677.  
 PR 07-JAN-1994; 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity; useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 ;  
 Db 2 u 2

RESULT 6  
 ID AAT86385/C  
 XX  
 AC AAT86385;  
 XX  
 DT 23-APR-1998 (first entry)  
 XX  
 DE Probe for target nucleic acid sequence p0.  
 XX  
 KW Point mutation detection; nucleic acid sequence analysis; probe;  
 KW viral disease diagnosis; genetic disease diagnosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers



CC This sequence represents a non-coding immunostimulatory polynucleotide  
CC (ISP) comprised of at least one strand of a palindromic, which includes  
CC at least one dinucleotide consisting of adjacent, unmethylated cytosine  
CC and guanine residues. ISP's could be used in vaccination methods  
CC for enhancing the immune response of a host to an antigen. Administration  
CC of naked gene expression vectors which encode antigens or their  
CC immunostimulatory fragments suppresses IgE antibody production  
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.  
X

SU Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
UB 1 t 1

## RESULT 9

AA17191  
ID AA17191 standard; cDNA; 4 BP.

XX AA17191;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 9648.

KW Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN W0200151628-A2.

XX 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI; 2001-451856/48.

PT New peptide useful as a marker for the diagnosis of breast cancer -

PS Claim 1; Page 1720; 3655pp; English.

CC The invention relates to human breast cancer expressed polynucleotides  
CC (AA107544-AA126789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.

SO Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 4 t 4

## RESULT 10

AA17191/C  
ID AA17191 standard; cDNA; 4 BP.

XX AA17191;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 9648.

KW Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

PN W0200151628-A2.

XX 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US00798.

PR 14-JAN-2000; 2000US-0176077.

PR 14-MAR-2000; 2000US-0189167.

PR 24-MAR-2000; 2000US-0192099.

PR 29-MAR-2000; 2000US-0193480.

PR 15-MAY-2000; 2000US-0205230.

PR 09-JUN-2000; 2000US-0211315.

PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI; 2001-451856/48.

PT New peptide useful as a marker for the diagnosis of breast cancer -

PS Claim 1; Page 1720; 3655pp; English.

CC The invention relates to human breast cancer expressed polynucleotides  
CC (AA107544-AA126789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.

SO Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 2 t 2

## RESULT 11

AA124357  
ID AA124357 standard; cDNA; 4 BP.

XX AA124357;

XX 07-DEC-2001 (first entry)  
 DT  
 XX  
 DE Human breast cancer expressed polynucleotide 16814.  
 XX  
 KW Human; breast cancer; cell marker; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200151628-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 10-JAN-2001: 2001WO-US00798.  
 XX  
 PR 14-JAN-2000: 2000US-0176077.  
 PR 14-MAR-2000: 2000US-0189167.  
 PR 24-MAR-2000: 2000US-0192099.  
 PR 29-MAR-2000: 2000US-0193480.  
 PR 15-MAY-2000: 2000US-0205230.  
 PR 09-JUN-2000: 2000US-0211315.  
 PR 25-JUL-2000: 2000US-0220534.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX  
 DR WPI: 2001-451656/48.  
 XX  
 PT New peptide useful as a marker for the diagnosis of breast cancer -  
 PS  
 XX  
 PS Claim 1: Page 3087: 3695pp: English.  
 CC  
 CC The invention relates to human breast cancer expressed polynucleotides  
 CC (AA107544-AA126789) and methods of assessing whether a patient is  
 CC afflicted with breast cancer by examining the correlation between the  
 CC expression of certain markers and the cancerous state of breast cells.  
 CC The polynucleotides and encoded polypeptides are potential markers for  
 CC detecting, diagnosing, monitoring, characterising treating and  
 CC potentially preventing breast cancer. The polynucleotides and encoded  
 CC polypeptides are also useful for isolating compounds with cytostatic  
 CC activity.  
 CC  
 SO Sequence 4 BP: 0 A; 1 C; 0 G; 3 T; 0 other;  
 CC  
 Query Match 100.0%; Score 1; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 t 1  
 DB 1 t 1  
 AC  
 AC AAF61450 standard; RNA: 4 BP.  
 XX  
 AC AAF61450:  
 XX  
 DT 18-JUN-2001 (first entry)  
 XX  
 DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.  
 XX  
 KW Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;  
 XX  
 KW cyclin E2F1; vasotropic; gene therapy; cell cycle arrest; ss.  
 OS  
 OS Synthetic.  
 XX  
 PN WO200121789-A1.  
 XX  
 PD 29-MAR-2001.

XX 22-SEP-1999; 99WO-EP07049.  
 PF  
 XX  
 PR 22-SEP-1999; 99WO-EP07049.  
 XX  
 PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.  
 XX  
 PI Grassi G, Kuhn AC, Kandolf R;  
 XX  
 DR WPI: 2001-257985/26.  
 XX  
 PT New catalytically acting RNA molecule comprising hammerhead ribozyme  
 PT directed against mRNA molecules encoding cyclin E or E2F1, useful for  
 PT inhibiting vascular smooth muscle cell proliferation and restenosis -  
 XX  
 PS Claim 12: Page 28; 40pp: German.  
 XX  
 CC This invention describes a novel catalytic RNA molecule which is directed  
 CC against mRNA molecules (11) which encode the cell relevant protein cyclin  
 CC E or E2F1. The products of the invention have vasotropic activity and can  
 CC be used for gene therapy. The use of (1), or a DNA molecule or a plasmid  
 CC of the invention is claimed for obtaining a vector for gene therapy and  
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic  
 CC compositions containing these components are also claimed. (1)  
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin  
 CC E and E2F1.  
 CC  
 SO Sequence 4 BP: 2 A; 0 C; 1 G; 0 U; 1 other;  
 CC  
 Query Match 100.0%; Score 1; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 t 1  
 DB 4 T 4  
 AC  
 AC AAN93676 standard; DNA: 5 BP.  
 XX  
 AC AAN93676:  
 XX  
 DT 24-JUN-1990 (first entry)  
 XX  
 DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber  
 DE variant (HSV-c) and HSV grape variant (HSV-g).  
 XX  
 KW Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.  
 XX  
 OS Hop growth retarding viroid.  
 OS  
 OS JP01040000-A.  
 XX  
 PN 10-FEB-1989.  
 XX  
 PD 05-AUG-1987; 87JP-0194377.  
 XX  
 PF 05-AUG-1987; 87JP-0195377.  
 XX  
 PR (YUKI ) YUKI GOSEI YAKUHIN.  
 XX  
 PA WPI: 1989-089715/12.  
 XX  
 DR Fractionating and detecting hop growth retarding viroids -  
 XX  
 PT using synthetic DNA probe contg. specific base sequence  
 XX  
 PS Disclosure; page 3; 5pp: Japanese.  
 PS  
 CC The synthetic probes is complementary to the RNA of HSV-g bases 53-59.  
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic

CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV  
CC infections in plants.  
XX  
SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 4 t 4

RESULT 14  
AA068752  
ID AA068752 standard; DNA: 5 BP.  
XX  
AC AA068752;

XX 24-JUN-1990 (first entry)

DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber  
DE variant (HSV-C) and HSV grape variant (HSV-G).

XX Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.

XX Hop growth retarding viroid.

XX JP01040000-A.

XX 10-FEB-1989.

XX 05-AUG-1987; 87JP-0194377.

XX 05-AUG-1987; 87JP-0195377.

XX (YUKI ) YUKI GOSEI YAKUHIN.

XX WPI: 1989-089715/12.

XX Fractionating and detecting hop growth retarding viroids -  
XX using synthetic DNA probe contg. specific base sequence

XX Disclosure: page 3; 5pp; Japanese.

XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.  
CC HSV, HSV-C and HSV-G are fractionated and detected using the synthetic  
CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV  
CC infections in plants.  
XX

SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 15  
AA068752  
ID AA068752 standard; DNA: 5 BP.  
XX  
AC AA068752;

XX 22-FEB-1995 (first entry)

XX CHA255 heavy chain CDR1 clone 3.3.3. coding sequence.

XX Polymerase chain reaction; primer; PCR; amplify; heavy; light;  
XX chain; complementarity determining region; CDR; variable; constant;  
XX region; monoclonal antibody; Mab; binding affinity; EDTA; DOTA;  
XX tumour; cancer; colorectal; breast; metal chelate; hapten; ss.

OS Synthetic.

XX AU9350602-A.

XX 26-MAY-1994.

XX 10-NOV-1993; 93AU-0050602.

XX 12-NOV-1992; 92US-0975230.

XX (HYBR-) HYBRITECH INC.

XX Abreweller PM, Moore MD:

XX WPI: 1994-209063/26.

XX P-PSDB: AAR54150.

XX Polypeptide used in imaging and treatment of carcinomas and  
XX tumours - comprising substd antibody CDR having binding affinity  
XX for metal chelate of EDTA or DETA or analogues

XX Claim 25; Fig 3a; 61pp; English.

XX The sequences given in AA068747-57 encode the wild type and mutagenised  
XX versions of the complementarity determining region 1 (CDR1) of the  
XX antibody designated CHA255. CHA255 is a murine monoclonal antibody  
XX (Mab) which is capable of binding complexes. Mutagenesis of these  
XX CDRs, causes the production of polypeptides with a particularly  
XX high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3  
XX of the heavy chain, and CDR2 and -3 of the light chain were targeted  
XX for mutagenesis. Five residues of both CDR1 and -3 of the CHA255  
XX heavy chain, five of seven residues of light chain CDR and six of  
XX nine light chain CDR3 residues were specifically targeted for  
XX codon-based mutagenesis. The mutagenised Mab's can be used in  
XX compositions for in vivo imaging of malignant tissues or tumours. They  
XX are also useful for the treatment of malignant tissues or tumours eg.  
XX colorectal or breast cancer. Both methods involve the use of  
XX radionuclides which bind to metal chelates or haptens which are  
XX specifically delivered to the target site by a targeting molecule. CDR  
XX derived peptides may be used to construct bi-functional antibodies  
XX having dual specificities, or as donor or recipients of CDR sequences.

SQ Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 3 t 3

RESULT 16  
AA081667  
ID AA081667 standard; RNA: 5 BP.  
XX  
AC AA081667;

XX 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #4.

XX Basic: fibroblast growth factor; bFGF; stem-loop structure;  
XX bubble structure; pseudoknot; receptor; heparin; competition;  
XX inhibition; enhance; neovascularisation; solid tumour; cancer;  
XX

KW metastasis; diagnosis; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994; 94WO-US06884.  
 XX  
 PR 18-JUN-1993; 93US-0079677.  
 PR 07-JAN-1994; 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PS New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 : :  
 Db 2 u 2

RESULT 17  
 AA081667/c  
 ID AA081667 standard; RNA: 5 BP.  
 XX  
 AC AA081667;  
 XX  
 DT 29-SEP-1995 (first entry)  
 XX  
 DE bFGF binding oligomer core sequence #4.  
 XX  
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9500528-A.  
 XX  
 PR 05-JAN-1995.  
 XX

XX  
 PF 17-JUN-1994; 94WO-US06884.  
 XX  
 PR 18-JUN-1993; 93US-0079677.  
 PR 07-JAN-1994; 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.  
 XX  
 PI Beutel BA, Joesten ME;  
 XX  
 DR WPI: 1995-051992/07.  
 XX  
 PS New oligo-nucleotide(s) that bind to basic fibroblast growth  
 PT factor - modulating, esp. inhibiting, its activity, useful in  
 PT treating cancer, preventing metastasis, and diagnosis.  
 XX  
 PS Claim 3; Page 25; 44pp; English.  
 XX  
 CC The sequences given in AA081642-95 are oligonucleotides which modulate  
 CC the activity of basic fibroblast growth factor (bFGF) by binding  
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67  
 CC represent core sequences of which at least one is present in each of  
 CC the binding oligos. These oligonucleotides may form a single  
 CC strand, double strand, a stem-loop structure, a bubble structure, a  
 CC pseudoknot or a closed, circular structure. bFGF binds to high  
 CC affinity receptor and low affinity heparin-like molecules on the  
 CC cell surface. These oligonucleotides bind to bFGF in competition  
 CC with its receptor and heparin. These oligonucleotides may inhibit  
 CC or enhance the activity of bFGF. Particularly, they inhibit  
 CC neovascularisation so they can be used to suppress growth of solid  
 CC tumours and to reduce the risk of metastasis. They can be used as  
 CC diagnostic reagents to determine the presence of thrombin, or used in  
 CC gene therapy.  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
 : :  
 Db 3 t 3

RESULT 18  
 AA081666  
 ID AA081666 standard; RNA: 5 BP.  
 XX  
 AC AA081666;  
 XX  
 DT 29-SEP-1995 (first entry)  
 XX  
 DE bFGF binding oligomer core sequence #3.  
 XX  
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;  
 KW bubble structure; pseudoknot; receptor; heparin; competition;  
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;  
 KW metastasis; diagnosis; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9500528-A.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 17-JUN-1994; 94WO-US06884.  
 XX  
 PR 18-JUN-1993; 93US-0079677.  
 PR 07-JAN-1994; 94US-0179491.  
 XX  
 PA (PHAR-) PHARMAGENICS INC.





CC to (11) and forms a cleavage site between p1 and p3; p3 (AA112043)  
 CC is an inhibitory element that binds to x2 and interacts with a  
 CC region of p1 corresp. to nucleotides 81-126 of MDV-1. p4 contributes  
 CC nucleotides to form the ribozyme with x1 and p2, or is the terminal  
 CC nucleotide of p1; x1 is a target region of (11); x2 and x3 are  
 CC terminal nucleotides or second or third target regions of (11); R1  
 CC is a ribozyme-forming area of (11); and R2 is a terminal nucleotide  
 CC of R1 or an area of (11) that binds to (11). x1 and R1 are  
 CC mutually exclusive and are represented by the sequences of AA112040 and  
 CC AA112041. For hairpin ribozymes, p2 is AA112045 and R1 is AA112046.  
 CC Probes bearing ribozymes are produced in a single step by transcription  
 CC of DNA of appropriate sequence, thereby reducing costs. The ribozymes  
 CC produce specific cleavage events, leading to a product RNA with  
 CC defined replication properties.

XX Sequence 5 BP; 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match Best Local Similarity 100.0%; Score 1; DB 17; Length 5;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
 Db 1 u 1

## RESULT 21

AAV61663 ID AAV61663 standard; DNA: 5 BP.

AC AAV61663;

PT 03-DEC-1998 (first entry)

DE Fusarium sp. 18S rRNA DNA fragment #7.

KW 18S rRNA; detection; identification; fungus; ss.

OS Fusarium sp.

PN JP10234380-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062104.

PR 28-FEB-1997; 97JP-0062104.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI: 1998-535034/46.

PT Use of oligo:nucleotide for detecting and identification of fungus  
 PT of Fusarium genus - as primer or probe to detect of identify  
 PT microbes rapidly and exactly

PS Claim 1; Page 7; 20pp; Japanese.

XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
 CC used in a method for the detection and identification of a fungus of  
 CC Fusarium genus. The process can be used to detect or identify microbes  
 CC rapidly and exactly.

SO Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 1; DB 19; Length 5;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
 Db 1

Db 1 t 1

## RESULT 22

AAV61663/C ID AAV61663 standard; DNA: 5 BP.

XX AAV61663;

DT 03-DEC-1998 (first entry)

DE Fusarium sp. 18S rRNA DNA fragment #7.

KW 18S rRNA; detection; identification; fungus; ss.

OS Fusarium sp.

PN JP10234380-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062104.

PR 28-FEB-1997; 97JP-0062104.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI: 1998-535034/46.

PT Use of oligo:nucleotide for detecting and identification of fungus  
 PT of Fusarium genus - as primer or probe to detect of identify  
 PT microbes rapidly and exactly

PS Claim 1; Page 7; 20pp; Japanese.

XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are  
 CC used in a method for the detection and identification of a fungus of  
 CC Fusarium genus. The process can be used to detect or identify microbes  
 CC rapidly and exactly.

SO Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 1; DB 19; Length 5;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
 Db 2 t 2

## RESULT 23

AA196299 ID AAT96299 standard; DNA: 5 BP.

XX AAT96299;

DT 08-APR-1998 (first entry)

DE Fungal telomeric nucleic acid sequence.

KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 KW malarial infection; malaria; ss.

OS Saccharomyces cerevisiae.

PN US5695932-A.

PD 09-DEC-1997.

PF 13-MAY-1993; 93US-0060952.

XX 13-MAY-1993; 93US-0060952.  
PR 13-MAY-1992; 92US-0882438.  
PR 24-MAR-1993; 93US-0038766.  
XX

PA (REGC ) UNIV CALIFORNIA.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX

P1 Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;  
XX WPI: 1998-041292/04.  
DR

PT Detection of eukaryotic pathogens, especially fungal or Plasmodium  
XX spp. - by detecting telomerase activity  
PS

PS Claim 5: Columns 81-82; 82pp; English.

CC The present sequence can be used in a novel method for detecting a  
CC eukaryotic pathogen in a patient. The method comprises obtaining a  
CC sample of somatic tissue or cells from the patient, determining if  
CC telomerase activity is present and correlating this with the  
CC presence of the pathogen. The method is useful for diagnosis of  
CC fungal infections, especially a fungus of the genus Candida,  
CC Kluveromyces, Saccharomyces, Sporothrix, Coccidioides,  
CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,  
CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially  
CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.  
XX  
SQ Sequence 5 BP: 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 1: DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 1 t 1

## RESULT 24

AA210695  
ID AA210695 standard; DNA: 5 BP.

AC AA210695;

DT 23-NOV-1999 (first entry)

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
XX skin cancer; ss.

OS Synthetic.

PN GB2336157-A.

PD 13-OCT-1999.

PF 24-MAR-1999; 99GB-0006758.

PR 26-MAR-1998; 98US-0048927.

PA (UYBO-) UNIV BOSTON.

P1 Gilchrist BA, Yaar M, Eller M;  
XX WPI: 1999-543520/46.  
DR

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
XX susceptibility to UV-induced hyperproliferative diseases -  
PT

XX Claim 11: Page 30; 44pp; English.  
XX

CC AA210692-97 represent DNA fragments that are used for increasing p53  
XX activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.  
XX

SQ Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1: DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 2 t 2

## RESULT 25

AA210695/c  
ID AA210695 standard; DNA: 5 BP.

AC AA210695;

DT 23-NOV-1999 (first entry)

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
XX skin cancer; ss.

OS Synthetic.

PN GB2336157-A.

PD 13-OCT-1999.

PF 24-MAR-1999; 99GB-0006758.

PR 26-MAR-1998; 98US-0048927.

PA (UYBO-) UNIV BOSTON.

P1 Gilchrist BA, Yaar M, Eller M;  
XX WPI: 1999-543520/46.  
DR

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
XX susceptibility to UV-induced hyperproliferative diseases -  
PT Claim 11: Page 30; 44pp; English.

CC AA210692-97 represent DNA fragments that are used for increasing p53  
XX activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.  
XX

SQ Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1: DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

## RESULT 26

AA210696  
ID AA210696 standard; DNA: 5 BP.

XX  
AC AA210696;

XX  
DT 23-NOV-1999 (first entry)

XX  
DE Oligonucleotide sequence that increases p53 activity in a cell.

KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KM skin cancer; ss.

OS Synthetic.

XX  
PN GB2336157-A.

XX  
PD 13-OCT-1999.

XX  
PF 24-MAR-1999; 99GB-0006758.

XX  
PR 26-MAR-1998; 98US-0048927.

XX  
PA (UYBO-) UNIV BOSTON.

XX  
P1 Gilchrist BA, Yaar M, Eller M;

XX  
DR WPI: 1999-543520/46.

XX  
PT DNA fragments useful for increasing p53 activity in a cell and reducing  
PT susceptibility to UV-induced hyperproliferative diseases .

XX  
PS Claim 11: Page 30; 44pp; English.

XX  
CC AA210692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.

XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

## RESULT 27

AA210696/C  
ID AA210696 standard; DNA: 5 BP.

XX  
AC AA210696;

XX  
DT 23-NOV-1999 (first entry)

DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX  
KM p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KM UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KM atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KM skin cancer; ss.

OS Synthetic.

XX  
PN GB2336157-A.

XX  
PD 13-OCT-1999.

XX  
PF 24-MAR-1999; 99GB-0006758.

XX  
PR 26-MAR-1998; 98US-0048927.

XX  
PA (UYBO-) UNIV BOSTON.

XX  
P1 Gilchrist BA, Yaar M, Eller M;

XX  
DR WPI: 1999-543520/46.

XX  
PT DNA fragments useful for increasing p53 activity in a cell and reducing  
PT susceptibility to UV-induced hyperproliferative diseases .

XX  
PS Claim 11: Page 30; 44pp; English.

XX  
CC AA210692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are are UV mimetics and  
CC protect cells against subsequent exposure to UV-irradiation or  
CC chemicals. The oligonucleotides are useful for increasing p53 activity  
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
CC and reducing susceptibility to skin cancer.

XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 4 T 4

## RESULT 28

AA211611  
ID AA211611 standard; DNA: 5 BP.

XX  
AC AA211611;

XX  
DT 16-NOV-1999 (first entry)

XX  
DE DNA enhancer sequence present in an upstream element.

XX  
KM Plant promoter; TATA motif; transcription start site; upstream element;  
KM gene expression; oxalate oxidase; plant resistance; pathogen; maize;  
KM Ubl-1 promoter; Syn II core promoter; ss.

XX  
OS Synthetic.

XX  
PN WO9943838-A1.

XX  
PD 02-SEP-1999.

XX  
PF 23-FEB-1999; 99WO-US03863.

XX  
PR 24-FEB-1998; 98US-0028819.



CC discriminate between perfect and imperfect duplexes. The methods also  
CC obviate the need for the fabrication and array placement of large numbers  
CC of immobilized oligomers.  
XX  
SQ Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

```
Query Match      100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy	1	6	1
	4	1	
Db	4	7	4

RESULT	31
AAV72348/C	
ID	AAV72348 standard; DNA; 5 BP.
XY	

AC AAV72348;

DT 28-JUL-1999 (first entry)

DE US5908745 primer #5.

KW DNA sequencing; disease-associated allele; polyacrylamide matrix;  
 KW continuous/contiguous stacking hybridization technique; detection;  
 KW mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.

01-JUN-1999 PD

PF 16-JAN-1996;

16-JAN-1996; 96US-05873332.

(UYCH-) UNIV CHICAGO.

P1 Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;  
P1 Barinov SV, Vorobeyev SV

WP1: 1999-347002/29.

PT detecting disease-associated alleles using continuous/contiguous  
PT stacking hybridization as a diagnostic tool

Example 1; Column 9; 16pp; English.

This invention describes novel methods for sequencing and analysing DNA samples to detect disease-associated alleles, by continuous/contiguous stacking hybridization techniques (utilizing universal bases) with oligonucleotides immobilized on polyacrylamide matrices. The methods may be used to detect multiple DNA base mutations which are specific for certain diseases. The methods of the invention provide accurate and efficient and sensitive methods for diagnosing disease by detecting multiple mutation sequences in patient DNA. The method require the minimum number of oligonucleotides and few stacking hybridization steps than prior art methods. The methods are also efficient enough to discriminate between perfect and imperfect duplexes. The methods also obviate the need for the fabrication and array placement of large numbers of immobilized oligomers.

Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

```
Query Match      100.0%; Score 1: DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1: Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

QY	1	t	1
Db	4	T	4

RESULT 32  
AAV72349/C  
ID AAV72349 standard; DNA; 5 BP.

AC AAV72349;

DT 28-JUL-1999 (first entry)

DE US5908745 primer #6.

KM DNA sequencing; disease-associated allele; polyacrylamide matrix;  
 KM continuous/contiguous stacking hybridization technique; detection;  
 KM mutation; diagnosis; primer; ss.

OS Synthetic.

PN US5908745-A.  
XX

01-JUN-1999  
PD  
XY

PF 16-JAN-1996; 96US-05873332.  
XX

PR 16-JAN-1996; 96US-05873332.

PA (UYCH-) UNIV CHICAGO.

Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD,

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XX 1000 245000 350

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stacking hybridization as a diagnostic tool

Example 1; Column 9; 16pp; English.

This invention describes novel methods for sequencing and analysing DNA samples to detect disease-associated alleles, by continuous/continuous stacking hybridization techniques (utilizing universal bases) with oligonucleotides immobilized on polyacrylamide matrices. The methods may be used to detect multiple DNA base mutations which are specific for certain diseases. The methods of the invention provide accurate and efficient and sensitive methods for diagnosing disease by detecting multiple mutation sequences in patient DNA. The method require the minimum number of oligonucleotides and few stacking hybridization steps than prior art methods. The methods are also efficient enough to discriminate between perfect and imperfect duplexes. The methods also obviate the need for the fabrication and array placement of large numbers of immobilized oligomers.

50 Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

```
Query Match      100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches      1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	t	1
pb	3	r	3

Result	33
AAV72350/c	
AAV72350 standard; DNA; 5 BP	

AAV72350	AAV72350;
XX	XX
XX	XX
ID	XX

```

DT 28-JUL-1999 (first entry)
XX
XX US5908745 primer #7.
DE
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
KM continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer: ss.
XX
XX Synthetic.
XX
XX US5908745-A.
XX
XX 01-JUN-1999.
XX
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX 16-JAN-1996: 96US-0587332.
XX
XX (UYCH-) UNIV CHICAGO.
XX
XX Baraki VE, Kirilov EV, Lysov YP, Mirzabekov AD;
PI Parinov SV, Yershov GM;
XX
XX WPI: 1999-347002/29.
XX
XX
XX Detecting disease-associated alleles using continuous/contiguous
PT stacking hybridization as a diagnostic tool
XX
XX Example 1: Column 9; 16pp: English.
XX
XX This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.
XX
XX Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other:
XX
XX
XX Query Match 100.0%; Score 1; DB 20; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 t 1
XX |
XX 3 T 3
XX
XX Db
XX
XX
XX RESULT 34
XX AAX56964/c
XX ID AAX56964 standard; DNA: 5 BP.
XX
XX AAX56964:
XX
XX 16-JUL-1999 (first entry)
XX
XX
XX Ras gene modulating liposomal entrapped oligonucleotide primer 8.
XX
XX
XX Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
KM cell growth inhibitor; treatment; cancer; ras protein; ss.
XX
XX Synthetic.
XX
XX OS
XX WO9922772-A1.
XX
XX PN
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PD 14-MAY-1999.
XX
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XX 28-OCT-1998: 98WO-US22821.
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XX 31-OCT-1997: 97US-0961469.
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XX
XX (ISIS-) ISIS PHARM INC.
XX
XX
XX Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;
PI Templin MV;
XX
XX WPI: 1999-313181/26.
XX
XX
XX Liposome-encapsulated oligonucleotides useful for treating or
PT preventing cancers associated with ras gene activation
XX
XX Example 1: Page 107; 120pp: English.
XX
XX
XX This invention describes novel compositions comprising oligonucleotides
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.
XX
XX Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other:
XX
XX
XX Query Match 100.0%; Score 1; DB 20; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 t 1
XX |
XX 3 T 3
XX
XX Db
XX
XX
XX RESULT 35
XX AAX21608/c
XX ID AAX21608 standard; DNA: 5 BP.
XX
XX AAX21608:
XX
XX 14-MAY-1999 (first entry)
XX
XX
XX Mutant H-ras specific antisense oligo ISIS #2563.
XX
XX
XX Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
KM diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX
XX Synthetic.
XX
XX OS
XX WO9902732-A1.
XX
XX PN
XX 21-JAN-1999.
XX
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XX 06-JUL-1998: 98WO-US13966.
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XX 08-JUL-1997: 97US-0889296.
XX
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX
XX Cowser LM, Manoharan M, Monia BP;
PI
XX WPI: 1999-120932/10.
XX
XX
XX New oligonucleotide targeting human N-ras nucleic acid - is
PT

```

capable of inhibiting human N-ras expression, useful for preventing or treating conditions arising from the activation of a human N-ras oncogene

Disclosure: Page 22: 97pp: English.

The invention relates to oligonucleotides, which target a nucleic acid encoding human N-ras, and are capable of inhibiting human N-ras expression. The antisense oligonucleotides form a pharmaceutical composition, which is useful for modulating the expression of human N-ras, inhibiting the proliferation of cancer cells, and preventing or treating conditions arising from the activation of a human N-ras oncogene. The oligonucleotides are also useful in diagnostics, therapeutics, and as research reagents and kits. The oligonucleotides enable the specific modulation of activated human N-ras expression, which is associated with tumour formation. Sequences AA21601-619 represent antisense oligonucleotides targeted to mutant H-ras.

Sequence 5 BP: 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 20; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 3 T 3

## RESULT 36

AA56981  
ID AA56981 standard; CDNA: 5 BP.

AA56981;

14-NOV-2000 (first entry)

Human colon cancer cell CDNA sequence #109.

Human: arbitrary primer; CDNA synthesis: contig sequence construction; open reading frame; ORF: low stringency; CDNA sequencing; ss.

Homo sapiens.

MO20001299-A2.

02-JUN-2000.

19-NOV-1999: 99MO-US27430.

20-NOV-1998: 98US-0196716.

(LUDW-) LUDWIG INST CANCER RES.

Simpson AJG, Dias Neto E, Brentani RR;

WPI; 2000-400100/34.

Method for determining open reading frames of the genome of an organism using primers at low stringency conditions, useful in the construction of contigs or constructs of sequenced nucleic acid molecules -

Example 6: Page 47: 113pp: English.

The present sequence is a CDNA sequence obtained using a method for determining open reading frames (ORFs) of the genome of an organism. An aliquot of mRNA from human colon cancer cells was mixed with a single, arbitrary primer, Moloney murine leukemia virus reverse transcriptase, reverse transcriptase buffer and dNTPs. The mixture was incubated under low stringency conditions to yield single stranded cDNA. The same primer was then used to amplify the cDNA by PCR. Rather than providing nucleotide sequence information from the non-coding

termini of nucleic acid molecules, the method provides information on the more interesting and relevant internal portions, such as ORFs. The method also permits the construction of contigs of sequenced nucleic acid molecules.

Sequence 5 BP: 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 21; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
DB 2 t 2

## RESULT 37

AA293601/c  
ID AA293601 standard; DNA: 5 BP.

AA293601;

24-JUL-2000 (first entry)

Transcription factor binding site of tobacco gene promoter sequence.

Regulatory sequence; meristem; genetic engineering;

gene expression; crop protection; transgenic plant; resistance;

tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

Synthetic.

Nicotiana glauca.

MO200012713-A1.

09-MAR-2000.

26-AUG-1999: 99MO-AU00692.

26-AUG-1998: 98AU-0005498.

(UYOU) UNIV QUEENSLAND.

Mudge SR, Birch RG;

WPI; 2000-237875/20.

Meristem-expressible nucleic acid sequences, useful for producing transgenic plants with improved characteristics such as resistance to pathogens

Example 9: Page 51: 102pp: English.

Isolated regulatory sequences of plants that are operable in dividing cells, in particular the meristem cells of plants are useful in the genetic engineering of plants. The regulatory sequences can be used to control the expression of foreign genes placed under their control. Such methods are useful for producing transgenic plants with altered shape and/or size. The sequences are also useful for producing transgenic plants capable of rapid regeneration following harvest or plants having improved resistance to pathogens. This sequence has been shown to bind a factor involved in the activation of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three times in the meristem regulatory sequence of tobacco described in GENESEQ record AA293567.

Sequence 5 BP: 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match  
Best Local Similarity 100.0%; Score 1; DB 21; Length 5;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 t 1  
DB 3 T 3

## RESULT 38

ID AA293602 standard; DNA: 5 BP.

XX AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; NIT2; nitrate; ss.

XX

OS Synthetic.

US Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYQU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

XX

PT Meristem-expressible nucleic acid sequences, useful for producing

transgenic plants with improved characteristics such as resistance to

pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

CC dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to regulate nitrate metabolism in the

CC fungus Neurospora crassa. It occurs multiple times in the meristem

CC regulatory sequence of tobacco described in GENESEQ record AA293567.

CC

SO Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 1 t 1

RESULT 39

AA293602/c

ID AA293602 standard; DNA: 5 BP.

XX AA293602;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; NIT2; nitrate; ss.

XX

OS Synthetic.

US Nicotiana acuminata.

PN WO200012713-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU00692.

PR 26-AUG-1998; 98AU-0005498.

PA (UYQU ) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI: 2000-237875/20.

XX

PT Meristem-expressible nucleic acid sequences, useful for producing

transgenic plants with improved characteristics such as resistance to

pathogens

XX Example 9; Page 51; 102pp; English.

PS Isolated regulatory sequences of plants that are operable in

CC dividing cells, in particular the meristem cells of plants are useful

CC in the genetic engineering of plants. The regulatory sequences can

CC be used to control the expression of foreign genes placed under their

CC control. Such methods are useful for producing transgenic plants with

CC altered shape and/or size. The sequences are also useful for

CC producing transgenic plants capable of rapid regeneration following

CC harvest or plants having improved resistance to pathogens. This

CC sequence has been shown to regulate nitrate metabolism in the

CC fungus Neurospora crassa. It occurs multiple times in the meristem

CC regulatory sequence of tobacco described in GENESEQ record AA293567.

CC

SO Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1

DB 2 T 2

RESULT 40

AA293603

ID AA293603 standard; DNA: 5 BP.

XX AA293603;

DT 24-JUL-2000 (first entry)

DE Transcription factor binding site of tobacco gene promoter sequence.

KW Regulatory sequence; meristem; genetic engineering;

KM gene expression; crop protection; transgenic plant; resistance;

KW tobacco; transcription factor; yeast; ss.

XX

OS Synthetic.

US Nicotiana acuminata.

PN WO200012713-A1.

```

XX 09-MAR-2000.
PD
XX
XX 26-AUG-1999; 99WO-AU00692.
PT
XX
XX 26-AUG-1998; 98AU-0005498.
PH
XX
XX (UYOU ) UNIV QUEENSLAND.
PA
XX
XX Mudge SR, Birch RG;
PI
XX WPI: 2000-237875/20.
DK
XX
XX Meristem-expressible nucleic acid sequences, useful for producing
PT transgenic plants with improved characteristics such as resistance to
PT pathogens
XX
XX Example 9; Page 51; 102pp; English.
PS
XX
XX Isolated regulatory sequences of plants that are operable in
CC dividing cells, in particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to activate yeast amino acid biosynthetic
CC enzymes. It occurs multiple times in the meristem regulatory sequence
CC of Tobacco described in GENESEQ record AA293567.
XX
SQ Sequence 5 BP; 1 A; 0 C; 0 G; 2 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 1 1
DB 1 1 1

```

```

RESULT 41
AA293603/C
ID AA293603 standard; DNA; 5 BP.
XX
XX AA293603;
AC
XX
XX 24-JUL-2000 (first entry)
DT
XX
XX Transcription factor binding site of tobacco gene promoter sequence.
DE
XX
XX Regulatory sequence; meristem; genetic engineering;
KW gene expression; crop protection; transgenic plant; resistance;
KW tobacco; transcription factor; yeast; ss.
XX
XX Synthetic.
OS Nicotiana glauca.
XX
XX WO200012713-A1.
PN
XX
XX 09-MAR-2000.
PD
XX
XX 26-AUG-1999; 99WO-AU00692.
PF
XX
XX 26-AUG-1998; 98AU-0005498.
PR
XX
XX (UYOU ) UNIV QUEENSLAND.
PA
XX Mudge SR, Birch RG;
PI
XX WPI: 2000-237875/20.
DR

```

```

XX Meristem-expressible nucleic acid sequences, useful for producing
PT transgenic plants with improved characteristics such as resistance to
PT pathogens
XX
XX Example 9; Page 51; 102pp; English.
PS
XX
XX Isolated regulatory sequences of plants that are operable in
CC dividing cells, in particular the meristem cells of plants are useful
CC in the genetic engineering of plants. The regulatory sequences can
CC be used to control the expression of foreign genes placed under their
CC control. Such methods are useful for producing transgenic plants with
CC altered shape and/or size. The sequences are also useful for
CC producing transgenic plants capable of rapid regeneration following
CC harvest or plants having improved resistance to pathogens. This
CC sequence has been shown to activate yeast amino acid biosynthetic
CC enzymes. It occurs multiple times in the meristem regulatory sequence
CC of Tobacco described in GENESEQ record AA293567.
XX
SQ Sequence 5 BP; 1 A; 0 C; 0 G; 2 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 1 1
DB 3 1 3

```

```

RESULT 42
AA289330
ID AA289330 standard; DNA; 5 BP.
XX
XX AA289330;
AC
XX
XX 13-JUN-2000 (first entry)
DT
XX
XX Human UCP3 promoter fragment #10.
DE
XX
XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KW fat metabolism; ss.
XX
XX Homo sapiens.
OS
XX
XX DE19838837-A1.
PN
XX
XX 02-MAR-2000.
PD
XX
XX 27-AUG-1998; 98DE-1038837.
PF
XX
XX 27-AUG-1998; 98DE-1038837.
PR
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Esterbauer H, Oberkofler H, Patsch W;
PI
XX WPI: 2000-272214/24.
DR
XX
XX Recombinant fat and muscle tissue specific uncoupling protein 3
PT promoters useful for identifying UCP3 modulators
XX
XX Claim 25; Page 12; 38pp; German.
PS
XX
XX This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases

```

CC With inappropriate fat tissue metabolism. This sequence represents a  
CC fragment of the human UCP-3 promoter which is used to illustrate the  
CC method of the invention.

Sequence 5 BP: 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 5 t 5

RESULT 43  
AA289330/c  
ID AA289330 standard; DNA; 5 BP.

AC AA289330;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #10.

UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

fat metabolism; ss.

Homo sapiens.

DE19838837-A1.

02-MAR-2000.

27-AUG-1998; 98DE-1038837.

27-AUG-1998; 98DE-1038837.

(BOEH ) BOEHRINGER INGELHEIM INT GMBH.

(NOVO ) NOVO-NORDISK AS.

Esterbauer H, Oberkofler H, Patsch W;

WPI: 2000-272214/24.

Recombinant fat and muscle tissue specific uncoupling protein 3  
promoters useful for identifying UCP3 modulators -

Claim 25; Page 12; 38pp; German.

This invention describes novel recombinant DNA molecules containing  
an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
cells but not functional in muscle cells or vice versa. The recombinant  
DNA molecules are useful for transcription of genes and, with host cells,  
to test for substances that can influence transcription. They can also be  
used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
metabolism and control of the promoter is useful in combating diseases  
with inappropriate fat tissue metabolism. This sequence represents a  
fragment of the human UCP-3 promoter which is used to illustrate the  
method of the invention.

Sequence 5 BP: 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 4 t 4

RESULT 44  
AA289331  
ID AA289331 standard; DNA; 5 BP.

AC AA289331;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #11.

UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

fat metabolism; ss.

Homo sapiens.

DE19838837-A1.

02-MAR-2000.

27-AUG-1998; 98DE-1038837.

27-AUG-1998; 98DE-1038837.

(BOEH ) BOEHRINGER INGELHEIM INT GMBH.

(NOVO ) NOVO-NORDISK AS.

Esterbauer H, Oberkofler H, Patsch W;

WPI: 2000-272214/24.

Recombinant fat and muscle tissue specific uncoupling protein 3  
promoters useful for identifying UCP3 modulators -

Claim 28; Page 12; 38pp; German.

This invention describes novel recombinant DNA molecules containing  
an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat  
cells but not functional in muscle cells or vice versa. The recombinant  
DNA molecules are useful for transcription of genes and, with host cells,  
to test for substances that can influence transcription. They can also be  
used to identify modulators of UCP3 promoters. UCP3 plays a role in fat  
metabolism and control of the promoter is useful in combating diseases  
with inappropriate fat tissue metabolism. This sequence represents a  
fragment of the human UCP-3 promoter which is used to illustrate the  
method of the invention.

Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 2 t 2

RESULT 45  
AA289331/c  
ID AA289331 standard; DNA; 5 BP.

AC AA289331;

DT 13-JUN-2000 (first entry)

DE Human UCP3 promoter fragment #11.

UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

fat metabolism; ss.

Homo sapiens.

XX	DE19838837-A1.
XX	
XX	02-MAR-2000.
PD	
XX	27-AUG-1998; 98DE-1038837.
XX	
XX	27-AUG-1998; 98DE-1038837.
PR	
XX	(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA	(NOVO ) NOVO-NORDISK AS.
XX	
XX	Esterbauer H, Oberkofler H, Patsch W;
P1	
XX	WP1: 2000-272214/24.
DK	
XX	
XX	Recombinant fat and muscle tissue specific uncoupling protein 3
P7	promoters useful for identifying UCP3 modulators
XX	
XX	Claim 28; Page 12; 38pp; German.
P5	
XX	
XX	This invention describes novel recombinant DNA molecules containing
CC	an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC	cells but not functional in muscle cells or vice versa. The recombinant
CC	DNA molecules are useful for transcription of genes and, with host cells,
CC	to test for substances that can influence transcription. They can also be
CC	used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC	metabolism and control of the promoter is useful in combating diseases
CC	with inappropriate fat tissue metabolism. This sequence represents a
CC	fragment of the human UCP-3 promoter which is used to illustrate the
CC	method of the invention.
XX	
XX	
XX	Sequence 5 BP: 1 A; 0 C; 2 G; 2 T; 0 other;

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:56:59 ; Search time 808.35 Seconds

(Without alignments)  
2.105 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3360\_3360

Perfect score: 1  
Sequence: 1 c 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

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2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	2	US-10-027-632-51869	Sequence 51869, A
2	100.0	1	2	US-10-027-632-52280	Sequence 52280, A
3	100.0	1	2	US-10-027-632-52357	Sequence 52357, A
4	100.0	1	2	US-10-027-632-53003	Sequence 53003, A
5	100.0	1	2	US-10-027-632-58305	Sequence 58305, A
6	100.0	1	2	US-10-027-632-175312	Sequence 175312, A
7	100.0	1	2	US-10-027-632-175337	Sequence 175337, A
8	100.0	1	2	US-10-027-632-175354	Sequence 175354, A
9	100.0	1	2	US-10-027-632-175401	Sequence 175401, A
10	100.0	1	2	US-10-027-632-175403	Sequence 175403, A
11	100.0	1	2	US-10-027-632-175415	Sequence 175415, A
12	100.0	1	2	US-10-027-632-175419	Sequence 175419, A
13	100.0	1	2	US-10-027-632-175426	Sequence 175426, A
14	100.0	1	2	US-10-027-632-175433	Sequence 175433, A
15	100.0	1	2	US-10-027-632-175849	Sequence 175849, A
16	100.0	1	2	US-10-027-632-176848	Sequence 176848, A
17	100.0	1	2	US-10-027-632-176849	Sequence 176849, A
18	100.0	1	2	US-10-027-632-176880	Sequence 176880, A
19	100.0	1	2	US-10-027-632-178420	Sequence 178420, A
20	100.0	1	2	US-10-027-632-178440	Sequence 178440, A
21	100.0	1	2	US-10-027-632-178440	Sequence 178440, A
22	100.0	1	2	US-10-027-632-178617	Sequence 178617, A
23	100.0	1	2	US-10-027-632-178640	Sequence 178640, A
24	100.0	1	3	PCT-US02-00351-20	Sequence 20, Appl
25	100.0	1	3	US-10-027-632-52136	Sequence 52136, A
26	100.0	1	3	US-10-027-632-52402	Sequence 52402, A

27	100.0	1	3	US-10-027-632-52403	Sequence 52403, A
28	100.0	1	3	US-10-027-632-52404	Sequence 52404, A
29	100.0	1	3	US-10-027-632-52410	Sequence 52410, A
30	100.0	1	3	US-10-027-632-52417	Sequence 52417, A
31	100.0	1	3	US-10-027-632-52418	Sequence 52418, A
32	100.0	1	3	US-10-027-632-52425	Sequence 52425, A
33	100.0	1	3	US-10-027-632-52425	Sequence 52425, A
34	100.0	1	3	US-10-027-632-52491	Sequence 52491, A
35	100.0	1	3	US-10-027-632-52495	Sequence 52495, A
36	100.0	1	3	US-10-027-632-52496	Sequence 52496, A
37	100.0	1	3	US-10-027-632-52508	Sequence 52508, A
38	100.0	1	3	US-10-027-632-52512	Sequence 52512, A
39	100.0	1	3	US-10-027-632-52513	Sequence 52513, A
40	100.0	1	3	US-10-027-632-52615	Sequence 52615, A
41	100.0	1	3	US-10-027-632-52633	Sequence 52633, A
42	100.0	1	3	US-10-027-632-52631	Sequence 52631, A
43	100.0	1	3	US-10-027-632-52753	Sequence 52753, A
44	100.0	1	3	US-10-027-632-52758	Sequence 52758, A
45	100.0	1	3	US-10-027-632-52761	Sequence 52761, A

## ALIGNMENTS

```
RESULT 1
US-10-027-632-51869
: Sequence 51869, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
: PRIOR FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: US 60/218, 006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198, 676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193, 483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185, 218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167, 363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156, 358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146, 002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 51869
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-51869

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 c 1
Db 2 c 2

RESULT 2
US-10-027-632-52280
: Sequence 52280, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52280
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52280
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 c 2
```

```
RESULT 3
US-10-027-632-52357
Sequence 52357, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52357
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-52357
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
```

```
Db 2 c 2
```

```
RESULT 4
US-10-027-632-53003
Sequence 53003, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53003
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-10-027-632-53003
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```
RESULT 5
US-10-027-632-58305
Sequence 58305, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58305
```

LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-58305

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 6  
US-10-027-632-175312/C  
Sequence 175312, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175312  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175312

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 7  
US-10-027-632-175337/C  
Sequence 175337, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175337  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175337

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 8  
US-10-027-632-175354/C  
Sequence 175354, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 175354  
LENGTH: 2  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-175354

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
Db 1 C 1

RESULT 9  
US-10-027-632-175401/C  
Sequence 175401, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.

```

: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175401
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175401

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 c 1
db       1 c 1
```

```

RESULT 10
US-10-027-632-175403/c
: Sequence 175403, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175403
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175403
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 c 1
db       1 c 1
```

```

RESULT 11
US-10-027-632-175415/c
: Sequence 175415, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175415
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175415
```

```

Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 c 1
db       1 c 1
```

```

RESULT 12
US-10-027-632-175419/c
: Sequence 175419, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
```



```
SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175419
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175419
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 13
US-10-027-632-175426/c
: Sequence 175426, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175426
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175426
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 14
US-10-027-632-175433/c
: Sequence 175433, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
```

```
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175433
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175433
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 1 C 1
```

```
RESULT 15
US-10-027-632-175849/c
: Sequence 175849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 175849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-175849
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 C 1
Db 2 C 2
```

```
RESULT 16
US-10-027-632-176848/c
: Sequence 176848, Application US/10027632
```

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: SOFTWARE: FASTSEQ for Windows Version 4.0
: NUMBER OF SEQ ID NOS: 325720
: SEQ ID NO 176848
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176848
```

```

Query Match      100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 c 1
Db 1 c 1
```

```

RESULT 17
US-10-027-632-176849/c
: Sequence 176849, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176849
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176849
```

```

Query Match      100.0%: Score 1; DB 6; Length 2;
```

```

Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 c 1
Db 1 c 1
```

```

RESULT 18
US-10-027-632-176880/c
: Sequence 176880, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176880
: LENGTH: 2
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-176880
```

```

Query Match      100.0%: Score 1; DB 6; Length 2;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 c 1
Db 1 c 1
```

```

RESULT 19
US-10-027-632-178420/c
: Sequence 178420, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
```

```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 c 1
        |
Db       2 c 2
```

```
RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 c 1
        |
Db       2 c 2
```

```
RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 c 1
        |
Db       1 c 1
```

```
RESULT 22
US-10-027-632-178617/c
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 c 1
        |
Db       2 c 2
```

RESULT 23

```
US-10-027-632-178640/C
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 2;
Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 c 2
```

```
RESULT 24
PCT-US02-00351-20
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ilan
; APPLICANT: Vitebo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: motif found in the URSS of both ech42 and prb1 genes
PCT-US02-00351-20
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;
Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 3 c 3
```

RESULT 25

```
US-10-027-632-52136/C
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136
```

```
Query Match
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;
Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 3 c 3
```

```
RESULT 26
US-10-027-632-52402
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402
```

Query Match 100.0%: Score 1: DB 6: Length 3:  
Best Local Similarity 100.0%: Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 c 1  
db 1 c 1

RESULT 27  
US-10-027-632-52403  
: Sequence 52403, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30  
: PRIOR APPLICATION NUMBER: US 60/218,006  
: PRIOR FILING DATE: 2000-07-12  
: PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: US 60/193,483  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: US 60/185,218  
: PRIOR FILING DATE: 2000-02-24  
: PRIOR APPLICATION NUMBER: US 60/167,363  
: PRIOR FILING DATE: 1999-11-23  
: PRIOR APPLICATION NUMBER: US 60/156,358  
: PRIOR FILING DATE: 1999-09-28  
: PRIOR APPLICATION NUMBER: US 60/146,002  
: PRIOR FILING DATE: 1999-08-09  
: NUMBER OF SEQ ID NOS: 325720  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 52403  
: LENGTH: 3  
: TYPE: DNA  
: ORGANISM: Human  
US-10-027-632-52403

Query Match 100.0%: Score 1: DB 6: Length 3:  
Best Local Similarity 100.0%: Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 c 1  
db 1 c 1

RESULT 28  
US-10-027-632-52404  
: Sequence 52404, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30  
: PRIOR APPLICATION NUMBER: US 60/218,006  
: PRIOR FILING DATE: 2000-07-12  
: PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: US 60/193,483  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: US 60/185,218  
: PRIOR FILING DATE: 2000-02-24  
: PRIOR APPLICATION NUMBER: US 60/167,363  
: PRIOR FILING DATE: 1999-11-23  
: PRIOR APPLICATION NUMBER: US 60/156,358

: PRIOR FILING DATE: 1999-09-28  
: PRIOR APPLICATION NUMBER: US 60/146,002  
: PRIOR FILING DATE: 1999-08-09  
: NUMBER OF SEQ ID NOS: 325720  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 52404  
: LENGTH: 3  
: TYPE: DNA  
: ORGANISM: Human  
US-10-027-632-52404

Query Match 100.0%: Score 1: DB 6: Length 3:  
Best Local Similarity 100.0%: Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 c 1  
db 1 c 1

RESULT 29  
US-10-027-632-52410  
: Sequence 52410, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30  
: PRIOR APPLICATION NUMBER: US 60/218,006  
: PRIOR FILING DATE: 2000-07-12  
: PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: US 60/193,483  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: US 60/185,218  
: PRIOR FILING DATE: 2000-02-24  
: PRIOR APPLICATION NUMBER: US 60/167,363  
: PRIOR FILING DATE: 1999-11-23  
: PRIOR APPLICATION NUMBER: US 60/156,358  
: PRIOR FILING DATE: 1999-09-28  
: PRIOR APPLICATION NUMBER: US 60/146,002  
: PRIOR FILING DATE: 1999-08-09  
: NUMBER OF SEQ ID NOS: 325720  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 52410  
: LENGTH: 3  
: TYPE: DNA  
: ORGANISM: Human  
US-10-027-632-52410

Query Match 100.0%: Score 1: DB 6: Length 3:  
Best Local Similarity 100.0%: Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 c 1  
db 1 c 1

RESULT 30  
US-10-027-632-52417  
: Sequence 52417, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30

```

: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52417
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52417
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 31
US-10-027-632-52418
: Sequence 52418, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52418
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52418
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 32
US-10-027-632-52419
: Sequence 52419, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52419
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52419
```

```

Query Match          100.0%: Score 1; DB 6; Length 3;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1 c 1
```

```

RESULT 33
US-10-027-632-52425
: Sequence 52425, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 52425
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
```

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 1 C 1

RESULT 34  
US-10-027-632-52491/c

; Sequence 52491, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52491  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 2 C 2

RESULT 35  
US-10-027-632-52495

; Sequence 52495, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52495  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 3 C 3

RESULT 36  
US-10-027-632-52496/c

; Sequence 52496, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52496  
; LENGTH: 3  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 C 1  
|  
Db 2 C 2

RESULT 37  
US-10-027-632-52508/c

; Sequence 52508, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129

```

: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52508
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52508
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 C 2
```

```

RESULT 38
US-10-027-632-52512
: Sequence 52512, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52512
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52512
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 1
```

```
Db 3 C 3
```

```

RESULT 39
US-10-027-632-52513/C
: Sequence 52513, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52513
: LENGTH: 3
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-52513
```

```
Query Match          100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 c 1
Db 2 C 2
```

```

RESULT 40
US-10-027-632-52615/C
: Sequence 52615, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 52615
: LENGTH: 3
```



```
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52615
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
        |
Db       2 C 2
```

```
RESULT 41
US-10-027-632-52633/C
; Sequence 52633, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52633
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52633
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
        |
Db       2 C 2
```

```
RESULT 42
US-10-027-632-52651/C
; Sequence 52651, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52651
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52651
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
        |
Db       2 C 2
```

```
RESULT 43
US-10-027-632-52753/C
; Sequence 52753, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52753
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52753
```

```
Query Match          100.0%: Score 1: DB 6: Length 3:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

```
OY      1 c 1
        |
Db       2 C 2
```

```
RESULT 44
US-10-027-632-52758
; Sequence 52758, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```



---

ET

```
1. 2
/db_xref="taxon:9606"
/organism="Homo sapiens"
/clone="DKFZp434f2010"
/clone_lib="434 (synonym: ntest). Vector pSport1; host
```



```

XX 11
RN 1-2
KP 1-2
KA Koehrer K., Beyer A., Mewes W., Cassenhuber J., Wiemann S.;
; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
KI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX clone from S. Wiemann, sequenced by MIPS within the cDNA
CC sequencing consortium of the German Genome Project
CC No st sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de
XX
XX Key location/Qualifiers
XX
XX source 1..2
XX /db_xref="taxon:9606"
XX /organism="Homo sapiens"
XX /clone="DKFZP586P0517"
XX /clone.lib="586 (synonym: butel). Vector pSPORT1; host
XX DH10B; sites NotI + SalI/MluI"
XX /dev_stage="adult"
XX /tissue_type="uterus"
XX
XX SO Sequence 2 BP; 0 A; 1 G; 0 C; 1 T; 0 other;

Query Match 100.0% Score 1; DB 2; Length 2;
Host Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 5
LACUS B1817789/c 2 bp mRNA linear EST 04-OCT-2001
DEFINITION G3-C22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to Putative ribosomal protein S2, mRNA sequence.
ACCESSION B1817789
VERSION B1817789.1 GI:35951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 2)
Voss,S.K., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
Expressed sequence tags from an axolotl limb regeneration library
unpublished (2001)
Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: srvoos@lamar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
srvoos@lamar.colostate.edu.

FEATURES
source
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone.lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

```

```

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0% Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 G 1

RESULT 6
LOCUS C55081 2 bp mRNA linear EST 16-SEP-1997
DEFINITION C55081 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone YK350C9 3', mRNA sequence.
ACCESSION C55081
VERSION C55081.1 GI:2399682
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea
; Rhabdilitidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 2)
Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
unpublished (1996)
Contact: Yuji Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
location/Qualifiers
1..2
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK350C9"
/clone.lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN
Query Match 100.0% Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 7
LOCUS BE351920 2 bp mRNA linear EST 18-JUL-2000
DEFINITION BE351920 y1 C. reinhardtii CC-1690, normalized, lambda zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
1 (bases 1 to 2)

```

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Grossman, A., Davies, J., Federspiel, N., Harris, E., Lelievre, P.,  
McJermott, J. P., Sillfow, C., Stern, D., and Surzycki, R.  
Analyses of the Chlamydomonas reinhardtii Genome: A Model,  
Unicellular System for Analyzing Gene Function and Regulation in  
Vascular Plants: project phase 2  
Unpublished (2000)  
Contact: Elizabeth H. Harris  
ICMB Box 91000  
Duke University  
Durham, NC 27708-1000, USA  
Tel: 919 613 8164  
Fax: 919 613 8177  
Email: eharris@duke.edu.

## FEATURES

## Source

Location/Qualifiers  
1. .2  
/organism="Chlamydomonas reinhardtii"  
/strain="CC-1690 wild type mt+ 21gr"  
/db.xref="taxon:3055"  
/clone\_1lb="C. reinhardtii CC-1690, normalized, lambda Zap  
11"

## BASE COUNT

0 a 0 c 2 g 0 t  
Note "Vector: Bluescript II SK-; Site1: EcoRI; Site2:  
XhoI; This library, constructed by John Davies and Jeffrey  
McJermott, combines cDNAs from CC-1690 cells grown to  
mid-log phase in YAP (acetate-containing) medium to the  
light, YAP medium in the dark, HS (minimal) medium in  
ambient levels of CO2 and HS medium bubbled with 5% CO2.  
polyA mRNA was purified from each sample, pooled and cDNA  
synthesized. The cDNA was directionally cloned into lambda  
Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.  
Zap clones by superinfection with ExAssist (Stratagene)  
phage. The library was normalized using method 4 described  
in Bonaldo et al (1996) Genome Research 6: 791-806."

Query Match 100.0%; Score 1: DB 10; Length 2:  
Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 1 g 1

## RESULT 8

## LOCUS

A2463604 2 bp DNA linear GSS 04-OCT-2000  
1M027205R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M027205 R, DNA sequence.

## ACCESSION

## VERSION

A2463604  
A2463604.1 GI:10621729

## KEYWORDS

## SOURCE

## ORGANISM

house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
and Wright, D., Weiss, R.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

## FEATURES

## Source

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0272 row: 3 column: 05  
Seq primer: CACACGACGAACACCTATGACAC  
Class: plasmid ends  
High quality sequence stop: 451.  
Location/Qualifiers  
1. .2  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db.xref="taxon:10090"  
/clone="UUCG1M027205"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42ny. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from The Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## BASE COUNT

0 a 0 c 1 g 1 t  
Note "Vector: pMD42ny. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from The Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 100.0%; Score 1: DB 12; Length 2:  
Best Local Similarity 100.0%; Pred. No. 0:  
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
1  
Db 1 g 1

## RESULT 9

## LOCUS

## DEFINITION

AM672605 3 bp mRNA linear EST 26-SEP-2001  
2XA Explanted metanephric mesenchyme induced to differentiate into  
epithelial structures of the nephron ex vivo. Rattus norvegicus  
cDNA similar to: gb|AF022811.1|AF022811 Mus musculus  
cornichon mRNA, mRNA sequence.

## ACCESSION

## VERSION

AM672605  
AM672605.1 GI:7541085

## KEYWORDS

## SOURCE

## ORGANISM

EST.  
Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 3)  
Pilsav, S. Y., Ivanov, S. V., Yoshino, K., Dove, L. F., Pilsava, T. M.,  
Higginbotham, K. G., Karavanova, I., Lerman, M., and Perantoni, A. O.,  
Mesenchymal-epithelial transition in the developing metanephric  
kidney: gene expression study by differential display  
Genesis 27 (1), 22-31 (2000)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

20321327  
Contact: Pilsav S. Y.  
Laboratory of Comparative Carcinogenesis  
National Cancer Institute  
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242  
 Fax: 301 846 4956  
 Email: plisov@mail.ncicrf.gov  
 PCR Primers  
 FORWARD: ctgcagctccgctc  
 BACFWARD: ttaagcttttttttc  
 Insert Length: 350 Std Error: 0.00  
 Seq primer: Sp6  
 High quality sequence stop: 261.  
 Location/Qualifiers  
 1..3  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_lib="Explicated metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."  
 /tissue\_type="Metanephric mesenchyme"  
 /cell\_type="Mesenchymal/Epithelial"  
 /dev\_stage="13 dpc-16dpc"  
 /lab\_host="JM109"  
 /note="Organ: Kidney; Vector: pGEM-Teasy (Promega).; Restriction Enzymes 1: ApaI, AatII, SphI, NcoI, BstXI, NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstZI, PstI, SalI, NdeI, SacI, BseXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis: cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."

BASE COUNT  
 ORIGIN 1 a 0 c 2 g 0 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 9; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 g 1  
 1  
 Db 1 c 1

RESULT 10  
 A2438202 3 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0228108F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION  
 A2438202  
 A2438202  
 A2438202.1 GI:10562215  
 GSS.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.  
 1 (bases 1 to 3)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0228 row: 1 column: 08  
 Seq primer: CGTGTAAACGACGCCGCGCT  
 Class: plasmid ends

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

High quality sequence stop: 302.  
 Location/Qualifiers  
 1..3  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0228108"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, f'-"  
 /note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrolidynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN 1 a 1 c 0 g 1 t

Query Match  
 Best Local Similarity 100.0%; Score 1; DB 12; Length 3;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 g 1  
 1  
 Db 1 g 1

RESULT 11  
 CNS00KCV 3 bp DNA linear GSS 03-JUN-1999  
 LOCUS  
 DEFINITION  
 CNS00KCV  
 Drosophila melanogaster genome survey sequence JET3 end of BAC: BACR17D19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL077515  
 AL077515.1 GI:4956992  
 GSS.  
 SOURCE  
 fruit fly.  
 ORGANISM  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 3)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segr@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using the BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT



P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
Source  
Location/Qualifiers

1.3  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCT-98"  
/clone="BACR17D19"  
/note="end : TET3"  
BASE COUNT 0 a 0 c 3 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 1 G 1

RESULT 12

BC926576 standard; RNA; EST: 4 BP.

AC BC926576;

SV BC926576.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.; "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritic Cartilage 9(7):641-653(2001).

RL Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

PH Location/Qualifiers

FT 1..4

FT /db\_xref="taxon:9606"  
FT /note="Vector: PSFOT I; Site\_1: SalI; Site\_2: NotI;  
FT Directional"  
FT /organism="Homo sapiens"  
FT /clone\_lib="HNC (Human Normal Cartilage)"  
FT /tissue\_type="Cartilage"

FT /lab\_host="E.coli DH10 B"  
XX Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1  
|  
Db 4 G 4

RESULT 13

BC926576/C standard; RNA; EST: 4 BP.

AC BC926576;

SV BC926576.1

09-JUN-2001 (Rel. 68, Created)

14-NOV-2001 (Rel. 69, Last updated, Version 2)

HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

DE EST.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

XX [1]

RP 1-4

XX MEDLINE: 21482651.

XX PUBMED: 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J., Sathie G.M., Mul P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.; "Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries";

RT Osteoarthritic Cartilage 9(7):641-653(2001).

RL Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598

CC Email: sanjay\_kumar-1@gsk.com

CC Seq primer: T7.

XX Key

PH Location/Qualifiers

FT 1..4

FT /db\_xref="taxon:9606"  
FT /note="Vector: PSFOT I; Site\_1: SalI; Site\_2: NotI;  
FT Directional"  
FT /organism="Homo sapiens"  
FT /clone\_lib="HNC (Human Normal Cartilage)"  
FT /tissue\_type="Cartilage"  
FT /lab\_host="E.coli DH10 B"

XX Sequence 4 BP: 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 3 G 3

RESULT 14  
ID HSM001901  
ID HSM003901 standard; RNA; EST; 4 BP.

AC AL039425;  
XX  
SV AL039425.1

DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434L0810\_s1 (from clone DKFZp434L0810)  
XX  
KW EST: expressed sequence tag.

OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

KN [1]  
RP 1-4  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

PH source

FT 1..4  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone\_lib="DKFZp434L0810"  
FT DH10B; sites NotI + SalI  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

SO Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1  
Db 4 G 4

RESULT 15  
ID HSM010467  
ID HSM010467 standard; RNA; EST; 4 BP.

AC AL045617;  
XX  
SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434O245\_r1 (from clone DKFZp434O245)

KW EST: expressed sequence tag.

XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]  
RP 1-4

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT 1..4  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone\_lib="DKFZp434O245"  
FT DH10B; sites NotI + SalI  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

SO Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1  
Db 4 G 4

RESULT 16  
ID HSM010467/c  
ID HSM010467 standard; RNA; EST; 4 BP.

AC AL045617;  
XX  
SV AL045617.1

DT 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434O245\_r1 (from clone DKFZp434O245)  
XX  
KW EST: expressed sequence tag.

OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]  
RP 1-4  
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC This clone is available at the RZPD in Berlin

BASE COUNT  
ORIGIN 1 a 0 c 3 g 0 t

Query Match 100.0% Score 1: DB 9: Length 4:  
Best Local Similarity 100.0% Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 g 1  
1  
Db 1 g 1

RESULT 18  
CNS004RB  
LOCUS 4 bp DNA linear GSS 03-JUN-1999  
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
AL054121  
AL054121.1 GI:4931932  
GSS  
fruit fly.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 4)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.  
Location/Qualifiers  
1..4  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"  
/clone="BACR10A06"  
/note="end : TET3"

BASE COUNT 1 a 1 c 0 g 2 t

ORIGIN

Query Match 100.0% Score 1: DB 12: Length 4:  
Best Local Similarity 100.0% Pred. No. 0:  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 g 1  
1  
Db 1 g 1

Db 4 C 4

RESULT 19  
HSM007310  
ID HSM007310 standard; RNA; EST: 5 BP.

XX AL042460;

SV AL042460.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434E1821\_r1 (from clone DKFZp434E1821)

XX EST: expressed sequence tag.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX RN

RP 1-5

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX FH

RP 1-5

RT source 1. .5

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434E1821"

FT /clone\_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX SO

RP 1-5

RT source 1. .5

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434E1821"

FT /clone\_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

Sequence 5 BP: 2 A: 0 C: 1 G: 2 T: 0 other:

Query Match 100.0%; Score 1; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

DB 1 g 1

RESULT 20

HSM007835/c

ID HSM007835 standard; RNA; EST: 5 BP.

XX AL042985;

SV AL042985.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434N1522\_r1 (from clone DKFZp434N1522)

XX EST: expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX RN

RP 1-5

RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the CDNA

CC sequencing consortium of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX FH

RP 1-5

RT source 1. .5

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434N1522"

FT /clone\_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX SO

RP 1-5

RT source 1. .5

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434D137\_r1

FT /clone\_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX SO

RP 1-5

RT source 1. .5

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434D137\_r1

FT /clone\_id="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434D137"
FT /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 g 1

RESULT 22
BG927410/c standard; RNA; EST; 6 BP.
XX
XX BG927410:
XX
XX BG927410.1
XX
XX 09-JUN-2001 (Rel. 68, Created)
XX 14-NOV-2001 (Rel. 69, last updated, Version 2)
XX
XX HNC1-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX EST.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX [1]
XX 1-6
XX MEDLINE: 21482651.
XX PUBMED: 11597177.
XX
XX Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
XX Sathie G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
XX "Identification and initial characterization of 5000 expressed sequenced
XX tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
XX libraries";
XX Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX Contact: Sanjay Kumar
XX UW2109
XX GlaxoSmithKline
XX 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
XX Tel: 610-270-7245
XX Fax: 610-270-5598
XX Email: sanjay.kumar-1@sk.com
XX Seq primer: 77.
XX
XX key Location/Qualifiers
FH
FH source 1..6
FT /db_xref="taxon:9606"
FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FT Directional"
FT /organism="Homo sapiens"
FT /clone_lib="HNC (Human Normal Cartilage)"
FT /tissue_type="cartilage"

```

```

FT
XX /lab_host="E.coli DH10 B"
XX
XX Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;
SQ

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 6 G 6

RESULT 23
HSM003844 standard; RNA; EST; 6 BP.
XX
XX HSM003844:
XX
XX AL039368;
XX
XX AL039368.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX [1]
XX 1-6
XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
XX No sl sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX key Location/Qualifiers
FH
FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434I0110"
FT /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 G 1

RESULT 24
HSM004423 standard; RNA; EST; 6 BP.
ID HSM004423

```

```

XX AC AL039947;
XX SV AL039947.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]
XX RP 1-6
XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_lib="DKFZp434J0112"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 25
HSM007334 standard; RNA; EST; 6 BP.
XX HSM007334
XX AC AL042484;
XX SV AL042484.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone_lib="DKFZp434F0321"
XX FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SO Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
DB 1 g 1

RESULT 26
HSM007683/C standard; RNA; EST; 6 BP.
XX HSM007683
XX AC AL042833;
XX SV AL042833.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX RN [1]
XX RP 1-6
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source 1..6
XX FT /db_xref="taxon:9606"

```

```

FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
XX
SQ      Sequence 6 BP: 2 A; 2 C; 0 G; 2 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      6 G 6

```

```

RESULT 27
HSM008014/c
ID      HSM008014 standard; RNA; EST: 6 BP.
XX
XX      AL043164;
AC
XX      AL043164.1
SV
XX
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434F1123_s1 (from clone DKFZp434F1123)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
XX      [1]
XX      1-6
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the CDNA
XX      sequencing consortium of the German Genome Project
XX      r1 sequence also available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
FH
FH      source      1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
XX
SQ      Sequence 6 BP: 1 A; 2 C; 0 G; 3 T; 0 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      5 G 5

```

```

RESULT 28
HSM010918
ID      HSM010918 standard; RNA; EST: 6 BP.
XX
XX      AL046068;
AC
XX      AL046068.1
SV
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
DE
XX      EST: expressed sequence tag.
XX
XX      Homo sapiens (human)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
XX      [1]
XX      1-6
XX      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by DKFZ within the CDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
FH
FH      source      1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
XX
SQ      Sequence 6 BP: 0 A; 2 C; 2 G; 0 T; 2 other;

```

```

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 g 1
DB      1 G 1

```

```

RESULT 29
HSM010918/c
ID      HSM010918 standard; RNA; EST: 6 BP.
XX
XX      AL046068;
AC
XX      AL046068.1
SV
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA: EST DKFZp434F1672_r1 (from clone DKFZp434F1672)
DE
XX      EST: expressed sequence tag.
XX
XX

```

```

OY      1 g 1
DB      5 G 5

```

```

DEFINITION 128628 MARC 1pIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE030526
VERSION BE030526.1 GI:8325535
KEYWORDS EST.
SOURCE plg.
ORGANISM Sus scrofa
            Fokaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 546)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
        Sloane,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
        and Keele,J.W.
        Design and use of two pooled tissue normalized cDNA libraries for
        EST discovery in swine
        Unpublished (2000)
        Contact: Smith TPJ
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
        PCR primers
        FORWARD: AGCAACACCTATGACCAT
        BACKWARD: GTTTCCTCAGTCACGACG
        Plate: 62 row: F column: 16
        Seq primer: ATTACGTGACACCTATAC.
FEATURES
    source
        1..546
        /organism="Sus scrofa"
        /db_xref="taxon:9823"
        /clone_id="MARC 1pIG"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
        Library made from pooled tissue from day 11, 13, 15, 20,
        and 30 embryos."
BASE COUNT 120 a 164 c 149 g 113 t
ORIGIN
Query Match 5.1%; Score 24; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 139 gacttggccttgcgggacatc 162
    ||||||||||||||||||
Db 83 CACTTGGCCTTGCCCGGACATC 106
RESULT 20
A1556371/c 357 bp mRNA linear EST 23-MAR-1999
LOCUS UI-R-C2P-rg-f-10-0-UI.s1 UI-R-C2P Rattus norvegicus cDNA clone
DEFINITION A1556371
ACCESSION UI-R-C2P-rg-f-10-0-UI 3', mRNA sequence.
VERSION A1556371.1 GI:4488734
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
            Rattus.
REFERENCE 1 (bases 1 to 357)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Program for Rat Gene Discovery and Mapping

```

```

FEATURES
    source
        University of Iowa
        451 Eckstein Medical Research Building Iowa City, IA 52242, USA
        Tel: 319 335 8250
        Fax: 319 335 9565
        Email: mscoare@blue.weeg.uiowa.edu
        cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone
        distribution: clones will be available through Research Genetics
        (www.resgen.com)
        Seq primer: M13 Forward.
        Location/Qualifiers
            1..357
            /organism="Rattus norvegicus"
            /strain="Sprague-Dawley"
            /db_xref="taxon:10116"
            /clone="UI-R-C2P-rg-f-10-0-UI"
            /clone_id="UI-R-C2P"
            /dev_stage="adult"
            /lab_host="DH10B (Life Technologies)"
            /note="Vector: p775D-Pac (Pharmacia) with a modified
            polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2P
            library is a subtracted library derived from the UI-R-C1
            library, which is a subtracted library derived from the
            UI-R-C0 library. The UI-R-C0 library consisted of a
            mixture of individually tagged normalized libraries
            constructed from rat placenta, adult lung, brain, liver,
            kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
            embryo. The tag is a string of 3-5 nucleotides present
            between the Not I site and the oligo-dT track which allows
            identification of the library of origin of a clone within
            the mixture. The subtracted library (UI-R-C2P) was
            constructed as follows: PCR amplified cDNA inserts from
            UI-R-C1 clones from which 3' ESTs had been derived was
            used as a driver in a hybridization with the UI-R-C1
            library in the form of a single-stranded circles. The
            remaining single-stranded circles (subtracted library) was
            purified by hydroxyapatite column chromatography,
            converted to double-stranded circles and electroporated
            into DH10B bacteria (Life Technologies) to generate the
            UI-R-C2P library. This procedure has been previously
            described (Bonaldo, Lennon and Soares, Genome Research 6:
            791-806, 1996)."
BASE COUNT 82 a 103 c 66 g 106 t
ORIGIN
Query Match 4.9%; Score 23; DB 9; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 124 gtggtgaagactgtgacttg 146
    ||||||||||||||||||
Db 130 GTGGTGAAGATCTGTGACTTTGG 108
RESULT 21
A0136157/c 409 bp DNA linear GSS 24-SEP-1998
LOCUS HS_3060_B1.G08_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION A0136157
ACCESSION A0136157
VERSION A0136157.1 GI:3527493
KEYWORDS GSS.
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
        Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
        Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

```





BASE COUNT 117 a 118 c 109 g 116 t 1 others  
ORIGIN

Query Match 4.9%; Score 23; DB 9; Length 461;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtaagatctgacttgacct 149  
|||||  
Db 394 GTCAAGATCTGTGACTTGCCCT 372

## RESULT 24

LOCUS AL039890 498 bp mRNA linear EST 29-FEB-2000  
DEFINITION DKF2P34G1012.r1 434 (synonym: htes3) Homo sapiens cDNA clone  
AL039890  
VERSION AL039890  
KEYWORDS EST.  
SOURCE human.  
ORIGIN Homo sapiens

REFERENCE 1 (bases 1 to 498)  
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Duesterhoeft, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Duesterhoeft A  
MIPS

Am Kioferplatz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
consortium of the German Genome Project.  
No 31 sequence available.

This clone (DKF2P34G1012) is available at the RZPD in Berlin,  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

Source  
1..498  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKF2P34G1012"  
/clone\_1lb="434 (synonym: htes3)"  
/tissue\_type="testis"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

BASE COUNT 127 a 117 c 113 g 139 t 2 others  
ORIGIN

Query Match 4.9%; Score 23; DB 9; Length 498;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtaagatctgacttgacct 149  
|||||  
Db 245 GTCAAGATCTGTGACTTGCCCT 267

## RESULT 25

LOCUS BF523018 604 bp mRNA linear EST 11-DEC-2000  
DEFINITION UI-R-C2p-rg-f-10-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone  
BF523018  
ACCESSION BF523018  
VERSION BF523018.1 GI:11631033  
KEYWORDS EST.

SOURCE Norway rat.  
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 604)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: mesores@blue.weeg.uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
This clone is also available through Research Genetics (www.resgen.com)  
LNL (info@image.llnl.gov). IMAGE ID= 1793119  
Seq primer: M13 Forward.

## FEATURES

Source  
1..604  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-C2p-rg-f-10-0-UI"  
/clone\_1lb="UI-R-C2p"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-C2p  
library is a subtracted library derived from the UI-R-C1  
library, which is a subtracted library derived from the  
UI-R-C0 library. The UI-R-C0 library consisted of a  
mixture of individually tagged normalized libraries  
constructed from rat placenta, adult lung, brain, liver,  
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day  
embryo. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dT track which allows  
identification of the library of origin of a clone within  
the mixture. The subtracted library (UI-R-C2p) was  
constructed as follows: PCR amplified cDNA inserts from  
UI-R-C1 clones from which 3' ESTs had been derived was  
used as a driver in a hybridization with the UI-R-C1  
library in the form of single-stranded circles. The  
remaining single-stranded circles (subtracted library) was  
purified by hydroxyapatite column chromatography,  
converted to double-stranded circles and electroporated  
into DH10B bacteria (Life Technologies) to generate the  
UI-R-C2p library. This procedure has been previously  
described (Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996)"

BASE COUNT 166 a 132 c 167 g 139 t  
ORIGIN

Query Match 4.9%; Score 23; DB 10; Length 604;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgacttggtg 146  
|||||  
Db 526 GTGTGAAGATCTGTGACTTGCG 548

## RESULT 26

LOCUS CNS0437Z 1003 bp DNA linear GSS 18-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence pUC-ori end of clone  
CNS0437Z  
079111 of library G from Tetraodon nigroviridis, genomic survey

sequence.  
AL272456  
AL272456.1 GI:7994531  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 1003)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL  
REFERENCE  
AUTHORS  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
2 (bases 1 to 1003)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 1003)  
Genoscope.  
TITLE  
Direct Submission  
JOURNAL  
COMMENT  
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetraodon>.  
Location/Qualifiers  
1..1003  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0BG079AE06SP1-end :  
PUC-Or1"

BASE COUNT 264 a 174 c 239 g 291 t 35 others

ORIGIN

Query Match 4.9% Score 23; DB 12; Length 1003;  
Best Local Similarity 100.0% Pred. No. 0.84;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 gtgaagatcgtgacttgccct 149  
|||||  
Db 727 GTCAAGATCTGCACTTGCCCT 705

RESULT 27  
CNS03S1B 1099 bp DNA linear GSS 17-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone  
DEFINITION 050010 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL257960  
AL257960.1 GI:7978972  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 1099)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE  
Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 1099)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 1099)  
Genoscope.  
TITLE  
Direct Submission  
JOURNAL  
COMMENT  
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetraodon>.  
Location/Qualifiers  
1..1099  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0BG050DB05SP1-end : T7"

BASE COUNT 226 a 322 c 324 g 216 t 11 others

ORIGIN

Query Match 4.9% Score 23; DB 12; Length 1099;  
Best Local Similarity 100.0% Pred. No. 0.85;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 gcccgagacatcacaaagacc 173  
|||||  
Db 882 GCCCGAGACTCTACCAAGACCC 860

RESULT 28  
AL642415 658 bp mRNA EST 12-DEC-2001  
LOCUS AL642415 XGC-neurula Slurana tropicalis cDNA clone TNeu025K14 5',  
DEFINITION mRNA sequence.  
AL642415  
AL642415.1 GI:16794540  
EST.  
western clawed frog.  
Slurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Slurana.  
1 (bases 1 to 658)  
Huckie,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.  
Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
Unpublished (2001)  
Contact: Huckie E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: tropesanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TNeu025K14.sp6  
Sequencing primer: Sp6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
Location/Qualifiers  
1..658  
/organism="Slurana tropicalis"  
/db\_xref="taxon:8964"  
/clone\_lib="XGC-neurula"  
/dev\_stage="neurula"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA  
was oligo dt primed from sug of poly A+ RNA from neurula.

ECORI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end.  
BASE COUNT 149 a 192 c 178 g 138 t 1 others  
ORIGIN

Query Match 4.7%; Score 22; DB 9; Length 658;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 128 tgaagatcgtgacttgacct 149  
|||||  
Db 428 tgaagatcgtgacttgacct 449

RESULT 29  
LOCUS B1556970 743 bp mRNA linear EST 05-SEP-2001  
DEFINITION 603238431p1 NIH-CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5291694 5',  
B1556970  
ACCESSION mRNA sequence.  
VERSION B1556970  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 743)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lohar Hennishausen Ph.D., Chu-Xia Deng Ph.D.  
CNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM1737 row: m column: 07  
High quality sequence stop: 700.

FEATURES  
source  
Location/Qualifiers  
1..743

/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5291694"  
/clone\_1lb="NIH-CGAP\_Mam3"  
/tissue\_type="tumor, gross tissue"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert 2 kb. Library constructed by Life  
Technologies, catalog #12017-018. Investigators providing  
samples: Lohar Hennishausen/Chu-Xia Deng, NIH Reference  
for transgenic model: Xu et al., Nature Genetics 22, 37-43  
(1999). Note: this is a NCI-CGAP Library."  
BASE COUNT 154 a 215 c 214 g 160 t  
ORIGIN

Query Match 4.7%; Score 22; DB 10; Length 743;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 gagaactgctgctcggaacat 104  
|||||  
Db 141 GAGACCTGGCTCTCGAACAT 162

RESULT 30  
BFI36721  
LOCUS BFI36721 793 bp mRNA linear EST 24-OCT-2000

DEFINITION 601780488F1 NCI-CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4008812 5',  
mRNA sequence.  
ACCESSION BFI36721  
VERSION BFI36721.1 GI:10975761  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 793)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM9243 row: o column: 21  
High quality sequence stop: 654.

FEATURES  
source  
Location/Qualifiers  
1..793

/organism="Mus musculus"  
/strain="C2ECB II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4008812"  
/clone\_1lb="NCI-CGAP\_Lu30"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; transgenic model MWT-1, expression driven by  
MWT-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"  
BASE COUNT 158 a 227 c 232 g 175 t 1 others  
ORIGIN

Query Match 4.7%; Score 22; DB 10; Length 793;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 gagaactgctgctcggaacat 104  
|||||  
Db 119 GAGACCTGGCTCTCGAACAT 140

RESULT 31  
B1686934 834 bp mRNA linear EST 18-SEP-2001  
LOCUS B1686934  
DEFINITION 60331809F1 NCI-CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5353635 5',  
B1686934  
ACCESSION mRNA sequence.  
VERSION B1686934  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 834)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
CNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://limage.llnl.gov>  
Plate: LLM11899 row: b column: 04  
High quality sequence stop: 781.  
Location/Qualifiers

## FEATURES

source

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1. 834
/organism="Mus musculus"
/strain="PVB/N"
/db_xref="taxon:10090"
/clone_image="5353635"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      175 a      245 c      247 g      167 t
ORIGIN
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Query Match 4.7%: Score 22; DB 10; Length 834;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 gagacctgagctcgcgaacat 104  
|||||  
Db 356 GAGACCTGCGTCGCGACAT 377

RESULT 32  
CNS04EJU/c 888 bp DNA linear GSS 21-MAY-2000  
LOCUS Tetradon nigroviridis genome survey sequence PUC-ori end of clone  
DEFINITION 104812 of library G from Tetradon nigroviridis, genomic survey  
sequence.

ACCESSION AL287139.1 GI:8025621  
VERSION GSS: genome survey sequence.  
KEYWORDS Tetradon nigroviridis.  
SOURCE Tetradon nigroviridis  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 888)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 888)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
COMMENT Human gene number estimate provided by genome wide analysis using  
Tetradon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 888)  
Genoscope.  
DIRECT SUBMISSION Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetradon>.  
LOCATION/Qualifiers  
1. 888  
/organism="Tetradon nigroviridis"

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
COMMENT

FEATURES  
source

```
/db_xref="taxon:99883"
/clone="104812"
/clone_lib="G"
/note="Genoscope sequence ID : C08C104DA06SP1-end : PUC-ori"
BASE COUNT      205 a      249 c      234 g      193 t      7 others
ORIGIN
```

Query Match 4.7%: Score 22; DB 12; Length 888;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 tctgctacagcttcagctgac 41  
|||||  
Db 872 TCTGCTACAGCTTCAGGTGCG 851

RESULT 33  
CNS03ZER/c 903 bp DNA linear GSS 15-MAY-2000  
LOCUS Tetradon nigroviridis genome survey sequence PUC-ori end of clone  
DEFINITION 206F22 of library G from Tetradon nigroviridis, genomic survey  
sequence.

ACCESSION AL224748.1 GI:7883622  
VERSION GSS: genome survey sequence.  
KEYWORDS Tetradon nigroviridis.  
SOURCE Tetradon nigroviridis  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei;  
Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 903)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 903)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
COMMENT Human gene number estimate provided by genome wide analysis using  
Tetradon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 903)  
Genoscope.  
DIRECT SUBMISSION Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetradon>.  
LOCATION/Qualifiers  
1. 903  
/organism="Tetradon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="206F22"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0AG206DC11SP1-end : PUC-ori"

FEATURES  
source

BASE COUNT 189 a 255 c 272 g 183 t 4 others  
ORIGIN

Query Match 4.7%: Score 22; DB 12; Length 903;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 agtgcacccagagacgtgac 92  
|||||

Db 236 ACTGCATCCACAGACCTGGC 215

RESULT 34  
CNS02YAK/C

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 180A18 of library G from Tetraodon nigroviridis, genomic survey

ACCESSION AL219413.1 GI:7878232

VERSION 1

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 967)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 967)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 967)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..967

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="180A18"

/clone\_1lb="G"

/note="Genoscope sequence ID : C0AG180BA09SP1-end : PUC-Or1"

BASE COUNT 253 a 252 c 247 g 211 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 967;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 tctgtctacagctccagggtgc 41  
|||||

Db 229 TCTGCTACAGCTTCCAGGTGGC 208

RESULT 35  
CNS02SAS/C

LOCUS 978 bp DNA linear GSS 12-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 236D19 of library G from Tetraodon nigroviridis, genomic survey

ACCESSION AL181837.1 GI:7819921

VERSION 1

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 978)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 978)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 978)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..978

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="236D19"

/clone\_1lb="G"

/note="Genoscope sequence ID : C0AG236CB10LP1-end : T7"

BASE COUNT 239 a 260 c 265 g 210 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 978;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 tctgtctacagctccagggtgc 41  
|||||

Db 605 TCTGCTACAGCTTCCAGGTGGC 584

RESULT 36  
CNS01UBA

LOCUS 1023 bp DNA linear GSS 12-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 196I14 of library G from Tetraodon nigroviridis, genomic survey

ACCESSION AL167598.1 GI:7805656

VERSION 1

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 1023)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1023)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1023)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..1023

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="196I14"

/clone\_1lb="G"

/note="Genoscope sequence ID : C0AG196I14LP1-end : T7"

BASE COUNT 239 a 260 c 265 g 210 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 tctgtctacagctccagggtgc 41  
|||||

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 978)

Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 978)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 978)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..978

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="236D19"

/clone\_1lb="G"

/note="Genoscope sequence ID : C0AG236CB10LP1-end : T7"

BASE COUNT 239 a 260 c 265 g 210 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 978;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 tctgtctacagctccagggtgc 41  
|||||

Db 605 TCTGCTACAGCTTCCAGGTGGC 584

RESULT 36  
CNS01UBA

LOCUS 1023 bp DNA linear GSS 12-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 196I14 of library G from Tetraodon nigroviridis, genomic survey

ACCESSION AL167598.1 GI:7805656

VERSION 1

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 1023)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1023)

AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1023)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..1023

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="196I14"

/clone\_1lb="G"

/note="Genoscope sequence ID : C0AG196I14LP1-end : T7"

BASE COUNT 239 a 260 c 265 g 210 t 4 others

ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 tctgtctacagctccagggtgc 41  
|||||

JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1023)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the tetradon nigroviridis genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetradon.

FEATURES  
source  
1..1023  
/organism="Tetradon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="196114"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : C0AG196BE07SP1-end : PUC-ori"

BASE COUNT 205 a 305 c 290 g 218 t 5 others  
ORIGIN

Query Match 4.7%; Score 22; DB 12; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 71 agtgcattccacagagactgac 92  
|||||  
Db 695 AGTCATTCACAGACCTGCG 716

RESULT 37  
BC013342 3397 bp mRNA linear HTC 04-SEP-2001  
LOCUS  
DEFINITION Mus musculus, clone IMAGE:4013934, mRNA.  
ACCESSION BC013342  
VERSION BC013342.1 GI:15426477  
KEYWORDS HTC.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 3397)  
REFERENCE 1 (bases 1 to 3397)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
http://www.systemsbiology.org  
contact: amadan@systemsbiology.org  
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan

REMARK  
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAK Plate: 18 Row: f Column: 15  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1089897  
This clone has the following problem: frame shifted.  
Location/Qualifiers  
1..3397  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4013934"  
/tissue\_type="mammary tumor metastasized to lung."  
MTV-LTR/MTL model. Expression driven by an MTV-LTR

enhancer."  
/clone\_1lb="NCI CGAP\_Lu30"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6"  
BASE COUNT 728 a 970 c 1014 g 685 t  
ORIGIN

Query Match 4.7%; Score 22; DB 11; Length 3397;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 gagacgtgctgctcggaacat 104  
|||||  
Db 2393 GAGACCTGCTGCTCGGAACAT 2414

RESULT 38  
AA895295 359 bp mRNA linear EST 06-APR-1998  
LOCUS  
DEFINITION vx49609.t1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1278568 5' similar to gb:U10717 TYROSINE-PROTEIN KINASE LYK I (HUMAN); gb:X55653 Mouse mRNA for protein-tyrosine kinase, tec type I (MOUSE);, mRNA sequence.  
ACCESSION AA895295  
VERSION AA895295.1 GI:3031714  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 359)  
REFERENCE 1 (bases 1 to 359)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HMI Mouse EST Project  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:670368  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 200.  
Location/Qualifiers  
1..359  
/organism="Mus musculus"  
/strain="C57BL/6 x CBA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1278568"  
/clone\_1lb="Stratagene mouse lung 937302"  
/sex="female"  
/tissue\_type="lung"  
/dev\_stage="6-8 month old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: lung; Vector: pluscript SK-; Site: 1; ECORI ; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo dt. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

TITLE  
JOURNAL  
COMMENT

High quality sequence stop: 200.  
Location/Qualifiers  
1..359  
/organism="Mus musculus"  
/strain="C57BL/6 x CBA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1278568"  
/clone\_1lb="Stratagene mouse lung 937302"  
/sex="female"  
/tissue\_type="lung"  
/dev\_stage="6-8 month old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: lung; Vector: pluscript SK-; Site: 1; ECORI ; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo dt. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

FEATURES  
source

BASE COUNT 94 a 76 c 97 g 92 t  
ORIGIN

Query Match 4.5%; Score 21; DB 9; Length 359;

Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 catcacagagacctgctgc 95  
|||||  
Db 111 CATCCACAGACCTGCTGC 131

RESULT 39  
BF147285  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF147285 458 bp mRNA linear EST 26-OCT-2000  
U66405.y1 Soares.mammary\_gland\_NMLMG Mus musculus cDNA clone  
IMAGE:3467145.5. similar to SW:TEC\_MOUSE P24604 TYROSINE-PROTEIN  
KINASE TEC ; mRNA sequence.  
BF147285  
BF147285.1 GI:11026680  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 458)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Unpublished (1997)  
Tumor Gene Index  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40R from GIBCO  
High quality sequence stop: 381.  
Location/Qualifiers  
1..458  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3467145"  
/clone\_lib="Soares.mammary\_gland\_NMLMG"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT73 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonadio."

BASE COUNT 120 a 99 c 125 g 113 t 1 others

Query Match 4.5%; Score 21; DB 10; Length 458;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 catcacagagacctgctgc 95  
|||||  
Db 161 CATCCACAGACCTGCTGC 181

RESULT 40  
AG094291  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AG094291 711 bp DNA linear GSS 03-NOV-2001  
Pan troglodytes DNA, clone: PTB-095A06.F, genomic survey sequence.  
AG094291  
AG094291.1 GI:16646093  
GSS: GSS (genome survey sequence).  
Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male  
BAC Library clone:PTB-095A06.F.  
Pan troglodytes

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1 (sites)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totohi,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 711)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totohi,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimps@gsc.riken.go.jp](mailto:chimps@gsc.riken.go.jp), [Yokohama\\_kanagawa\\_230-0045\\_Japan](mailto:Yokohama_kanagawa_230-0045_Japan),  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1..711  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-095A06.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 147 a 260 c 158 g 146 t

Query Match 4.5%; Score 21; DB 12; Length 711;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 ggtggccagagagatgagct 56  
|||||  
Db 502 GGTGGCCAGAGGATGAGCTT 482

RESULT 41  
B1111982  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

B1111982 845 bp mRNA linear EST 26-JUN-2001  
602901317F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5031052.5',  
mRNA sequence.  
B1111982  
B1111982.1 GI:14562883  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 845)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
Unpublished (1999)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Lohar Hemphausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1087 row: a column: 05  
High quality sequence stop: 837.



FEATURES  
source  
Location/Qualifiers  
1. 845  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5031052"  
/clone\_1lb="NCI CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 211 a 188 c 238 g 208 t

ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 845;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 catccacagagactgctgc 95  
|||||

Db 88 CATCCACAGACGCTGCTGC 108

RESULT 42  
BF119392 945 bp mRNA linear EST 24-OCT-2000  
LOCUS 601758315F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3992642 5',  
DEFINITION mRNA sequence.  
ACCESSION BF119392  
VERSION BF119392.1 GI:10958432  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 945)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: L1AM9207 row: n column: 03  
High quality sequence stop: 661.  
Location/Qualifiers  
1. 945  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3992642"  
/clone\_1lb="NCI CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 255 a 235 c 237 g 217 t 1 others

ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 945;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttgacct 150  
|||||

Db 452 AAGATCTGTGACTTGGCCTT 472

RESULT 43  
B1153717 1019 bp mRNA linear EST 05-JUL-2001  
LOCUS 602871357F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5003055 5',  
DEFINITION mRNA sequence.  
ACCESSION B1153717  
VERSION B1153717.1 GI:14613718  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1019)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: L1AM11039 row: b column: 16  
High quality sequence start: 2  
High quality sequence stop: 442.  
Location/Qualifiers  
1. 1019  
/organism="Mus musculus"  
/strain="FVB/N-3"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5003055"  
/clone\_1lb="NCI CGAP\_Mam2"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Gilbert Smith, NIH"

BASE COUNT 308 a 294 c 276 g 141 t

ORIGIN

Query Match 4.5%; Score 21; DB 10; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 gaagacctggtctggaaca 103  
|||||

Db 318 GAAGACCTGCTCGGACCA 338

RESULT 44  
BC018230 2564 bp mRNA linear HTC 06-DEC-2001  
LOCUS BC018230  
DEFINITION Mus musculus, similar to cytoplasmic tyrosine kinase, Dscr28c related (Prosopha1a), clone IMAGE:4484096, mRNA.  
ACCESSION BC018230  
VERSION BC018230.1 GI:17390527  
KEYWORDS HTC.

SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2564)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [vllation@bcm.tmc.edu](mailto:vllation@bcm.tmc.edu)  
Villation, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAX Plate: 31 Row: 1 Column: 24  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 7305568  
This clone has the following problem: frame shifted.  
FEATURES  
source  
1..2564  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4484096"  
/tissue\_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."  
/clone\_1lb="NCI\_CGAP\_Mam1"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
BASE COUNT 789 a 521 c 656 g 598 t  
ORIGIN  
Query Match 4.5%; Score 21; DB 11; Length 2564;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 75 catccacagagacctgctgc 95  
|||||  
Db 1538 CATCCACAGAGACTGCTGC 1558  
RESULT 45  
AUI29676 253 bp mRNA linear EST 24-OCT-2000  
LOCUS AUI29676 NT2RP2 Homo sapiens cDNA clone NT2RP2006021 5', mRNA  
DEFINITION sequence.  
ACCESSION AUI29676  
VERSION AUI29676.1 GI:10990030  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 253)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Makamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
TITLE HRI human cDNA project  
JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)  
HRI human cDNA project: 5'-6 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
FEATURES  
source  
1..253  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NT2RP2006021"  
/clone\_1lb="NT2RP2"  
/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note="Vector: pME18SFU3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."  
BASE COUNT 63 a 64 c 58 g 65 t 3 others  
ORIGIN  
Query Match 4.2%; Score 20; DB 9; Length 253;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 130 aaguctctgacttgacct 149  
|||||  
Db 32 AAGATCTGTGACTTTGGCCT 51

Search completed: July 15, 2002, 20:07:35  
Job time: 14493 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:56:48 ; Search time 808.35 Seconds  
(without alignments)  
991.681 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514

Perfect score: 471

Sequence: 1 ctgaccatggaagatctgtg.....gacctgctcgcgagctg 471

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/prodata/2/pna/US06\_NEW\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/prodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	471	100.0	4416	5	US-09-053-375B-132
2	471	100.0	4416	5	US-09-442-384B-447
3	96	20.4	476	5	US-09-539-331D-34177
4	23	4.9	476	5	US-09-539-331D-34177
5	23	4.9	6373	6	US-10-027-400-1
6	23	4.9	6373	5	US-09-053-375B-419
7	22	4.7	22	5	US-09-704-167A-8
8	22	4.7	4479	5	US-09-053-375B-724
9	21	4.5	744	6	US-10-027-632-15064
10	21	4.5	997	6	US-10-027-632-30946
11	21	4.5	2574	6	US-10-045-428A-2
12	20	4.2	366	5	US-09-721-544-17950
13	20	4.2	461	5	US-09-721-544-17950
14	20	4.2	462	5	US-09-918-995-24204
15	20	4.2	484	5	US-09-721-544-17950
16	20	4.2	698	6	US-10-027-632-148136
17	20	4.2	1611	5	US-09-053-375B-130
18	20	4.2	1611	5	US-09-053-375B-130
19	20	4.2	1611	6	US-10-171-311-126
20	20	4.2	1611	6	US-10-171-311-126
21	20	4.2	5279	6	US-10-105-299-752
22	20	4.2	5427	5	US-09-053-375B-420
23	20	4.2	5427	5	US-09-442-384B-437
24	20	4.2	5427	6	US-10-027-400-3
25	20	4.2	5570	6	US-10-007-926A-209
26	19	4.0	303	5	US-09-539-331D-17143

27	19	4.0	465	5	US-09-442-384B-358	Sequence 358, App
28	19	4.0	466	5	US-09-442-366A-66	Sequence 66, App1
29	19	4.0	504	5	US-09-911-904-130	Sequence 130, App
30	19	4.0	1063	6	US-10-106-698-2068	Sequence 2068, App
31	19	4.0	1706	5	US-09-937-060A-17	Sequence 17, App
32	19	4.0	1939	6	US-10-104-047-1465	Sequence 1465, App
33	19	4.0	1948	6	US-10-027-632-97991	Sequence 97991, A
34	19	4.0	1948	6	US-10-027-632-97992	Sequence 97992, A
35	19	4.0	2344	5	US-09-053-375B-907	Sequence 907, App
36	19	4.0	2526	5	US-09-053-375B-1006	Sequence 1006, App
37	19	4.0	3949	5	US-09-442-384B-773	Sequence 773, App
38	19	4.0	3949	5	US-09-721-544-12422	Sequence 12422, A
39	18	3.8	340	5	US-10-121-925-5	Sequence 5, App1
40	18	3.8	361	6	US-10-121-925-5	Sequence 5, App1
41	18	3.8	361	6	US-09-918-995-1503	Sequence 1503, App
42	18	3.8	449	5	US-09-918-995-11621	Sequence 11621, A
43	18	3.8	738	6	US-10-027-632-15007	Sequence 15007, A
44	18	3.8	738	6	US-10-027-632-15007	Sequence 15007, A
45	18	3.8	738	6	US-10-027-632-15008	Sequence 15008, A

## ALIGNMENTS

```
RESULT 1
US-09-053-375B-132
: Sequence 132, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chemchik, Alex
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053, 375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 132
: LENGTH: 4416
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
: NAME/KEY: misc-feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
: US-09-053-375B-132

Query Match 100.0%; Score 471; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.6e-246;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgaccatggaagatctgtgctgctcaagcttgcgaggaaggaagtcctg 60
    |||||||
Db 3044 ctgaccatggaagatctgtgctgctcaagcttgcgaggaaggaagtcctg 3103
    |||||||

QY 61 gcttccggaagatgcatccacagagacgtgctgctggaacatctgctgcggaagc 120
    |||||||
Db 3104 gcttccggaagatgcatccacagagacgtgctgctggaacatctgctgcggaagc 3163
    |||||||

QY 121 gacgtgtgaagatctgtgacttgccttgcgaggaatctcaagaagaccctgactac 180
    |||||||
Db 3164 gacgtgtgaagatctgtgacttgccttgcgaggaatctcaagaagaccctgactac 3223
    |||||||

QY 181 gtcgcaagggcagtgcccgctgcccctgaagtgaatgagccctgaagacatctcgac 240
    |||||||
```

```
Db 3224 gtcgcgaagggcagtgcccgctgcccctgaagtgatgcccctgaagacatcttcgac 3283
Oy 241 aaggtgtacaccacgacagatgacgtgtgtcttcttggtgtcttcttcctcggagatcttc 300
Db 3284 aaggtgtacaccacgacagatgacgtgtgtcttcttggtgtcttcttcctcggagatcttc 3343
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagttcttcgacgagctg 360
Db 3344 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagttcttcgacgagctg 3403
Oy 361 aagagcgacgaagaagatgagggcccgagctggtccatcccgccatcacgcccacatcag 420
Db 3404 aagagcgacgaagaagatgagggcccgagctggtccatcccgccatcacgcccacatcag 3463
Oy 421 ctgaactgtgtctccggaagaccacgaagcgaaacctgacatctcggagctg 471
Db 3464 ctgaactgtgtctccggaagaccacgaagcgaaacctgacatctcggagctg 3514
```

## RESULT 2

```
US-09-442-384B-447
: Sequence 447, Application US/09442384B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Lukashov, Matvey
: TITLE OF INVENTION: Hematology/Immunology Array
: FILE REFERENCE: CLON-006C1P15
: CURRENT APPLICATION NUMBER: US/09/442, 384B
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053, 375
: PRIOR FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 830
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 447
: LENGTH: 4416
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
: NAME/KEY: misc_feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-447
```

Query Match 100.0%; Score 471; DB 5; Length 4416;  
Best Local Similarity 100.0%; Pred. No. 3 6e-246;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 ctgacctggaagatctgtctgtctacagcttcccaagtgccagaggaatgagtttctg 60
Db 3044 ctgacctggaagatctgtctgtctacagcttcccaagtgccagaggaatgagtttctg 3103
Oy 61 gcttccgaagaagtcacacacagagacctgtgctcgcgcgaacatcttgcctctggaagc 120
Db 3104 gcttccgaagaagtcacacacagagacctgtgctcgcgcgaacatcttgcctctggaagc 3163
Oy 121 gacgtgtggaagatctgtgacttctgaccttgcgcgcgagacatctacaagaacctgactac 180
Db 3164 gacgtgtggaagatctgtgacttctgaccttgcgcgcgagacatctacaagaacctgactac 3223
Oy 181 gtcgcgaagggcagtgcccgctgcccctgaagtgaatgagccctgaagaacatcttcgac 240
Db 3224 gtcgcgaagggcagtgcccgctgcccctgaagtgaatgagccctgaagaacatcttcgac 3283
Oy 241 aaggtgtacaccacgacagatgacgtgtgtcttcttggtgtcttcttcctcggagatcttc 300
Db 3284 aaggtgtacaccacgacagatgacgtgtgtcttcttggtgtcttcttcctcggagatcttc 3343
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagttcttcgacgagctg 360
```

```
Db 3344 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagttcttcgacgagctg 3403
Oy 361 aagagcgacgaagaagatgagggcccgagctggtccatcccgccatcacgcccacatcag 420
Db 3404 aagagcgacgaagaagatgagggcccgagctggtccatcccgccatcacgcccacatcag 3463
Oy 421 ctgaactgtgtctccggaagaccacgaagcgaaacctgacatctcggagctg 471
Db 3464 ctgaactgtgtctccggaagaccacgaagcgaaacctgacatctcggagctg 3514
```

## RESULT 3

```
US-09-539-331D-34177
: Sequence 34177, Application US/09539331D
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539, 331D
: CURRENT FILING DATE: 2000-03-30
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 34177
: LENGTH: 476
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177
```

Query Match 20.4%; Score 96; DB 5; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5.4e-42;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 42 cagagagatgagcttctgcttcccgaaagtgcacccacagagactggtgtcgaa 101
Db 24 cagagagatgagatcttctgcttcccgaaagtgcacccacagagactggtgtcgaa 83
Oy 102 catctcgtgtcggaaagcgacgtgtgtgaagatctg 137
Db 84 catctcgtgtcggaaagcgacgtgtgtgaagatctg 119
```

## RESULT 4

```
US-09-539-331D-34177/C
: Sequence 34177, Application US/09539331D
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539, 331D
: CURRENT FILING DATE: 2000-03-30
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 34177
: LENGTH: 476
: TYPE: DNA
: ORGANISM: Homo sapiens
```

FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu01173578  
US-09-539-331D-34177

Query Match 4.9%: Score 23; DB 5; Length 476;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 tctgtacagcttgagctggcc 42  
|||||  
Db 27 tctgtacagcttgagctggcc 5

RESULT 5  
US-10-027-400-1  
Sequence 1, Application US/10027400  
GENERAL INFORMATION:  
APPLICANT: WILLIAMS, Lewis T.  
ESCHEDO, Jaime A.  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market, Stewart Street Tower, 20th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/027,400  
FILING DATE: 19-Dec-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,917  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 07/151,414  
FILING DATE: 02-FEB-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6373 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 129..3398  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-027-400-1

Query Match 4.9%: Score 23; DB 6; Length 6373;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtaagaatcgtgacttgcc 149  
|||||  
Db 2622 gtaagaatcgtgacttgcc 2644

RESULT 6  
US-09-053-375B-419  
Sequence 419, Application US/09053375B  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Bibilashvili, Robert  
TITLE OF INVENTION: Nucleic Acid Arrays  
FILE REFERENCE: CLON-006  
CURRENT APPLICATION NUMBER: US/09/053,375B  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 1543  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 419

LENGTH: 6378  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-053-375B-419

Query Match 4.9%: Score 23; DB 5; Length 6378;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtaagaatcgtgacttgcc 149  
|||||  
Db 2633 gtaagaatcgtgacttgcc 2655

RESULT 7  
US-09-704-167A-8/C  
Sequence 8, Application US/09704167A  
GENERAL INFORMATION:  
APPLICANT: Havemann, Klaus  
TITLE OF INVENTION: Production and Use of Endothelial-like Cells  
FILE REFERENCE: BPD-100  
CURRENT APPLICATION NUMBER: US/09/704,167A  
CURRENT FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent version 3.1  
SEQ ID NO 8

LENGTH: 22  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: VEGFR-3 3'-primer for RT-PCR, VEGFR-3 Genbank accession no. NM  
US-09-704-167A-8

Query Match 4.7%: Score 22; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 117 aagcagcgtgctgaagatcgt 138  
|||||  
Db 22 AAGCAGCgtgctgaagatcgt 1

RESULT 8  
US-09-053-375B-724  
Sequence 724, Application US/09053375B  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Bibilashvili, Robert  
TITLE OF INVENTION: Nucleic Acid Arrays  
FILE REFERENCE: CLON-006  
CURRENT APPLICATION NUMBER: US/09/053,375B  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 1543  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 724

LENGTH: 4479  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-053-375B-724

Query Match 4.7% Score 22: DB 5: Length 4479;  
Best Local Similarity 100.0%: Pred. No. 0.11;

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 83 gagacctgctgcgcgaacat 104  
|||||  
DB 2309 gagacctgctgcgcgaacat 2330

RESULT 9

US-10-027-632-15064/C  
Sequence 15064, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15064  
LENGTH: 744  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-15064

Query Match 4.5% Score 21: DB 6: Length 744;  
Best Local Similarity 100.0%: Pred. No. 0.37;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 36 ggtggccagagagatgagtt 56  
|||||  
DB 275 GGTGGCCAGAGAGATGAGTT 255

RESULT 10

US-10-027-632-30946/C  
Sequence 30946, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30946  
LENGTH: 997  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-30946

Query Match 4.5% Score 21: DB 6: Length 997;  
Best Local Similarity 100.0%: Pred. No. 0.37;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 36 ggtggccagagatgagtt 56  
|||||  
DB 604 GGTGGCCAGAGATGAGTT 584

RESULT 11

US-10-045-428A-2  
Sequence 2, Application US/10045428A  
GENERAL INFORMATION:  
APPLICANT: Mano, Hiroyuki  
APPLICANT: Sakata, Tsuneaki  
APPLICANT: Hasegawa, Mamoru  
APPLICANT: Tabata, Toshiaki  
TITLE OF INVENTION: Promoter  
FILE REFERENCE: 50026/011003  
CURRENT APPLICATION NUMBER: US/10/045,428A  
PRIOR FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: 09/735,103  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 09/142,529  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: PCT/JP97/00741  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: JP 8/54294  
PRIOR FILING DATE: 1996-03-12  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 2574  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-045-428A-2

Query Match 4.5% Score 21: DB 6: Length 2574;  
Best Local Similarity 100.0%: Pred. No. 0.38;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 75 catccacagagacctgctgc 95  
|||||  
DB 1566 catccacagagacctgctgc 1586

RESULT 12

US-09-721-544-17950  
Sequence 17950, Application US/09721544  
GENERAL INFORMATION:  
APPLICANT: Arterburn, Matthew  
APPLICANT: Asghari, Vida  
APPLICANT: Damavandi, Simin  
APPLICANT: Dickson, Mark  
APPLICANT: Drake, Jim

```

: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Gledt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jessen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Raistl, Farida
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: FILE REFERENCE: 728CIP
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 17950
: LENGTH: 366
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-721-544-17950

```

```

Query Match      4.2%: Score 20; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 73 aagatctgtgacttgacct 92

```

```

RESULT 13
US-09-721-544-7766
: Sequence 7766, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Arterburn, Matthew
: APPLICANT: Asgnari, Vida
: APPLICANT: Damavandi, SlmIn
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Gledt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jessen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Nogra, Margie
: APPLICANT: Palencia, Servando

```

```

: APPLICANT: Raistl, Farida
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: FILE REFERENCE: 728CIP
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7766
: LENGTH: 461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(461)
: OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7766

```

```

Query Match      4.2%: Score 20; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 170 aagatctgtgacttgacct 189

```

```

RESULT 14
US-09-918-995-24204
: Sequence 24204, Application US/09918995
: GENERAL INFORMATION:
: APPLICANT: Hysq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 24204
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(462)
: OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24204

```

```

Query Match      4.2%: Score 20; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 130 aagatctgtgacttgacct 149
      |||
Db 91 aagatctgtgacttgacct 110

```

RESULT 15



```

US-09-721-544-7765
: Sequence 7765, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Artzburn, Mathew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Simin
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radojce
: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Gledt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jensen, Aaron
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phong
: APPLICANT: Mogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Raisl, Fariba
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verra, Ron
: APPLICANT: Yang, Fel
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
: FILE REFERENCE: 728CIP
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7765
: LENGTH: 484
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(484)
: OTHER INFORMATION: n ~ A,T,C or G
US-09-721-544-7765

```

ORGANISM: Homo sapiens  
US-09-053-175B-130

Query Match 4.2% Score 20: DB 5: Length 1611:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 130 aagatctgacttgacct 149  
|||||  
DB 109 AACATCTGCACTTGCGCT 90

RESULT 19  
US-10-171-311-126  
Sequence 126, Application US/10171311

GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Chen, Yan  
APPLICANT: Zhao, Xumei  
APPLICANT: Monahan, John  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Glatl, Karen  
APPLICANT: Gannavarapu, Manjula  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
FILE REFERENCE: MRI-035  
CURRENT APPLICATION NUMBER: US/10/171,311  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: US 60/298,159  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,155  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/335,936  
PRIOR FILING DATE: 2001-11-14  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 126  
LENGTH: 1611  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-171-311-126

Query Match 4.2% Score 20: DB 6: Length 1611:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 130 aagatctgacttgacct 149  
|||||  
DB 817 aagatctgacttgacct 836

RESULT 20  
US-10-171-311-126/c  
Sequence 126, Application US/10171311

GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Chen, Yan  
APPLICANT: Zhao, Xumei  
APPLICANT: Monahan, John  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Glatl, Karen  
APPLICANT: Gannavarapu, Manjula  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
FILE REFERENCE: MRI-035  
CURRENT APPLICATION NUMBER: US/10/171,311  
CURRENT FILING DATE: 2002-06-12

PRIOR APPLICATION NUMBER: US 60/298,159  
PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,155  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/335,936  
PRIOR FILING DATE: 2001-11-14  
NUMBER OF SEQ ID NOS: 238

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 126  
LENGTH: 1611  
TYPE: DNA

ORGANISM: Homo sapiens  
US-10-171-311-126

Query Match 4.2% Score 20: DB 6: Length 1611:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 130 aagatctgacttgacct 149  
|||||  
DB 109 AACATCTGCACTTGCGCT 90

RESULT 21  
US-10-105-299-752  
Sequence 752, Application US/10105299

GENERAL INFORMATION:  
APPLICANT: Rosen, et. al  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS950  
CURRENT APPLICATION NUMBER: US/10/105,299  
CURRENT FILING DATE: 2002-03-26  
NUMBER OF SEQ ID NOS: 15197  
Prior Application removed - See File Wrapper or Palm  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 752  
LENGTH: 5279  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1371)..(1371)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-105-299-752

Query Match 4.2% Score 20: DB 6: Length 5279:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 130 aagatctgacttgacct 149  
|||||  
DB 547 aagatctgacttgacct 566

RESULT 22  
US-09-053-375B-420

Sequence 420, Application US/09053375B  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: Nucleic Acid Arrays  
FILE REFERENCE: CLON-006  
CURRENT APPLICATION NUMBER: US/09/053,375B  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 1543  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 420  
LENGTH: 5427  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-053-375B-420

Query Match 4.2%: Score 20: DB 5: Length 5427:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 130 aagatctgtgacttggcct 149  
|||||  
Db 2707 aagatctgtgacttggcct 2726

## RESULT 23

US-09-442-384B-437  
Sequence 437, Application US/09442384B  
GENERAL INFORMATION:  
APPLICANT: Chemchik, Alex  
APPLICANT: Lukashiev, Matvey  
TITLE OF INVENTION: Hematology/Immunology Array  
FILE REFERENCE: CLON-006CIP15  
CURRENT APPLICATION NUMBER: US/09/442,384B  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 09/053,375  
NUMBER OF SEQ ID NOS: 830  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 437  
LENGTH: 5427  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-442-384B-437

Query Match 4.2%: Score 20: DB 5: Length 5427:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 130 aagatctgtgacttggcct 149  
|||||  
Db 2707 aagatctgtgacttggcct 2726

## RESULT 24

US-10-027-400-3  
Sequence 3, Application US/10027400  
GENERAL INFORMATION:  
APPLICANT: WILLIAMS, Lewis T.  
APPLICANT: ESCOBEDO, Jaime A.  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market, Stewart Street Tower, 20th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/027,400  
FILING DATE: 19-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,917  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 07/151,414  
FILING DATE: 02-FEB-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5427 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 187..3507  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-027-400-3

Query Match 4.2%: Score 20: DB 6: Length 5427:  
Best Local Similarity 100.0%: Pred. No. 1.3:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 130 aagatctgtgacttggcct 149  
|||||  
Db 2707 AAGATCTGTGACTTTGGCCT 2726

## RESULT 25

US-10-007-926A-209  
Sequence 209, Application US/10007926A  
GENERAL INFORMATION:  
APPLICANT: BERTUCCI, FRANCOIS  
APPLICANT: HOULATTE, REMI  
APPLICANT: BIRNBAUM, DANIEL  
APPLICANT: NGUYEN, CATHERINE  
APPLICANT: VIENS, PATRICE  
APPLICANT: FERT, VINCENT  
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
FILE REFERENCE: 1546-R-00  
CURRENT APPLICATION NUMBER: US/10/007,926A  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/254,090  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 209  
LENGTH: 5570  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: beta polypeptide (PDGFRB) gene.  
US-10-007-926A-209

Query Match 4.2%: Score 20: DB 6: Length 5570:  
Best Local Similarity 100.0%: Pred. No. 1.4:  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 130 aagatctgtgacttggcct 149  
|||||  
Db 2877 aagatctgtgacttggcct 2896

## RESULT 26

US-09-538-331D-17143  
Sequence 17143, Application US/09539331D  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Deleage, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.

```
; APPLICANT: Mullaby, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 17143
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incycle ID No: hu00007038
; NAME/KEY: unsure
; LOCATION: 3, 99, 284
; OTHER INFORMATION: d, t, c, g, or other
US-09-539-331D-17143
```

```
Query Match          4.0%; Score 19; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 128 tgaagatctgactctg 146
      |||
Db 112 tgaagatctgactctg 130
```

```
RESULT 27
US-09-442-384B-358
; Sequence 358, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-358
```

```
Query Match          4.0%; Score 19; DB 5; Length 465;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 gagacctgctgctcgaa 101
      |||
Db 54 gagacctgctgctcgaa 72
```

```
RESULT 28
US-09-442-366A-66
; Sequence 66A, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
```

```
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-66
```

```
Query Match          4.0%; Score 19; DB 5; Length 466;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 83 gagacctgctgctcgaa 101
      |||
Db 54 gagacctgctgctcgaa 72
```

```
RESULT 29
US-09-911-904-130
; Sequence 130, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-130
```

```
Query Match          4.0%; Score 19; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 209 tgaagtgtgctgctcga 227
      |||
Db 127 tgaagtgtgctgctcga 145
```

```
RESULT 30
US-10-106-698-2068/c
; Sequence 2068, Application US/1010698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2068
```

LENGTH: 1063  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-106-698-2068

Query Match 4.0%; Score 19; DB 6; Length 1063;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 tgaagatctgtgacttgg 146  
|||||  
DB 454 TCACATCTGTGACTTTCG 436

RESULT 31  
US-09-937-060A-17  
Sequence 17, Application US/09937060A  
GENERAL INFORMATION:  
APPLICANT: INCYTE PHARMACEUTICALS, INC.  
APPLICANT: BANDMAN, Olga  
APPLICANT: TANG, Y. Tom  
APPLICANT: YUE, Henry  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: AZIMZAI, Yaida  
APPLICANT: LU, Dyung Alina M.  
TITLE OF INVENTION: REGULATORS OF INTRACELLULAR PHOSPHORYLATION  
FILE REFERENCE: PF-0683 PCT  
CURRENT APPLICATION NUMBER: US/09/937,060A  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188  
PRIOR FILING DATE: 1999-03-18; 1999-05-20; 1999-07-09  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PERL Program  
SEQ ID NO 17  
LENGTH: 1706  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: 1425842CB1  
US-09-937-060A-17

Query Match 4.0%; Score 19; DB 5; Length 1706;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 tgaagatctgtgacttgg 146  
|||||  
DB 577 tgaagatctgtgacttgg 595

RESULT 32  
US-10-104-047-1465  
Sequence 1465, Application US/10104047  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: NOVEL full length cDNA  
FILE REFERENCE: H1-A0105  
CURRENT APPLICATION NUMBER: US/10/104,047  
CURRENT FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE:  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1465  
LENGTH: 1939  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-104-047-1465

Query Match 4.0%; Score 19; DB 6; Length 1939;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 gtggccagaggatggagt 55  
|||||  
DB 1014 gtggccagaggatggagt 1032

RESULT 33  
US-10-027-632-97991  
Sequence 97991, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/198,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97991  
LENGTH: 1948  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-97991

Query Match 4.0%; Score 19; DB 6; Length 1948;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 acatctacaagaccctga 176  
|||||  
DB 958 acatctacaagaccctga 976

RESULT 34  
US-10-027-632-97992  
Sequence 97992, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23

```

: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 97992
: LENGTH: 1948
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-97992
```

```

Query Match          4.0%; Score 19; DB 6; Length 1948;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 158 acatctacaagaccctga 176
    |||||||
Db 958 acatctacaagaccctga 976
```

```

RESULT 35
US-09-053-375B-907/c
: Sequence 907, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 907
: LENGTH: 2344
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-053-375B-907
```

```

Query Match          4.0%; Score 19; DB 5; Length 2344;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 380 gggcccgagcgtgcgcac 398
    |||||||
Db 1579 GGGCCCCGAGCTGCCAC 1561
```

```

RESULT 36
US-09-053-375B-1006
: Sequence 1006, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1006
: LENGTH: 2526
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-053-375B-1006
```

```

Query Match          4.0%; Score 19; DB 5; Length 2526;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 209 tgaagtgatgccccctga 227
    |||||||
Db 2048 tgaagtgatgccccctga 2066
```

```

RESULT 37
US-09-053-375B-57
: Sequence 57, Application US/09053375B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Bibilashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 57
: LENGTH: 3949
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-053-375B-57
```

```

Query Match          4.0%; Score 19; DB 5; Length 3949;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 83 ggaacctgctgctcgaa 101
    |||||||
Db 2185 ggaacctgctgctcgaa 2203
```

```

RESULT 38
US-09-442-384B-773
: Sequence 773, Application US/09442384B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Lukashov, Matvey
: TITLE OF INVENTION: Hematology/Immunology Array
: FILE REFERENCE: CLON-006CIP15
: CURRENT APPLICATION NUMBER: US/09/442,384B
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053,375
: PRIOR FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 830
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 773
: LENGTH: 3949
: TYPE: DNA
: ORGANISM: homo sapiens
US-09-442-384B-773
```

```

Query Match          4.0%; Score 19; DB 5; Length 3949;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 83 ggaacctgctgctcgaa 101
    |||||||
Db 2185 ggaacctgctgctcgaa 2203
```

```

RESULT 39
US-09-721-544-12422/c
: Sequence 12422, Application US/09721544
: GENERAL INFORMATION:
: APPLICANT: Arterburn, Matthew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Simin
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
```

```

: APPLICANT: Engleman, Carrie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Garcia, Veronica
: APPLICANT: Giedt, Gretchen
: APPLICANT: Hunter, Kelly
: APPLICANT: Jones, Aaron
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroya, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nguyen, Phuong
: APPLICANT: Mogra, Margie
: APPLICANT: Palencia, Servando
: APPLICANT: Ralsi, Fariba
: APPLICANT: Smith, Benjamin
: APPLICANT: Tkach, Joe
: APPLICANT: Tran, Lien
: APPLICANT: Verna, Ron
: APPLICANT: Yang, Pei
: APPLICANT: Yim, Kenneth
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
: FILE REFERENCE: 728C1P
: CURRENT APPLICATION NUMBER: US/09/721,544
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 09/515,128
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: 09/034,341
: PRIOR FILING DATE: 1998-02-13
: NUMBER OF SEQ ID NOS: 24489
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 12422
: LENGTH: 340
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-721-544-12422

Query Match          3.8%; Score 18; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8  tgaagaatctgtctgtct 25
      |||
Db 288 TCGAAGATCTTGTCTGCT 271

RESULT 40
: US-10-121-925-5
: Sequence 5, Application US/10121925
: GENERAL INFORMATION:
: APPLICANT: ROBINSON, KEITH E.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
: TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
: FILE REFERENCE: MNI-090
: CURRENT APPLICATION NUMBER: US/10/121,925
: CURRENT FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US/09/948,802
: PRIOR FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: 09/387,212
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: All occurrences of n indicate any nucleotide
: US-10-121-925-5
```

```

Query Match          3.8%; Score 18; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 gacctgctgcgcgaac 102
      |||
Db 244 gacctgctgcgcgaac 261

RESULT 41
: US-10-121-995-5
: Sequence 5, Application US/10121995
: GENERAL INFORMATION:
: APPLICANT: ROBINSON, KEITH E.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
: TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
: FILE REFERENCE: MNI-090
: CURRENT APPLICATION NUMBER: US/10/121,995
: CURRENT FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US/09/948,802
: PRIOR FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: 09/387,212
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: All occurrences of n indicate any nucleotide
: US-10-121-995-5

Query Match          3.8%; Score 18; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 gacctgctgcgcgaac 102
      |||
Db 244 gacctgctgcgcgaac 261

RESULT 42
: US-09-918-995-1503
: Sequence 1503, Application US/09918995
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1503
: LENGTH: 449
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(449)
: OTHER INFORMATION: n = A,T,C or G
: US-09-918-995-1503

Query Match          3.8%; Score 18; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 gacctgctgcgcgaac 102
```

Db 250 gaccgtgctgcgcgcgcac 267  
|||||

RESULT 43  
US-09-918-995-31621  
: Sequence 31621, Application US/09918995  
: GENERAL INFORMATION:  
: APPLICANT: Hyseq, Inc.  
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
: FILE REFERENCE: 20411-756  
: CURRENT APPLICATION NUMBER: US/09/918,995  
: PRIOR FILING DATE: 2001-07-30  
: PRIOR APPLICATION NUMBER: US/09/235,076  
: NUMBER OF SEQ ID NOS: 38054  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 31621  
: LENGTH: 489  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc-feature  
: LOCATION: (1)..(489)  
: OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-31621

Query Match  
Best Local Similarity 3.8%; Score 18; DB 5; Length 489;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 262 gacgtgctgcgcgcgcgcac 279  
|||||

Db 463 gacgtgctgcgcgcgcgcac 480  
|||||

RESULT 44  
US-10-027-632-15007  
: Sequence 15007, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30  
: PRIOR APPLICATION NUMBER: US 60/218,006  
: PRIOR FILING DATE: 2000-07-12  
: PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: US 60/193,483  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: US 60/185,218  
: PRIOR FILING DATE: 2000-02-24  
: PRIOR APPLICATION NUMBER: US 60/167,363  
: PRIOR FILING DATE: 1999-11-23  
: PRIOR APPLICATION NUMBER: US 60/156,358  
: PRIOR FILING DATE: 1999-09-28  
: PRIOR APPLICATION NUMBER: US 60/146,002  
: PRIOR FILING DATE: 1999-08-09  
: NUMBER OF SEQ ID NOS: 325720  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 15007  
: LENGTH: 738  
: TYPE: DNA  
: ORGANISM: Human  
US-10-027-632-15007

Query Match 3.8%; Score 18; DB 6; Length 738;  
Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 23 gctacagcttcacagtg 40  
|||||

Db 460 gctacagcttcacagtg 477  
|||||

RESULT 45  
US-10-027-632-15008  
: Sequence 15008, Application US/10027632  
: GENERAL INFORMATION:  
: APPLICANT: Wang, David G.  
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
: FILE REFERENCE: 108827.129  
: CURRENT APPLICATION NUMBER: US/10/027,632  
: PRIOR FILING DATE: 2002-04-30  
: PRIOR APPLICATION NUMBER: US 60/218,006  
: PRIOR FILING DATE: 2000-07-12  
: PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: US 60/193,483  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: US 60/185,218  
: PRIOR FILING DATE: 2000-02-24  
: PRIOR APPLICATION NUMBER: US 60/167,363  
: PRIOR FILING DATE: 1999-11-23  
: PRIOR APPLICATION NUMBER: US 60/156,358  
: PRIOR FILING DATE: 1999-09-28  
: PRIOR APPLICATION NUMBER: US 60/146,002  
: PRIOR FILING DATE: 1999-08-09  
: NUMBER OF SEQ ID NOS: 325720  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 15008  
: LENGTH: 738  
: TYPE: DNA  
: ORGANISM: Human  
US-10-027-632-15008

Query Match 3.8%; Score 18; DB 6; Length 738;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 23 gctacagcttcacagtg 40  
|||||

Db 460 gctacagcttcacagtg 477  
|||||

Search completed: July 16, 2002, 02:56:59  
Job time: 24557 sec



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GenCore version 4.5  
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UM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:49:56 ; Search time 12941.8 Seconds  
(without alignments)  
787.375 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514  
471

Perfect score: 1 ctgacctggaagatctgt.....gacctgacctctgagagcgc 471

Sequence: OLIGO\_NUC  
Gap 60.0 , Gapext 60.0

Scoring table: 21979536 seqs, 10817449327 residues

Searched: Word size : 0  
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending-Patents\_NA\_Main:\*

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4: /cgn2\_6/ptodata/2/pna/US09.COMB.seq:\*  
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63: /cgn2\_6/ptodata/2/pna/US6024.COMB.seq:\*  
64: /cgn2\_6/ptodata/2/pna/US6025.COMB.seq:\*  
65: /cgn2\_6/ptodata/2/pna/US6026.COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471	100.0	4111	1 PCT-US99-06133-1	Sequence 1, Appl1
2	471	100.0	4111	17 US-09-375-248-1	Sequence 1, Appl1
3	471	100.0	4195	3 US-07-959-951A-1	Sequence 1, Appl1
4	471	100.0	4195	6 US-08-257-754-1	Sequence 1, Appl1
5	471	100.0	4195	15 US-09-169-079-1	Sequence 36, Appl1
6	471	100.0	4416	10 US-08-601-132-36	Sequence 36, Appl1
7	471	100.0	4416	10 US-08-671-573A-36	Sequence 36, Appl1
8	471	100.0	4416	17 US-09-355-700-1	Sequence 1035, Ap
9	471	100.0	4416	18 US-09-440-302A-1035	Sequence 447, App
10	471	100.0	4416	18 US-09-442-384A-447	Sequence 636, App
11	471	100.0	4416	20 US-09-442-589B-636	Sequence 1, Appl1
12	471	100.0	4416	18 US-09-534-376A-1	Sequence 36, Appl1
13	471	100.0	4416	24 US-09-631-092-36	Sequence 36, Appl1
14	471	100.0	4425	8 US-08-446-648-31	Sequence 31, Appl1
15	471	100.0	4425	11 US-08-770-449-31	Sequence 889, App
16	471	100.0	4425	14 US-09-023-655-889	Sequence 31, Appl1
17	471	100.0	4425	36 US-09-982-610-31	Sequence 101, App
18	471	100.0	4425	36 US-09-982-610-31	Sequence 15763, A
19	471	100.0	4425	55 US-60-167-943-103	Sequence 3, Appl1
20	471	100.0	4425	55 US-60-172-373-15763	Sequence 3, Appl1
21	471	100.0	4795	3 US-07-959-951A-3	Sequence 3, Appl1
22	471	100.0	4795	6 US-08-257-754-3	Sequence 3, Appl1
23	471	100.0	4795	15 US-09-169-079-3	Sequence 45, Appl1
24	471	100.0	9108	8 US-08-446-648-45	Sequence 455, App
25	471	100.0	9108	36 US-09-209-009-455	Sequence 951, App
26	420	89.2	3277	59 US-60-213-360-951	Sequence 4300, Ap
27	420	89.2	3277	71 US-60-324-185-4300	Sequence 4274, Ap
28	420	89.2	4459	71 US-60-324-185-4274	Sequence 19, Appl
29	420	89.2	6826	6 US-08-256-769B-19	Sequence 17, Appl
30	420	89.2	6827	8 US-08-446-648-17	
31	420	89.2			

C	32	420	89.2	6827	11	US-08-770-449-17	Sequence 17, Appl
C	33	420	89.12	6827	36	US-09-982-610-17	Sequence 17, Appl
	34	401	85.1	415	60	US-60-213-178-1247	Sequence 1247, Appl
	35	105	64.8	4133	37	US-10-081-126-1	Sequence 1, Appl
	36	105	64.8	4450	1	PCT-US99-08079-1	Sequence 1, Appl
	37	105	64.8	4450	1	PCT-US99-08079-1	Sequence 1, Appl
	38	189	40.1	4450	37	US-10-012-214-1	Sequence 1, Appl
	39	189	40.1	4450	28	US-09-710-286-674	Sequence 674, Appl
	40	183	38.9	535	28	US-09-710-286-6884	Sequence 2884, Appl
C	41	126	26.8	1077	60	US-09-716-953-1245	Sequence 1245, Appl
C	42	126	26.8	1077	60	US-60-213-178-4	Sequence 1824, Appl
C	43	126	26.8	1077	60	US-60-170-574-1824	Sequence 4, Appl
C	44	125	26.5	496	60	US-60-213-178-929	Sequence 297, Appl
C	45	113	24.0	516	60	US-60-213-178-954	Sequence 954, Appl
						US-60-178-305-929	Sequence 929, Appl

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RESULT 3
US-07-959-951A-1
: Sequence 1, Application US/0795951A
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/959,951A
: FILING DATE: 19921009
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Gruber, Lewis S.
: REGISTRATION NUMBER: 30,060
: REFERENCE/DOCKET NUMBER: 28113/31104
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-07-959-951A-1

Query Match 100.0%; Score 471; DB 3; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgaccatggaagatctgtctgctacagctcccaagtgccagaggaatgagttctctg 60
|||||
DB 3044 CTGACCATGGAAGATCTTGTCTCTACAGCTTCACAGTGCACAGAGGATGAGTCTCTG 3103

OY 61 gcttccgaagaagtgatccacagaagactgctgctcgtggaacattctgctggaagc 120
|||||
DB 3104 GCTTCCGAAAGTGACATCCACAGAGACTGCTGCTCGAAGCATTTCTGCTGCGAAGC 3163

OY 121 gacgtggaagaatctgagcttgacctgcccggagacattcaacaagacctgactac 180
|||||
DB 3164 GACGTGCTGAAGATCTGTGACTTTGGCTTGCCTTCCCTCTCTCTGCGAGATCTTTC 3223

OY 181 gtccgaagagcagtgcccgactgcccctgaaatggaatggcccttgaagacattctcga 240
|||||
DB 3224 GTCCGCAAGGAGAGTGGCCCGCTGCCCTGAAGTGATGGCCCTGAAGACATCTTTCGAC 3283

OY 241 aaggtgtacacacagcagagtgacgtgtgtgtcccttggagtgctctctctggaagcttc 300
|||||
DB 3284 AAGGTGTACACACAGCAGAGTGAAGTGTGTGTCTTGGGGTCTCTCTGCGAGATCTTTC 3243

OY 301 tctctggagagccctcccgctacctgaggtgacagatcaatgaagagttcttgcagcgagctg 360
|||||
DB 3344 TCTCTGGGAGCTTCCCGTACCTCTGGGGTGCAGATCAATGAGAGTTCTGCGAGGCTG 3403
```

```
OY 361 agagacgcacaaagatgaagggcccgagacttgaccactccgcacataccgcatcatg 420
|||||
DB 3404 AGAGACGCACAAAGATGAGGGCCCGAGCTGGCCACTCCGCCCATACGCCGATCATG 3463

OY 421 ctgaactgtgtctcggagaccccaagcgagacattctcggagctg 471
|||||
DB 3464 CTGAAGTGTGTGTCTCGAGACCCCAAGGCGAGACCTGATCTCGAGGCTG 3514

RESULT 4
US-08-257-754-1
: Sequence 1, Application US/08257754
: GENERAL INFORMATION:
: APPLICANT: Alltalo, Karl
: APPLICANT: Kaipainen, Arja
: APPLICANT: Korhonen, Jaana
: APPLICANT: Mustonen, Tuija
: APPLICANT: Pajusola, Karl
: APPLICANT: Matikainen, Marja-Terttu
: APPLICANT: Karmani, Paivi
: TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/257,754
: FILING DATE: 09-JUN-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28344/32133
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-08-257-754-1

Query Match 100.0%; Score 471; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgaccatggaagatctgtctgctacagctcccaagtgccagaggaatgagttctctg 60
|||||
DB 3044 CTGACCATGGAAGATCTTGTCTCTACAGCTTCACAGTGCACAGGATGAGTCTCTG 3103

OY 61 gcttccgaagaatgacacagaagactgctgctcgtggaacattctgctggaagc 120
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```
Db 3104 GCTTCCGGAAGTGCATCCACAGAGACTTGCTGCTCGAAGATTCCTGCTCGAAGAC 3163
OY 121 gacgtgtgaagatctgtgaacttggccttgcgcggagacatctcaagaagccctgaac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTGGCCGGACATCTACAAAGACCTGACTAC 3223
OY 181 gtcgcgaagggacgtgcgcgcgtgcgcgcctgaagtgagatggccctcaaaacatcttcagc 240
Db 3224 GTCGCCAAGGCGCAGTCCCGGCTGCCCTGAATGATGGCCCTTAAAGCATCTTTCGAC 3283
OY 241 aaggtttacaccacgcagagtgacgtgtgttccttgggggtccttcctcgtggagatcttc 300
Db 3284 AAGGTTTAACACCGACGAGTACGTGTGCTTGGGGGTCTTCTTGAGGATCTTC 3343
OY 301 tctctgggggctccctccgtacccctgggtgcagatcaatgaagagttctgcgcagcgctg 360
Db 3344 TCTCTGGGGGCTCCCTCCGTACCTTGAGGTGACAGATCAATGAAGAGATTCTGCCAGCGCTG 3403
OY 361 agagacgcacaaagatgaaggagcccgagcgtgcacatcccgccatagcgccatcatg 420
Db 3404 AGAGACGCGACAAAGATGAGGCGCCCGGAGCTGGCCACTCCGCCATACGCCCATCATG 3463
OY 421 ctgaactgtgtgtccggagaccaccaagcgagacatctgcagactg 471
Db 3464 CTGAACGTGCTGTGCTCGGAGACCCCAAGCGAGACCTGCTGCTCGAGACTG 3514
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RESULT 5  
US-09-169-079-1

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Sequence 1, Application US/09169079
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Kalpalen, Arja
APPLICANT: Valtoia, Reija
APPLICANT: Jussila, Lotta
TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
FILE REFERENCE: 28113/34891
CURRENT APPLICATION NUMBER: US/09/169,079
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: 08/901,710
EARLIER FILING DATE: 1997-07-28
EARLIER APPLICATION NUMBER: 08/340,011
EARLIER FILING DATE: 1994-11-14
EARLIER APPLICATION NUMBER: 08/257,754
EARLIER FILING DATE: 1994-07-09
EARLIER APPLICATION NUMBER: 07/959,951
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4195
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (20)..(3913)
US-09-169-079-1
```

Query Match 100.0%; Score 471; DB 15; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ctgaccatggaagatctgtctgtctacagcttcaggctggccaggaagatgagttccctg 60
Db 3044 ctgaccatggaagatctgtctgtctacagcttcaggctggccaggaagatgagttccctg 3103
OY 61 gcttcccgaaagtgcattccacagagacctgtgctccggaacatctgtctgcggaagc 120
Db 3104 gcttcccgaaagtgcattccacagagacctgtgctccggaacatctgtctgcggaagc 3163
OY 121 gacgtgtgaagatctgtgaacttggccttgcgcggagacatctcaagaagccctgaactac 180
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```
Db 3164 gacgtgtgaagatctgtgaacttggccttgcgcggagacatctcaagaagccctgaactac 3223
OY 181 gtcgcgaagggacgtgcgcgcgtgcgcgcctgaagtgagatggccctcaaaacatcttcagc 240
Db 3224 gtcgcgaagggacgtgcgcgcgtgcgcgcctgaagtgagatggccctcaaaacatcttcagc 3283
OY 241 aaggtttacaccacgcagagtgacgtgtgttccttgggggtccttcctcgtggagatcttc 300
Db 3284 aaggtttacaccacgcagagtgacgtgtgttccttgggggtccttcctcgtggagatcttc 3343
OY 301 tctctgggggctccctccgtacccctgggtgcagatcaatgaagagttctgcgcagcgctg 360
Db 3344 TCTCTGGGGGCTCCCTCCGTACCTTGAGGTGACAGATCAATGAAGAGATTCTGCCAGCGCTG 3403
OY 361 agagacgcacaaagatgaaggagcccgagcgtgcacatcccgccatagcgccatcatg 420
Db 3404 agagacgcacaaagatgaaggagcccgagcgtgcacatcccgccatagcgccatcatg 3463
OY 421 ctgaactgtgtgtccggagaccaccaagcgagacatctgcagactg 471
Db 3464 CTGAACGTGCTGTGCTCGGAGACCCCAAGCGAGACCTGCTGCTCGAGACTG 3514
```

RESULT 6  
US-08-601-132-36

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Sequence 36, Application US/08601132
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,132
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET INFORMATION: 28113/33118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-601-132-36
```

Query Match 100.0%; Score 471; DB 10; Length 4416;  
Best Local Similarity 100.0%; Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgaccatggaagatctgtctgtctacagcttcaggctggccaggaagatgagttccctg 60
Db 3044 CTGACCATGGAAGATCTGTGCTGCTACAGCTTCCAGGTCGCCAGAGGATGAGTCTCTG 3103
```

OY	61	gctcccggaagctgcatcccaagaagaccgctgcctcgaacaatctctgctgcggaagc	120
Db	3104	gctttccccaaggtcattccACAGAGACcttgctgcgAACATTctgctgcgAAAC	3163
OY	121	gaagctggaagactctgacttgacttgacctgcgcgagacatcaagaagaaccttactac	180
Db	3164	GACGtGGtGAAGAtCTGTGAtCTTGGCTTGGCCGGACATTCAAAACACCTGTGACTAC	3222
OY	181	gtccgcaaggcagctgcccgactgcctccctgaaatgtaatggcccttgaaagacatcttcgac	240
Db	3224	gtccCAAGGcCACTGCCCGGCTCCCTCAATGGATGGCCCTGAAGCAATCTTCAC	3283
OY	241	aagctgtaaccacgaagagatgaaagcttgatctcttgagggtctctctcggagaacttc	300
Db	3284	AAGGtTtACACACACCGAGtGAAGctGTGGtCTCTTGGGGTCTCTTCGGAGATCTTC	3343
OY	301	ctctctggggcctcccgtaaccctcgggtgtagatcaatgaagagtctctgcagagcgtc	360
Db	3344	TCTCTGGGGCCCTCCCGTACCCTCGGGGTCAATCAATGAGAGATTCTGCCAGCGGCTG	3403
OY	361	agaagacggcacaagaatgaaggcccggaagctgagcaatcccgcaatacgcgcatacga	420
Db	3404	AGAAcCGGCAACAAGGAtGAGAGGGCCCGGAGACtGGCACTCCGCAATAGCGCCATCATG	3463
OY	421	ctgaacatgcgtctcgcagagaccccaaggagagaaactgaaattcttgagctg	471
Db	3464	CTGAACtGtGtGTCCGAGACGCCCAAGGCGAGACCTGCATTCTGGAGACTG	3514

RESULT 7  
US-08-671-573A-36  
Sequence 36, Application US/08671573A  
GENERAL INFORMATION:  
APPLICANT: Allaio, Karl  
APPLICANT: Jourkov, Vladimir  
TITLE OF INVENTION: Receptor Ligand  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray  
STREET: 6300 Sears Tower, 233 South Wacker Dr  
City: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
Zip: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,573A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: ??-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28113/33348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 4416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-671-573A-36

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Query Match	100.0%	Score 471;	DB 10;	Length 4416;
Best Local Similarity	100.0%	Pred. No. 1.2e+239;		
Matches 471; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ctgacgatgaaagatctctgtctctcaagcttccaaagtgtgcagaagaaatgaaatctctcg	60
Db	3044	CTGACCATGGAAAGATCTTGTCTGCTAAGCTTCCAGGTGGCCAGAGGAGATGGAGTTCCCG	3103
QY	61	gctctccgaagaatgacatccacaagaagactgctgcctcgcagaacatctgctctgcgaagac	120
Db	3104	GCTTCCCGAAAGTGCAATCCACAGAGACCTGGCTGCGAACAATTGCTGTCCGAAAC	3165
QY	121	gaagtggtgaagatctgtgactttgaccttgccggagacatctacaagaaccctgactac	180
Db	3164	GACCTGTGTGAAGATCTGTGACTTTGGCTTTGCCCGGAGACATCTACAAAGACCTTGACTAC	3222
QY	181	gtccgaagaagcaatgtcccgctgcgccctgaagaatgaaatgacccctgaagaacatcttgac	240
Db	3224	GTCGCGAAGGGCACTGTGCCCGCTGCCCTTGAAATGGATGGCCCTTGAAGCAATTTTCGAC	3283
QY	241	aagatgtacacacacgaagatgaagctgtgagctcctttggtgtctctctcctggaagatcttc	300
Db	3284	AAGGTGTACACCAACGAGAGATGTAGCTGTGGTCTTTGGGGTCTTCTTGAGAGATCTTC	3344
QY	301	tctctgtaggaacccctcccgtaaccttgtaggtgtgcagatcaatgaaggaattctgcgaagcgtctg	360
Db	3344	TCTCTGGGGGCTCTCCCGTAACCTTGGGGGTGCAGATCAATGAAGAGATTCTGCCAGCGCTG	3403
QY	361	agagacgcgacaaagatlgagggcccccggagcttgcgaactctccgcacatacgcgcacatca	420
Db	3404	AGAGACGCGCACAAAGATGAGGGCCCGCGAGCTGTGCCACTCCCGCATATGCGCCGCAATCAT	3465
QY	421	ctgaactgtcgtgcggagagaccccaaggagaaactgcatcttcggaagctg 471	
Db	3464	CTGAACGTCTGCTCCGAGAACCCCAAGGGGAGAACCTGCATTTCTCGGACCTG 3514	

RESULT 8  
US-08-671-573B-36  
Sequence 36, Application US/08671573B  
GENERAL INFORMATION:  
APPLICANT: Alitelo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Receptor Ligand  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,573B  
FILING DATE: 28-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4416 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-671-573b-36

Query Match  
Best Local Similarity 100.0%; Score 471; DB 10; Length 4416;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgaccatgtaagaatctgtctgtctacagcttcacagtgccagagatgagttctc 60  
Db 3044 CTGACACATGCAAGATCTGTCTGTCTACAGCTTCACAGCGCCGACAGCATGATTCCTG 3103  
Oy 61 gctccgcaagaatgcatccacagagagactgctgtcggaaactctgtctcggaaagc 120  
Db 3104 GCTTCCGCAAGATGATTCACAGAGACCTGCTCGGAACATTCCTGTCTCGAAAGC 3163  
Oy 121 gaagtgtaagaatctgtacttgccttcgctccgagacatctacaagaccctgactac 180  
Db 3164 GACCTGTGAAGATCTGTGACTTTGGCTTGGCCGGGACATCTACAAAGACCTGACTAC 3223  
Oy 181 gtcgcaaggcgaatgcccggctgcccctgaagtgaatgagccctgaagcatcttcgac 240  
Db 3224 GTCCGCAAGGCGATGCGCCGCTGCCCTGAGTGAAGTGCCTCCGAAAGCATCTTCGAC 3283  
Oy 241 aaggtgtacacacagcagagatgacgtgtgtctcttgagtgctctctcgtggagatcttc 300  
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTTTGGGTCTTCTCTGGAGATCTTC 3343  
Oy 301 tctctgggggcccctcccgtaacctgggggtgacagatcaatgagagttcttcgacgagctg 360  
Db 3344 TCTCTGGGGCCCTCCCGTACCTGGGGGTGACATCAATGAGAGATTCTGCGACGGCTG 3403  
Oy 361 agagacgacacagagatgagggcccgagacttgccactccgcgaatgagcgcacatcatg 420  
Db 3404 AGAGACGCGCAAGATGAGGGCCCGGAGCTGCGCATTCGCCCATACGCCCATCATCATG 3463  
Oy 421 ctgaactgtgtctcggagagaccccaagcgagacactgcatcttcgagagctg 471  
Db 3464 CTGAACGTGTGCTCGGAGACCCCAAGCGAGACGTGCAATTCTCGAGAGCTG 3514

RESULT 9  
US-09-355-700-1  
Sequence 1, Application US/09355700

GENERAL INFORMATION:  
APPLICANT: Ludwig Institute for Cancer Research  
Helsinki University Licensing  
Aittalo, Kari(U.S. only)  
Joukov, Vladimir (U.S. only)  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/355,700  
FILING DATE: 05-Nov-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/795,430  
FILING DATE: 05-FEB-1997  
APPLICATION NUMBER: PCT/FT196/00427  
FILING DATE: 01-AUG-1996  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/34140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4416 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-355-700-1

Query Match  
Best Local Similarity 100.0%; Score 471; DB 17; Length 4416;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgaccatgtaagaatctgtctgtctacagcttcacagtgccagagatgagttctc 60  
Db 3044 CTGACACATGCAAGATCTGTCTGTCTACAGCTTCACAGCGCCGACAGCATGATTCCTG 3103  
Oy 61 gctccgcaagaatgcatccacagagagactggtctcggaaactctgtcggaaagc 120  
Db 3104 GCTTCCGCAAGATGATTCACAGAGACCTGCTGCTCGAAGATTCCTGTGGAAGAC 3163  
Oy 121 gaagtgtaagaatctgtacttgccttcgctccgagacatctacaagaccctgactac 180  
Db 3164 GACCTGTGAAGATCTGTGACTTTGGCTTGGCCGGGACATCTACAAAGACCTGACTAC 3223  
Oy 181 gtcgcaaggcgaatgcccggctgcccctgaagtgaatgagccctgaagcatcttcgac 240  
Db 3224 GTCCGCAAGGCGATGCGCCGCTGCCCTGAGTGAAGTGAAGCGCCCTGAAAGCATCTTCGAC 3283  
Oy 241 aaggtgtacacacagcagagatgacgtgtgtctcttgagtgctctcgtggagatcttc 300  
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTTTGGGTCTTCTCTGGAGATCTTC 3343  
Oy 301 tctctgggggcccctcccgtaacctgggggtgacagatcaatgagagttcttcgacgagctg 360

```
Db 3344 TCTCTGGGGCTCCCTCCCTGACCTGGGTGCAGATCAATGAGAGTTCGACGCGCTG 3403
OY 361 agagacgacacagatgagagggcccgagctgagccatcccgacatagccgacatcag 420
Db 3404 ACAGACGGCACAAGATGAGGGCCCCGGAGCTGGCCACTCCGCCCATACGGCATATCAG 3463
OY 421 ctgaactgctgctcggagagaccccaagcgagacatcctcggagctg 471
Db 3464 CTGAACCTGCTCGGAGACCCCAAGCGAGACCTGCATTCGAGACTG 3514
```

```
RESULT 10
US-09-440-302A-1035
; Sequence 1035, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey E.
; FILE REFERENCE: Human Neurobiology Array
; CURRENT APPLICATION NUMBER: US/09/440.302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053.375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1035
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-440-302A-1035
```

Query Match Best Local Similarity 100.0%; Score 471; DB 18; Length 4416;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgaccatgagaatctctgtctacagcttcagatgacagagagatgagctctg 60
Db 3044 ctgaccatgagaatctctgtctacagcttcagatgacagagagatgagctctg 3103
OY 61 gctccggaagtgatcctccacagagacctgctcggaacatctgctcggaagc 120
Db 3104 gctccggaagtgatcctccacagagacctgctcggaacatctgctcggaagc 3163
OY 121 gacgtgtagaagatctgacttgccttcgcccggagacatctacaaagacctgactac 180
Db 3164 gacgtgtagaagatctgacttgccttcgcccggagacatctacaaagacctgactac 3223
OY 181 gtcgcaagggcagtgcccgagctgcccctgaagtgaatggccccctgaagacatctcgac 240
Db 3224 gtcgcaagggcagtgcccgagctgcccctgaagtgaatggccccctgaagacatctcgac 3283
OY 241 aaggtgacacacagagatgacgtggtctcttgagggtctctctcctgagagatctc 300
Db 3284 aaggtgacacacagagatgacgtggtctcttgagggtctctctcctgagagatctc 3343
OY 301 tctctgggggctcccccgtacccctgggggtgacagatcaatgaagagatctcgcagcgctg 360
Db 3344 tctctgggggctcccccgtacccctgggggtgacagatcaatgaagagatctcgcagcgctg 3403
OY 361 agagacgacacagatgagagggcccgagacctgacacatccgcacatagccgacatcag 420
Db 3404 agagacgacacagatgagagggcccgagacctgacacatccgcacatagccgacatcag 3463
OY 421 ctgaactgctgctcggagagaccccaagcgagacatctcggagctg 471
Db 3464 ctgaactgctgctcggagagaccccaagcgagacatctcggagctg 3514
```

```
RESULT 11
US-09-442-384A-447
; Sequence 447, Application US/09442384A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; FILE REFERENCE: Hematology/Immunology Array
; CURRENT APPLICATION NUMBER: US/09/442.384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053.375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-384A-447
```

Query Match Best Local Similarity 100.0%; Score 471; DB 18; Length 4416;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgaccatgagaatctctgtctacagcttcagatgacagagagatgagctctg 60
Db 3044 ctgaccatgagaatctctgtctacagcttcagatgacagagagatgagctctg 3103
OY 61 gctccggaagtgatcctccacagagacctgctcggaacatctgctcggaagc 120
Db 3104 gctccggaagtgatcctccacagagacctgctcggaacatctgctcggaagc 3163
OY 121 gacgtgtagaagatctgacttgccttcgcccggagacatctacaaagacctgactac 180
Db 3164 gacgtgtagaagatctgacttgccttcgcccggagacatctacaaagacctgactac 3223
OY 181 gtcgcaagggcagtgcccgagctgcccctgaagtgaatggccccctgaagacatctcgac 240
Db 3224 gtcgcaagggcagtgcccgagctgcccctgaagtgaatggccccctgaagacatctcgac 3283
OY 241 aaggtgacacacagagatgacgtggtctcttgagggtctctctcctgagagatctc 300
Db 3284 aaggtgacacacagagatgacgtggtctcttgagggtctctctcctgagagatctc 3343
OY 301 tctctgggggctcccccgtacccctgggggtgacagatcaatgaagagatctcgcagcgctg 360
Db 3344 tctctgggggctcccccgtacccctgggggtgacagatcaatgaagagatctcgcagcgctg 3403
OY 361 agagacgacacagatgagagggcccgagacctgacacatccgcacatagccgacatcag 420
Db 3404 agagacgacacagatgagagggcccgagacctgacacatccgcacatagccgacatcag 3463
OY 421 ctgaactgctgctcggagagaccccaagcgagacatctcggagctg 471
Db 3464 ctgaactgctgctcggagagaccccaagcgagacatctcggagctg 3514
```

```
RESULT 12
US-09-442-589B-636
; Sequence 636, Application US/09442589B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; FILE REFERENCE: Human Cardiovascular Array
```



RESULT 13  
 US-09-534-376A-1  
 : Sequence 1, Application US/09534376A  
 : GENERAL INFORMATION:  
 : APPLICANT: Aitalo, Karl  
 : TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
 : TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF  
 : FILE REFERENCE: 28967/24140A  
 : CURRENT APPLICATION NUMBER: US/09/534, 376A  
 : CURRENT FILING DATE: 2000-03-24  
 : PRIOR APPLICATION NUMBER: 09/355,700

OY	1	ctgacacatggaagatcctgtctgctacagcttccaaagtggccaaagagatggaatctctg	60
Db	3044	ctgacacatggaagatcctgtctgctacaaagcttccaaagtggccaaagagatggaatctctg	3103
OY	61	gcttccccaagtgatccacagaagacctgagctcgcagacacatctgtctgtccgaaagc	120
Db	3104	gcttccccaagtgatccacagaagacctgagctcgcagacacatctgtctgtcggaaagc	3163
OY	121	gaacgtgtgaatatctgtgatttgacctggacctggccggagacatctacaagaacctgtacct	180
Db	3164	gaacgtgtgaaatatctgtgatttgacctggacctggccggagacatctacaagaacctgtacct	3223
OY	181	gtccgcaaaaggacgtccggctgtccctctgaagtgaatggccccgtgaagaagatctctgac	240
Db	3224	gtccgcaaaaggacgtccggctgtccctctgaagtgaatggccccgtgaagaagatctctgac	3283
OY	241	aaggtgtacacacaaagcagatgacatgctgtgctcttgggtgctctctctggaagatcttc	300
Db	3284	aaggtgtacacacaaagcagatgacatgctgtgctcttgggtgctctctctggaagatcttc	3343
OY	301	tctctgggggctccctccgctacccctgggggtgacagatcaatgaagagattcttggccaaagctg	360
Db	3344	tctctgggggctccctccgctacccctgggggtgacagatcaatgaagagattcttggccaaagctg	3403
OY	361	agagacggcacaagaagatgataggggcccggagactggccactcccgccatatagcgcgcatcatg	420
Db	3404	agagacggcacaagaagatgataggggcccggagactggccactcccgccatatagcgcgcatcatg	3463
OY	421	ctggaactgtgctgtccggagagcccccaaggagagaaaccttgatctctggagctg	471
Db	3464	ctggaactgtgctgtccggagagcccccaaggagagaaaccttgatctctggagctg	3514

RESULT 14  
 US-09-631-0992-36  
 : Sequence 36, Application US/09631092  
 : GENERAL INFORMATION:  
 : APPLICANT: Alltalo, Karl  
 : Jukov, Vladimir  
 : TITLE OF INVENTION: Receptor Ligand



Db 3235 GTCCCGACAGCGCAGTCCCGCGCTGCCCTGAAGTGGATGCGCCCGCAAGCATCTTCGAC 3294  
QY 241 aaggtgtacacacagagatgactgtgtgttccttgggggtgtctcttggagacatcttc 300  
Db 3295 AAGGTTACACACGACAGTACGTGTCTTGGCGTCTCTCGGAGATCTTC 3354  
QY 301 tctctgggggactcccgtaacctgtgggtgacatcaatgaaggaattctgtcagcgctg 360  
Db 3355 TCTCTGGGGCGCTCCCGCTACCTGGGTGCGATGAGAGATTCTGCGACGCGCTG 3414  
QY 361 aagagagagacaaagatgtaggggcccggagctgtgacctccgcacatacgccgacatg 420  
Db 3415 AGAGACGGCACAAAGATAGGGCCCGGAGCTGCGCACTCCCGCATACGCCGATCATG 3474  
QY 421 ctgaactgtgtctccggagaccacaaaggcgagactgtatcttggagctg 471  
Db 3475 CTGAAGTGTGCTCGGAGACCCCAAGCGGAGACCTGCATTCTCGAGCTG 3525

## RESULT 16

US-08-770-449-31

Sequence 31, Application US/08770449

GENERAL INFORMATION:

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David

APPLICANT: Lee, James M.

APPLICANT: Matthews, William

APPLICANT: Tsai, Shao Ping

APPLICANT: Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Francisco Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Minipatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,449

FILING DATE: 20-Dec-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00586

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/826935

FILING DATE: 22-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0821P201

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 910/371-7168

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 4425 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-770-449-31

Query Match 100.0% Score 471: DB 11: Length 4425:  
Best Local Similarity 100.0%: Pred. No. 1.2e-239:  
Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgaacatggaagatctgtctgtacaaagcttcacaggtgagcagaagatgagtcctg 60  
Db 305 CTGACCATGGAAGATCTTCTCTACAGCTTCAGGTGCGCAGAGGATGAGTCTCTG 3114  
QY 61 gctccgaagatgacatccacagaagacctgctgtctcggaacatctgtctggaagc 120  
Db 3115 GCTTCCCGAAGTGCATCCACAGACAGCTGTGCTCGGACATTCTGTCGGAAGC 3174  
QY 121 gacgtgtgaagatctgtgacttgccttgcgcggagacatcaaaagaccctgacac 180  
Db 3175 GACGTGTGAAGATCTGTGACTTTGGCCTTGCCGGGACATCTACAAAGACCTGACTAC 3234  
QY 181 gtccgaagagcagatgacccggtcgcctgaagtgtatgtgcccctgaagacatctcgac 240  
Db 3235 GTCCGCAAGGAGTGTGCCGCTGCCCTGAAGTGTGATGCGCCCTGAAGCATCTTCGAC 3294  
QY 241 aaggtgtacacacagcagaagatgacgtgtgttccttgggggtgtctcttggagacatctc 300  
Db 3295 AAGGTTACACACGACAGTACGTGTGTCTTGGGTGCTTCTCTCGGAGATCTTC 3354  
QY 301 tctctgggggacctcccgtaacctgtgggtgacatcaatgaaggaattctgtcagcgctg 360  
Db 3355 TCTCTGGGGCGCTCCCGCTACCTGGGTGCGATGAGAGATTCTGCGACGCGCTG 3414  
QY 361 aagagagagacaaagatgtaggggcccggagctgtgacctccgcacatacgccgacatg 420  
Db 3415 AGAGACGGCACAAAGATAGGGCCCGGAGCTGCGCACTCCCGCATACGCCGATCATG 3474  
QY 421 ctgaactgtgtctccggagaccacaaaggcgagactgtatcttggagctg 471  
Db 3475 CTGAAGTGTGCTCGGAGACCCCAAGCGGAGACCTGCATTCTCGAGCTG 3525

## RESULT 17

US-09-023-655-889

Sequence 889, Application US/09023655

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Sellhammer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 889:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1150990  
US-09-023-655-889

Query Match 100.0%; Score 471; DB 14; Length 4425;  
Best Local Similarity 100.0%; Pred. No. 1.2e-239;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgcgaagagatctgtctgtacagcttccaggtgcccgaagagatgagcttcctg 60  
DB 3055 CTGACCATGGAGATCTGTCTGTCTACAGCTTCACAGGTGGCCAGAGGATGAGTTCTTG 3114  
OY 61 gctccgaagatgcatccacagagacctgctcgcgaacattctgtctggaagc 120  
DB 3115 GCTTCCCGAAGTGCAATCCACAGACCTGGCTCTCGGACATTCTCTCGGAAAGC 3174  
OY 121 gaagtgatgaagatctgtgacttggccttgcccggagacatctacaagacctgactac 180  
DB 3175 GACGTGTGAAGATCTGTGACTTTGGCCCTTCCCGGACATCTCAAAAGACCTGACTAC 3234  
OY 181 gtccgaagagcagctgcccgcctggaagtgaatgagtgcccttgaaagatcttcgac 240  
DB 3235 CTCGCGCAAGGCACTGCCCGCTCTGAGAGTGGCCCTGAAAGCATCTTTCGAC 3294  
OY 241 aaggtgacacacacagcagatgacgtgltgctcttgagggtgctctctcgtggaatcttc 300  
DB 3295 AAGCTGTACACACAGCAGAGTGAAGTGTGCTTGGGGTGTCTCTGGAATCTTTC 3354  
OY 301 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagaagctctcgcagcgctg 360  
DB 3355 TCTCTGGGGGCTCCCGCTACCTGGGGTGTGAGATCAATGAGGATTTCTGCCACCGCTG 3414  
OY 361 agagacgagcacaagatgaaaggcccgagagctgagccatcccgacatagccgcatcatc 420  
DB 3415 AGAGACGCGCAAGAGATGAGGGCCCGGAGCTGGCCACTCCCGCATACCGCGCATATG 3474  
OY 421 ctgaactgctggtcggagagaccacaaggcgagacctgcatctctcgagctg 471  
DB 3475 CTGAACCTGTGTCTGGAGACCCCAAGCGAGACTGCTATTCTCGAGCTG 3525

RESULT 18  
US-09-982-610-31  
Sequence 31, Application US/09982610  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
Bennett, Brian D.  
Goeddel, David

Lee, James M.  
Matthews, William  
Tsai, Siao Ping  
Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,610  
FILING DATE: 17-Oct-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/446,648  
FILING DATE: 1996-MAY-23  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4425 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-982-610-31

Query Match 100.0%; Score 471; DB 36; Length 4425;  
Best Local Similarity 100.0%; Pred. No. 1.2e-239;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctaccatgtaaatctgtctgtctacagcttccaggtgcccgaagagatgagcttcctg 60  
DB 3055 CTGACCATGGAGATCTGTCTGTCTACAGCTTCACAGGTGGCCAGAGGATGAGTTCTTG 3114  
OY 61 gctccgaagatgcatccacagagacctgctcgcgaacattctgtctggaagc 120  
DB 3115 GCTTCCCGAAGTGCAATCCACAGACCTGGCTCTCGGACATTCTCTCGGAAAGC 3174  
OY 121 gaagtgatgaagatctgtgacttggccttgcccggagacatctacaagacctgactac 180  
DB 3175 GACGTGTGAAGATCTGTGACTTTGGCCCTTCCCGGACATCTCAAAAGACCTGACTAC 3234  
OY 181 gtccgaagagcagctgcccgcctggaagtgaatgagtgcccttgaaagatcttcgac 240  
DB 3235 CTCGCGCAAGGCACTGCCCGCTCTGAGAGTGGCCCTGAAAGCATCTTTCGAC 3294  
OY 241 aaggtgacacacacagcagatgacgtgltgctcttgagggtgctctcgtggaatcttc 300  
DB 3295 AAGCTGTACACACAGCAGAGTGAAGTGTGCTTGGGGTGTCTCTGGAATCTTTC 3354  
OY 301 tctctgggggctccctccgtacccctgggggtgcaagatcaatgagaagctctcgcagcgctg 360  
DB 3355 TCTCTGGGGGCTCCCGCTACCTGGGGTGTGAGATCAATGAGGATTTCTGCCACCGCTG 3414  
OY 361 agagacgagcacaagatgaaaggcccgagagctgagccatcccgacatagccgcatcatc 420  
DB 3415 AGAGACGCGCAAGAGATGAGGGCCCGGAGCTGGCCACTCCCGCATACCGCGCATATG 3474  
OY 421 ctgaactgctggtcggagagaccacaaggcgagacctgcatctctcgagctg 471  
DB 3475 CTGAACCTGTGTCTGGAGACCCCAAGCGGAGACTGCTATTCTCGAGCTG 3525

RESULT 19  
US-60-167-943-103  
Sequence 103, Application US/60167943  
GENERAL INFORMATION:  
APPLICANT: Hodgson, David M.  
Lincoln, Stephen E.  
Jones, Antsaa L.  
Yu, Jimmy Y.

```

: APPLICANT: Russo, Frank D.
: APPLICANT: Sapiro, Peter A.
: APPLICANT: Barville, Steve C.
: APPLICANT: Bratcher, Shawn R.
: APPLICANT: Dufour, Gerard E.
: APPLICANT: Cohen, Howard J.
: APPLICANT: Rosen, Bruce
: APPLICANT: Shah, Purvi
: APPLICANT: Chalup, Michael S.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: RECEPTOR MOLECULES
: FILE REFERENCE: PT-0093 P
: CURRENT APPLICATION NUMBER: US/60/167,943
: CURRENT FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 244
: SOFTWARE: PERL Program
: SEQ ID NO 103
: LENGTH: 4461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 902563.1
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-167-943-103
```

```

Query Match
Best Local Similarity 100.0%; Score 471; DB 55; Length 4461;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtacacgcttcacaggtggcgaagagatggagttccctg 60
Db 3056 ctgacatggaagatctgtctgtacacgcttcacaggtggcgaagagatggagttccctg 3115
Oy 61 gctcccgaaagtgcacacacagagaccctgctcgaacattctgtctcgaagc 120
Db 3116 gctcccgaaagtgcacacacagagaccctgctcgaacattctgtcgcgcggaagc 3175
Oy 121 gacgtggtgaagatctgtacttggcttcgctccggaacatctacaagaacctgtactc 180
Db 3176 gacgtggtgaagatctgtacttggcttcgctccggaacatctacaagaacctgtactc 3235
Oy 181 gtcgcaaggagcagtgccggtgcgccctgaagtgatggccctgaagacatcttcgac 240
Db 3236 gtcgcaaggagcagtgccggtgcgccctgaagtgatggccctgaagacatcttcgac 3295
Oy 241 aaggtgtacacacacgagatgacgtgtgtcttcttgggtgtcttctcgtggaatcttc 300
Db 3296 aaggtgtacacacacgagatgacgtgtgtcttcttgggtgtcttctcgtggaatcttc 3355
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagcttcgtccagcgctg 360
Db 3356 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagcttcgtccagcgctg 3415
Oy 361 agagacggcacaagatgaggggcccggagctgcacatcccgcatatgcgcgcatatg 420
Db 3416 agagacggcacaagatgaggggcccggagctgcacatcccgcatatgcgcgcatatg 3475
Oy 421 ctgaactgtctgctcggagaccccaaggcgaagctgtcatctcggagctg 471
Db 3476 ctgaactgtctgctcggagaccccaaggcgaagctgtcatctcggagctg 3526
```

```

RESULT 20
US-60-172-373-15763
: Sequence 15763, Application US/6017373
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
```

```

: APPLICANT: Died, Diah
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Poly
: CURRENT APPLICATION NUMBER: US/60/172,373
: CURRENT FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 25,772
: SOFTWARE: PERL Program
: SEQ ID NO 15763
: LENGTH: 4462
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 902563.2
: NAME/KEY: unsure
: LOCATION: 2402-2421, 2907, 3602
: OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15763
```

```

Query Match
Best Local Similarity 100.0%; Score 471; DB 56; Length 4462;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtacacgcttcacaggtggcgaagagatggagttccctg 60
Db 3058 ctgacatggaagatctgtctgtacacgcttcacaggtggcgaagagatggagttccctg 3117
Oy 61 gctcccgaaagtgcacacacagagaccctgctcgaacattctgtctcgaagc 120
Db 3118 gctcccgaaagtgcacacacagagaccctgctcgaacattctgtcgcgcggaagc 3177
Oy 121 gacgtggtgaagatctgtacttggcttcgctccggaacatctacaagaacctgtactc 180
Db 3178 gacgtggtgaagatctgtacttggcttcgctccggaacatctacaagaacctgtactc 3237
Oy 181 gtcgcaaggagcagtgccggtgcgccctgaagtgatggccctgaagacatcttcgac 240
Db 3238 gtcgcaaggagcagtgccggtgcgccctgaagtgatggccctgaagacatcttcgac 3297
Oy 241 aaggtgtacacacacgagatgacgtgtgtcttcttgggtgtcttctcgtggaatcttc 300
Db 3298 aaggtgtacacacacgagatgacgtgtgtcttcttgggtgtcttctcgtggaatcttc 3357
Oy 301 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagcttcgtccagcgctg 360
Db 3358 tctctgggggctccctccgtacccctgggtgtcagatcaatgaagagcttcgtccagcgctg 3417
Oy 361 agagacggcacaagatgaggggcccggagctgcacatcccgcatatgcgcgcatatg 420
Db 3418 agagacggcacaagatgaggggcccggagctgcacatcccgcatatgcgcgcatatg 3477
Oy 421 ctgaactgtctgctcggagaccccaaggcgaagctgtcatctcggagctg 471
Db 3478 ctgaactgtctgctcggagaccccaaggcgaagctgtcatctcggagctg 3528
```

```

RESULT 21
US-07-959-951A-3
: Sequence 3, Application US/0795951A
: GENERAL INFORMATION:
: APPLICANT: Alltato, Karl, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/959,951A
: FILING DATE: 19921009
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Gruber, Lewis S.
: REGISTRATION NUMBER: 30,060
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEEX: 25-3856
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4795 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..4111
:
: US-07-959-951A-3

```

Query Match 100.0%; Score 471; DB 3; Length 4795;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-239;  
 Matches 471: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ctgaccatgtaagatctgtctgtctacagcttcagatgagcagaaggaatgagctc 60
Db 3044 CTCACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCAGAGGAGTGTCTG 3103
OY 61 gctccccaagatgacacacagagacctgtctctggaacatctcgtctcggaaagc 120
Db 3104 GCTTCCCAAGATGCTATCCACAGAACCTGCTCTCGAATCTTCTCGAAGC 3163
OY 121 gaagtgtaagatctgtactgtgaccttgccggagacatctcaagaacctgactac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTCCGGGACATCTCAAGACCTTGACTAC 3223
OY 181 gtccgaagggcaatgcccgcctgagatgagatgagccctgaagatcttcac 240
Db 3224 GTCCGCAAGGGCAATGCCCCGCTTCCGTAAGTATGCCCCCTGAAGCATCTTCGAC 3283
OY 241 aaggtgtaaccacagatgagctgtgctccttgagggtgactctctcggagatcttc 300
Db 3284 AAGGTGTACACACGACGAGTGTGCTTGGGCTTGGGCTTCTCTCGACATCTTC 3343
OY 301 tctctggggacctcccgtaaccttgggtgagatcaatgagatctcgcgcgcgcgc 360
Db 3344 TCTCTGGGGCCCTCCCTGACCTGGGCTGACATCAATGAGAGTCTCTCGACGCGCTG 3403
OY 361 aaggaagggcagaaggaagggcccggaatctggcaatcccgcatcagcgcatatg 420
Db 3404 AGGAGCGGCAAGAGGAGAGGCGCCCGGAGCTGGCCACTCCCGCAATACCCCGATCATG 3463
OY 421 ctgaactgctgtcccgagagaccgaagcgagacctcattctcggagctc 471
Db 3464 CTGAAGTGTGTCTCGGAGACCCCAAGGCGACACCTGCAATCTCTCGAGACTG 3514

```

```

: APPLICANT: Korhonen, Jaana
: APPLICANT: Mustonen, Tuja
: APPLICANT: Pajusola, Karl
: APPLICANT: Mälikäinen, Marja-Terttu
: APPLICANT: Karjalainen, Paivi
: TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/257,754
: FILING DATE: 09-JUN-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28344/32133
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEEX: 25-3856
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4795 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..4111
:
: US-08-257-754-3

```

Query Match 100.0%; Score 471; DB 6; Length 4795;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-239;  
 Matches 471: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ctgaccatgtaagatctgtctgtctacagcttcagatgagcagaaggaatgagctc 60
Db 3044 CTCACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCAGAGGAGTGTCTG 3103
OY 61 gctccccaagatgacacacagagacctgtctctggaacatctcgtctcggaaagc 120
Db 3104 GCTTCCCAAGATGCTATCCACAGAACCTGCTCTCGAATCTTCTCGAAGC 3163
OY 121 gaagtgtaagatctgtactgtgaccttgccggagacatctcaagaacctgactac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTCCGGGACATCTCAAGACCTTGACTAC 3223
OY 181 gtccgaagggcaatgcccgcctgagatgagatgagccctgaagatcttcac 240
Db 3224 GTCCGCAAGGGCAATGCCCCGCTTCCGTAAGTATGCCCCCTGAAGCATCTTCGAC 3283
OY 241 aaggtgtaaccacagagatgagctgtgctccttgagggtgactctcgtggagatcttc 300
Db 3284 AAGGTGTACACACGACGAGTGTGCTTGGGCTTGGGCTTCTCTCGAGAGTCTTC 3343
OY 301 tctctggggacctcccgtaaccttgggtgagatcaatgagatctcgcgcgcgcgc 360

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Db 3344 TCTCTGGGGGCTCCCTGTAACCTGGGCTGCGATCAATGAGAGACTTCTGCCAGCGCTG 3403  
OY 361 agagagcgacaaagatgagggcccgagactggccactcccgcaatacagcagcatctg 420  
Db 3404 AGAGACGGCCACAAGATGAGGGCCCGGAGCTGGCAGCTCCGCCATACGCCCATCATC 3463  
OY 421 ctgaactgctgtctcgagagaccccaagcgagactgcatctcggagctg 471  
Db 3464 CTGAACTGCTGTCTCGAGAGACCCCAAGCGGAGAGACCTTCGAGACTG 3514

## RESULT 23

US-09-169-079-3  
Sequence 3, Application US/09169079  
GENERAL INFORMATION:  
APPLICANT: Alltalo, Karl  
APPLICANT: Kaipainen, Arja  
APPLICANT: Valtola, Reija  
APPLICANT: Jussila, Lotta  
TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera  
FILE REFERENCE: 28113/34891  
CURRENT FILING DATE: US/09/169, 079  
EARLIER FILING DATE: 1998-10-09  
EARLIER FILING DATE: 1997-07-28  
EARLIER FILING DATE: 1997-07-28  
EARLIER FILING DATE: 1997-07-28  
EARLIER FILING DATE: 1994-11-14  
EARLIER FILING DATE: 1994-11-14  
EARLIER FILING DATE: 1994-07-09  
EARLIER FILING DATE: 1994-07-09  
EARLIER FILING DATE: 1992-10-09  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 3  
LENGTH: 4795  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (20)..(4108)  
US-09-169-079-3

Query Match 100.0%: Score 471; DB 15; Length 4795;  
Best Local Similarity 100.0%: Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttcacagctggcagagagatgagatctctg 60  
Db 3044 ctgacacatggaagatctgtctgtctacagcttcacagctggcagagagatgagatctctg 60  
OY 61 gctcccggaagatgacatccacagagacctggtctcgtcgaacatctctcgtcgaagc 120  
Db 3104 gctcccggaagatgacatccacagagacctggtctcgtcgaacatctctcgtcgaagc 120  
OY 121 gacgtgtgaaagatctgtactctgtcctctgcgcggaacatctcgaacatctcgaac 180  
Db 3164 gacgtgtgaaagatctgtactctgtcctctgcgcggaacatctcgaacatctcgaac 180  
OY 181 gtcgcgaagagcagatgcccgtcgtcccttgaagtgatgacgcccgaagacatctcgaac 240  
Db 3224 gtcgcgaagagcagatgcccgtcgtcccttgaagtgatgacgcccgaagacatctcgaac 240  
OY 241 aaggtgtacacacgacagatgagctgtgtcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300  
Db 3284 aaggtgtacacacgacagatgagctgtgtcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300  
OY 301 tctctgt 360  
Db 3344 tctctgt 360  
OY 361 agagagcgacaaagatgagggcccgagactggccactcccgcaatacagcagcatctg 420

Db 3404 agagagcgacaaagatgagggcccgagactggccactcccgcaatacagcagcatctg 3463  
OY 421 ctgaactgctgtctcgagagaccccaagcgagactgcatctcggagctg 471  
Db 3464 ctgaactgctgtctcgagagaccccaagcgagactgcatctcggagctg 3514

## RESULT 24

US-08-446-648-45  
Sequence 45, Application US/08446648  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao ping  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446, 648  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9108 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-446-648-45

Query Match 100.0%: Score 471; DB 8; Length 9108;  
Best Local Similarity 100.0%: Pred. No. 1.2e-239;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttcacagctggcagagagatgagatctctg 60  
Db 3987 ctgacacatggaagatctgtctgtctacagcttcacagctggcagagagatgagatctctg 60  
OY 61 gctcccggaagatgacatccacagagacctggtctcgtcgaacatctctcgtcgaagc 120  
Db 4047 gctcccggaagatgacatccacagagacctggtctcgtcgaacatctctcgtcgaagc 120  
OY 121 gacgtgtgaaagatctgtactctgtcctctgcgcggaacatctcgaacatctcgaac 180  
Db 4107 gacgtgtgaaagatctgtactctgtcctctgcgcggaacatctcgaacatctcgaac 180





```
Db 645 gacgtgtgaagatctgtacttgccttgcgggacatctacaagaagcccgactac 704
Oy 181 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatctcgac 240
Db 705 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatctcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 824
Oy 301 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 360
Db 825 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 884
Oy 361 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 420
Db 885 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 944
Oy 421 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 471
Db 945 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 995

RESULT 27
US-60-213-360-951
: Sequence 951, Application US/60213360
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
: FILE REFERENCE: GX-0014 P
: CURRENT APPLICATION NUMBER: US/60/213,360
: NUMBER OF SEQ ID NOS: 2000-06-21
: SOFTWARE: PERL Program
: SEQ ID NO 951
: LENGTH: 3277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-213-360-951

Query Match 89.2%; Score 420; DB 60; Length 3277;
Best Local Similarity 99.8%; Pred. No. 1.7e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtacagcttccaggtgagcagaagatggaagcttcctg 60
Db 525 ctgacatggaagatctgtctgtacagcttccaggtgagcagaagatggaagcttcctg 584
Oy 61 gcttccgaaagtgcattccacagagacctgtgtctcgaaacatcttgcgtctcgaaagc 120
Db 585 gcttccgaaagtgcattccacagagacctgtgtctcgaaacatcttgcgtctcgaaagc 644
Oy 121 gacgtgtgaagatctgtactttggcttgccttcggcgagacatctacaagaagccctgactac 180
Db 645 gacgtgtgaagatctgtactttggcttgccttcggcgagacatctacaagaagccctgactac 704
Oy 181 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatcttcgac 240
Db 705 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatcttcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 824
Oy 301 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 360
```

```
Db 825 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 884
Oy 361 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 420
Db 885 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 944
Oy 421 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 471
Db 945 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 995

RESULT 28
US-60-324-185-4300
: Sequence 4300, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324,185
: NUMBER OF SEQ ID NOS: 2001-09-21
: SOFTWARE: PERL Program
: SEQ ID NO 4300
: LENGTH: 3277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-324-185-4300

Query Match 89.2%; Score 420; DB 71; Length 3277;
Best Local Similarity 99.8%; Pred. No. 1.7e-212;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgtacagcttccaggtgagcagaagatggaagcttcctg 60
Db 525 ctgacatggaagatctgtctgtacagcttccaggtgagcagaagatggaagcttcctg 584
Oy 61 gcttccgaaagtgcattccacagagacctgtgtctcgaaacatcttgcgtctcgaaagc 120
Db 585 gcttccgaaagtgcattccacagagacctgtgtctcgaaacatcttgcgtctcgaaagc 644
Oy 121 gacgtgtgaagatctgtactttggcttgccttcggcgagacatcttgcgtctcgaaagc 180
Db 645 gacgtgtgaagatctgtactttggcttgccttcggcgagacatcttgcgtctcgaaagc 704
Oy 181 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatcttcgac 240
Db 705 gtccgaagggaatgcccggctgccccttcgaatgagatgagcccttgaaagacatcttcgac 764
Oy 241 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 300
Db 765 aaggtgtacacacagagatgagatgtgtgcttcttgagggtgtgcttcttgaggatcttc 824
Oy 301 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 360
Db 825 tctctgggggcttcccgctacacctgggggtgacatcaatgaaagatcttgcacagcgctg 884
Oy 361 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 420
Db 885 agaaacggcacaagaatgaaagggcccgagctgacaccccgccgacatgcgcacatg 944
Oy 421 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 471
Db 945 ctgaactgctgtgtccggaagaccccaaggcgagacctgcatctctcgagctg 995
```

## RESULT 29

```
US-60-324-185-4274
: Sequence 4274, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324,185
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4274
: LENGTH: 4459
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1082992.1
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-4274
```

Query Match 89.2% Score 420; DB 71; Length 4459;  
Best Local Similarity 99.8%; Pred. No. 1.8e-212;

Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ctgacatggaagatcttctctcctcagctccagctgagcagaagagatgagctctc 60
Db 3055 ctgacatggaagatcttctctcctcagctccagctgagcagaagagatgagctctc 60
OY 61 gctccggaagatgcatcccaagagacgctgctcgcgaagatctctcgcgaagc 120
Db 3115 gctccggaagatgcatcccaagagacgctgctcgcgaagatctctcgcgaagc 120
OY 121 gacgtggtgaagatctctgacttgacttgacttgacttgacttgacttgacttgact 180
Db 3175 gacgtggtgaagatctctgacttgacttgacttgacttgacttgacttgacttgact 180
OY 181 gtcgcaagggcagtgcccgctgacctgaagtgaatgagccctggaagatctctgac 240
Db 3235 gtcgcaagggcagtgcccgctgacctgaagtgaatgagccctggaagatctctgac 240
OY 241 aaggtgtacacacagcagaatgagctgctgctctgctgctgctgctgctgctgctg 300
Db 3295 aaggtgtacacacagcagaatgagctgctgctctgctgctgctgctgctgctgctg 300
OY 301 tctctgggggctcccgctgacctggtgtgctgacctgacctgacctgacctgacctg 360
Db 3355 tctctgggggctcccgctgacctggtgtgctgacctgacctgacctgacctgacctg 360
OY 361 agagacgacacaagatgagggcccgagctgagcactcccgacatagcgcgacatg 420
Db 3415 agagacgacacaagatgagggcccgagctgagcactcccgacatagcgcgacatg 420
OY 421 ctgaactgctgctcggagaccccaagcgagacatgcatctcggagctg 471
Db 3475 ctgaactgctgctcggagaccccaagcgagacatgcatctcggagctg 471
```

## RESULT 30

```
US-08-256-769B-19/c
: Sequence 19, Application US/08256769B
: GENERAL INFORMATION:
: APPLICANT: Avraham, Hava
: APPLICANT: Groopman, Jerome
: APPLICANT: Cowley, Sally
```

```
APPLICANT: Scadden, David
APPLICANT: Mon Lee, James
APPLICANT: Bennett, Brian D.
APPLICANT: Wood, William I.
APPLICANT: Goeddel, David
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASES
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,769B
FILING DATE: 22-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: NEDH91-11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (1880..2923)
US-08-256-769B-19
```

Query Match 89.2% Score 420; DB 6; Length 6826;  
Best Local Similarity 99.8%; Pred. No. 1.8e-212;

Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ctgacatggaagatcttctctcctcagctccagctgagcagaagagatgagctctc 60
Db 2749 ctgacatggaagatcttctctcctcagctccagctgagcagaagagatgagctctc 60
OY 61 gctccggaagatgcatcccaagagacgctgctgctcgcgaagatctctcgcgaagc 120
Db 2689 gctccggaagatgcatcccaagagacgctgctgctcgcgaagatctctcgcgaagc 120
OY 121 gacgtggtgaagatctctgacttgacttgacttgacttgacttgacttgacttgact 180
Db 2629 gacgtggtgaagatctctgacttgacttgacttgacttgacttgacttgacttgact 180
OY 181 gtcgcaagggcagtgcccgctgacctgaagtgaatgagccctggaagatctctgac 240
Db 2569 gtcgcaagggcagtgcccgctgacctgaagtgaatgagccctggaagatctctgac 240
OY 241 aaggtgtacacacagcagaatgagctgctgctctgctgctgctgctgctgctgctg 300
Db 2509 aaggtgtacacacagcagaatgagctgctgctctgctgctgctgctgctgctgctg 300
OY 301 tctctgggggctcccgctgacctggtgtgctgacctgacctgacctgacctgacctg 360
Db 2449 tctctgggggctcccgctgacctggtgtgctgacctgacctgacctgacctgacctg 360
```

Oy 361 agagacgacacaaagatgaagagcccgagctggcccaatcccccacatagcgcacatg 420  
|||||  
Db 2389 AGAGACGGCACACAGATGAGCGCCCGGAGCTGGCCACTCCCGCATACGCCCATCATC 2330  
Oy 421 ctgaactgctgctcgagagaccccaagcgagacatctctcgagctg 471  
|||||  
Db 2329 CTGAACCTGCTGCTCCGGAGACCCCAAGCGACACTCTCATTTCTCGAGCTG 2279

## RESULT 31

US-08-446-648-17/C  
; Sequence 17, Application US/08446648  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPacIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446, 648  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P3PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6827 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-08-446-648-17

Query Match 89.2%; Score 420; DB 8; Length 6827;  
Best Local Similarity 99.8%; Pred. No. 1.8e-212;  
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgacatggaagatctgtctgctacagcttcacagtgagccagagagatgaatctcg 60  
|||||  
Db 2749 CTGACCATGGAAGATCTTGTCTCTACAGCTTCACAGTGGCCAGAGGATGAGTTCTG 2690  
Oy 61 gctcccgaaagatgctacacagagaccgctgctcggaacatctgctcggaagc 120  
|||||  
Db 2689 GCTTCCGGAAGTGCATCCACAGACGTGCTGCTCGGAACATTTCTGTCGGAAGC 2630  
Oy 121 gacgtggtgaagatctgctgacttggccttgcgggacatactaaagaccctgactac 180  
|||||

Db 2629 GACGTGCTGAAGATCTGTACTTTTGCTTGCCCTGCGCGGACATCTACAAAGACCCGACTAC 2570  
Oy 181 gtcgcgaagggagatgcccgcgctgcccctgaatgagatgcccctgaagacatctgac 240  
|||||  
Db 2569 CTCGCCAAGGCGAGTGGCCGGCTGCCCTGAAGTGAATGGCCCTGAAACCATCTTCGAC 2510  
Oy 241 aagtgtaacacacagcagaatgaatgctggtccttgggtgctctctgaggaatcttc 300  
|||||  
Db 2509 AAGGTACACACGACGACAGATGAGCTGTGCTTTGGGCTCTTCTCTGGAGATCTTC 2450  
Oy 301 tctctggggcctccctccgtaacctggggtgagatcaaaagagatctgccaagcgctg 360  
|||||  
Db 2449 TCTCTGGGGCTCCCTCCGTACCCCTGGGTGCAGATCAATGAGAGTTCTCCAGCGGCTG 2390  
Oy 361 agagacgacacaaagatgaagagcccgagctggcccaatcccccacatagcgcacatg 420  
|||||  
Db 2389 AGAGACGGCACACAGATGAGCGCCCGGAGCTGGCCACTCCCGCATACGCCCATCATC 2330  
Oy 421 ctgaactgctgctcgagagaccccaagcgagacatctctcgagctg 471  
|||||  
Db 2329 CTGAACCTGCTGCTCCGGAGACCCCAAGCGACACTCTCATTTCTCGAGCTG 2279

## RESULT 32

US-08-770-449-17/C  
; Sequence 17, Application US/08770449  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPacIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770, 449  
; FILING DATE: 20-Dec-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00586  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/826935  
; FILING DATE: 22-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P2D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6827 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single

TOPOLOGY: Linear  
US-08-770-449-17

Query Match 89.2%; Score 420; DB 11; Length 6827;  
Best Local Similarity 99.8%; Pred. No. 1.8e-212;  
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ctgacacatggaagatctgtctgtacagcttcagagtgccagaggaagagatctctg 60
DB 2749 ctgacacatggaagatctgtctgtacagcttcagagtgccagaggaagagatctctg 2690
OY 6 gtctccgaagatgcatccacagagaccltgctcgaacatctgtctggaagac 120
DB 2689 gcttcccccaaatccatccacagacacctgcctcgcgaatcttgcctgcgaagac 2630
OY 121 gacgtggaagatctgtacatttgcccttgccggagacatctcaagaagccctgactac 180
DB 2629 gacgtggaagatctgtacatttgcccttgccggagacatctcaagaagacacctgac 2570
OY 181 gtccgaagagcagtgccgagctgcccctgaagtgagtgccctgaagacatctcagac 240
DB 2569 gtcccccaagagcagtgccgagctgcccctgaagtgagtgccctgaagacatctcagac 2510
OY 241 aaggtgacacacagcagagtgagtggtcttgggtgtctctcgtggagatcttc 300
DB 2509 aaggtgacacacagcagagtgagtggtcttgggtgtctctcgtggagatcttc 300
OY 301 tctctgagggcctcccgctacccctgagtgagtgagtgagtgagtgagtgagtgagtgag 360
DB 2449 tctctgagggcctcccgctacccctgagtgagtgagtgagtgagtgagtgagtgagtgag 2290
OY 361 agagaagcgaacagatgagagggccgagagtgagtgagtgagtgagtgagtgagtgagtgag 420
DB 2389 agagaagcgaacagatgagagggccgagagtgagtgagtgagtgagtgagtgagtgagtgag 2230
OY 421 ctgacgtgctgtgctcgaagagccccaagagcagagtgagtgagtgagtgagtgagtgag 471
DB 2329 ctgacgtgctgtgctcgaagagccccaagagcagagtgagtgagtgagtgagtgagtgag 2279
```

## RESULT 33

US-09-982-610-17/c

Sequence 17, Application US/09982610

GENERAL INFORMATION:

APPLICANT:

Bennett, Brian D.

Goeddel, David

Lee, James M.

Matthews, William

Tsai, Siao Ping

Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,610

FILING DATE: 17-Oct-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,648

FILING DATE: 1996-May-23

APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6827 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear

US-09-982-610-17  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Query Match 89.2%; Score 420; DB 36; Length 6827;  
Best Local Similarity 99.8%; Pred. No. 1.8e-212;  
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ctgacacatggaagatctgtctgtacagcttcagagtgccagaggaagagatctctg 60
DB 2749 ctgacacatggaagatctgtctgtacagcttcagagtgccagaggaagagatctctg 2690
OY 6 gtctccgaagatgcatccacagagaccltgctcgaacatctgtctggaagac 120
DB 2689 gcttcccccaaatccatccacagacacctgcctcgcgaatcttgcctgcgaagac 2630
OY 121 gacgtggaagatctgtacatttgcccttgccggagacatctcaagaagccctgactac 180
DB 2629 gacgtggaagatctgtacatttgcccttgccggagacatctcaagaagacacctgac 2570
OY 181 gtccgaagagcagtgccgagctgcccctgaagtgagtgccctgaagacatctcagac 240
DB 2569 gtcccccaagagcagtgccgagctgcccctgaagtgagtgccctgaagacatctcagac 2510
OY 241 aaggtgacacacagcagagtgagtggtcttgggtgtctctcgtggagatcttc 300
DB 2509 aaggtgacacacagcagagtgagtggtcttgggtgtctctcgtggagatcttc 300
OY 301 tctctgagggcctcccgctacccctgagtgagtgagtgagtgagtgagtgagtgagtgag 360
DB 2449 tctctgagggcctcccgctacccctgagtgagtgagtgagtgagtgagtgagtgagtgag 2290
OY 361 agagaagcgaacagatgagagggccgagagtgagtgagtgagtgagtgagtgagtgagtgag 420
DB 2389 agagaagcgaacagatgagagggccgagagtgagtgagtgagtgagtgagtgagtgagtgag 2230
OY 421 ctgacgtgctgtgctcgaagagccccaagagcagagtgagtgagtgagtgagtgagtgag 471
DB 2329 ctgacgtgctgtgctcgaagagccccaagagcagagtgagtgagtgagtgagtgagtgag 2279
```

## RESULT 34

US-60-213-178-1247

Sequence 1247, Application US/60213178

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: C1000689

CURRENT APPLICATION NUMBER: US/60/213,178

NUMBER OF SEQ ID NOS: 1425

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1247

LENGTH: 415

TYPE: DNA



```
FILE REFERENCE: 20093-001000US
CURRENT APPLICATION NUMBER: US/10/012.214
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: PCT/US99/08079
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (22)..(3915)
US-10-012-214-1
```

```
Query Match          64.8% Score 305; DB 37; Length 4450;
Best Local Similarity 99.7% Pred. NO. 3.4e-151;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ctgaccatggaagatctctgtctacagctccagtgccagagagatgagctctg 60
Db 3046 ctgaccatggaagatctctgtctacagctccagtgccagagagatgagctctg 3105
OY 61 gctccgaaagtgatccacagagagctgtctgtggaacatctgtctgtggaagc 120
Db 3106 gctccgaaagtgatccacagagagctgtctgtggaacatctgtctgtggaagc 3165
OY 121 gacgtgtggaagatctgtgtctgtccctgtcccgagacatctacaagaccctgac 180
Db 3166 gacgtgtggaagatctgtgtctgtccctgtcccgagacatctacaagaccctgac 3225
OY 181 gtcgcaagggcagtgccggctgccccttgagtgagatgagccctgaaacatcttcgac 240
Db 3226 gtcgcaagggcagtgccggctgccccttgagtgagatgagccctgaaacatcttcgac 3285
OY 241 aaggtgacacacagcagagtgacgtgtgtctgtgggtgtctctctgtggagatcttc 300
Db 3286 aaggtgacacacagcagagtgacgtgtgtctgtgggtgtctctctgtggagatcttc 3345
OY 301 tctctgggggctccctccgtacccctgggggtgacatcaatgagagatctgtccagcg 356
Db 3346 tctctgggggctccctccgtacccctgggggtgacatcaatgagagatctgtccagcg 3401
```

```
RESULT 38
US-09-710-286-674
; Sequence 674, Application US/09710286
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2005-001
; CURRENT APPLICATION NUMBER: US/09/710.286
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,255
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-286-674
```

```
Query Match          40.1% Score 189; DB 28; Length 443;
Best Local Similarity 100.0% Pred. NO. 2e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 219 gcccctgaaagcatcttcgacaaggtgtacacacagcagatgagctgtgctcttg 278
Db 25 gcccctgaaagcatcttcgacaaggtgtacacacagcagatgagctgtgctcttg 84
OY 279 ggtctctctggagatctctctctctgtggggtccctccgtacacctgggtgacatcaa 338
Db 85 ggtctctctggagatctctctctctgtggggtccctccgtacacctgggtgacatcaa 144
OY 339 tgaagatcttcgacagcgtgagagacgacacaagatgtagggcccgagcttgccac 398
Db 145 tgaagatcttcgacagcgtgagagacgacacaagatgtagggcccgagcttgccac 204
OY 399 tcccgcat 407
Db 205 tcccgcat 213
```

```
RESULT 39
US-09-710-286-2884
; Sequence 2884, Application US/09710286
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2005-001
; CURRENT APPLICATION NUMBER: US/09/710.286
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,255
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2884
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1046)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-286-2884
```

```
Query Match          40.1% Score 189; DB 28; Length 1046;
Best Local Similarity 100.0% Pred. NO. 2.1e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 219 gcccctgaaagcatcttcgacaaggtgtacacacagcagatgagctgtgctcttg 278
Db 1 gcccctgaaagcatcttcgacaaggtgtacacacagcagatgagctgtgctcttg 60
OY 279 ggtctctctggagatctctctctctgtggggtccctccgtacacctgggtgacatcaa 338
Db 61 ggtctctctggagatctctctctctgtggggtccctccgtacacctgggtgacatcaa 120
OY 339 tgaagatcttcgacagcgtgagagacgacacaagatgtagggcccgagcttgccac 398
Db 121 tgaagatcttcgacagcgtgagagacgacacaagatgtagggcccgagcttgccac 180
OY 399 tcccgcat 407
Db 181 tcccgcat 189
```

```
RESULT 40
US-09-716-953-1245
; Sequence 1245, Application US/09716953
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
```

FILE OF INVENTION: THEREFOR  
FILE REFERENCE: 1600,2044-001  
CURRENT APPLICATION NUMBER: US/09/716,953  
CURRENT FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 60/167,413  
PRIOR FILING DATE: 1999-11-24  
NUMBER OF SEQ ID NOS: 2620  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1245  
LENGTH: 535  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(535)  
OTHER INFORMATION: n = A,T,C or G  
US-09-716-953-1245

Query Match 38.9%; Score 183; DB 28; Length 535;  
Best Local Similarity 99.6%; Pred. No. 3.2e-86;  
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 238 gacaaagtgatcacacacagcagaatgagctgtgtcccttgagggtgtctctccttgaggatc 297  
DB 15 gacaaagtgatcacacacagcagaatgagctgtgtcccttgagggtgtctctccttgaggatc 74  
OY 298 ttctctctgaggagctccctccgtacccctgagggtgagatcaatgaggagttctgcacagg 357  
DB 75 ttctctctgaggagctccctccgtacccctgagggtgagatcaatgaggagttctgcacagg 134  
OY 358 ctgagagacgagcacaagaatgagggcccgagagctggccacatcccgacatagccgcgcatc 417  
DB 135 ctgagagacgagcacaagaatgagggcccgagagctggccacatcccgacatagccgcgcatc 194  
OY 418 atgctgacgagctgtgtcgcgagagaccacaaaggagacctcatctctcggagctg 471  
DB 195 atgctgacgagctgtgtcgcgagagaccacaaaggagacctcatctctcggagctg 248  
RESULT 41  
US-60-170-374-1824/C  
Sequence 1824, Application US/60170374  
GENERAL INFORMATION:  
APPLICANT: Bonazzi, Vivien  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES  
FILE REFERENCE: CL000146  
CURRENT APPLICATION NUMBER: US/60/170,374  
CURRENT FILING DATE: 1999-12-13  
NUMBER OF SEQ ID NOS: 3666  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1824  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Human  
US-60-170-374-1824

Query Match 26.8%; Score 126; DB 56; Length 610;  
Best Local Similarity 100.0%; Pred. No. 7.7e-56;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 agtgcatacagaagacctgctgtcgtgaacatctcgtctgcgaaagcgaagctgtga 130  
DB 568 AGTGATCTGATCCACAGACAGCTGGCTGCTCGAATCTCTGCTCGAAGACGACAGCTGTGA 509  
OY 131 agatctgtagcttgctgtccctgcgagacatctacaagaacctgactacgtccgaagg 190  
DB 508 AGATCTGTGATCTTTGGCTTGGCCCGGACATCTACAAAGACCTGTACTGCTCCGACAGC 449  
OY 191 gcagtg 196

DB 448 GCAGTG 443

RESULT 42  
US-60-213-178-4/C  
Sequence 4, Application US/60213178  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL000689  
CURRENT APPLICATION NUMBER: US/60/213,178  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 1425  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 1077  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1077)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-178-4

Query Match 26.8%; Score 126; DB 60; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 7.8e-56;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 agatctcacagaagacctgctgtcccgagacatctcgtctgtggaagcgaagctgtga 130  
DB 1007 AGTGATCTGATCCACAGACAGCTGGCTGCTCGAATCTCTGCTCGAAGACGACGCTGTGA 948  
OY 131 agatctgtagcttgctgtccctgcgagacatctacaagaacctgactacgtccgaagg 190  
DB 947 AGATCTGTGATCTTTGGCTTGGCCCGGACATCTACAAAGACCTGTACTGCTCCGACAGC 888  
OY 191 gcagtg 196  
DB 887 GCAGTG 882

RESULT 43  
US-60-213-178-297/C  
Sequence 297, Application US/60213178  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL000689  
CURRENT APPLICATION NUMBER: US/60/213,178  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 1425  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 297  
LENGTH: 32768  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(32768)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-178-297

Query Match 26.8%; Score 126; DB 60; Length 32768;  
Best Local Similarity 100.0%; Pred. No. 8.9e-56;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 agtgcacacagagacccgtgctgctcggaacattctgctcggaagcgagctggtga 130  
|||||  
Db 29337 AGTGCATCCACAGACGCTGCTCGACATTCTCTGCGAAGCGACGTGCTGA 29478  
OY 131 agatcgtgacttggccttgcgggagacatctacaagaccctgactacgtcgcaag 190  
|||||  
Db 29477 AGATCTGTGACTTTGGCTTCCCGGACATCTACAAAGCCTGACTACGTCGCCAAG 29418  
OY 191 gcaagt 196  
|||||  
Db 29417 GCAGTC 29412

RESULT 44  
US-60-213-178-954

; Sequence 954, Application US/60213178  
; GENERAL INFORMATION:  
; APPLICANT: Bgasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL000689  
; CURRENT APPLICATION NUMBER: US/60/213,178  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 1425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 954  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Human  
US-60-213-178-954

Query Match 26.5%; Score 125; DB 60; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.6e-55;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 tgcacacacagagacccgtgctgctcggaacattctgctcggaagcgagctggtgaag 132  
|||||  
Db 2 tgcacacacagagacccgtgctgctcggaacattctgctcggaagcgagctggtgaag 61  
OY 133 atcgtgacttggccttgcgggagacatctacaagaccctgactacgtcgcaagggc 192  
|||||  
Db 62 atcgtgacttggccttgcgggagacatctacaagaccctgactacgtcgcaagggc 121  
OY 193 agtgc 197  
|||||  
Db 122 agtgc 126

RESULT 45

US-60-178-305-229/C  
; Sequence 229, Application US/60178305  
; GENERAL INFORMATION:  
; APPLICANT: BONAZZI, VIVIEN  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE  
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL000207  
; CURRENT APPLICATION NUMBER: US/60/178,305  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 1740  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 229  
; LENGTH: 516  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-178-305-229

Query Match 24.0%; Score 113; DB 56; Length 516;  
Best Local Similarity 100.0%; Pred. No. 6.5e-49;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 gcccgctgcccctggaagtgaatggccccggaagcattctgacaaagtgtaaccacag 255  
|||||  
Db 473 GCCCGCTGCCCTGAAGTGGATGGCCCCGGAAGCATCTTGACAAAGGTGACACACG 414  
OY 256 caagatgactgtgtgctccttgggtgctctctcgggaagacctctctcggg 308  
|||||  
Db 413 CAGAGTACGTGTGCTCTTGGGGTCTCTCGGAGATCTCTCTCGG 361

Search completed: July 16, 2002, 02:50:25  
Job time: 31278 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:17 : Search time 223.79 seconds

(without alignments)  
516.973 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514

Perfect score: 471  
1 ctgaccatcgaagatctgtc.....gacctgcatctcgagctg 471

Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/lna/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/2/lna/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/2/lna/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/lna/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/lna/PCRTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/lna/Backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	4195	1 US-08-340-011-1	Sequence 1, Appl1
2	471	100.0	4195	3 US-08-901-710-1	Sequence 1, Appl1
3	471	100.0	4416	1 US-08-795-430-1	Sequence 1, Appl1
4	471	100.0	4425	1 US-08-223-616-31	Sequence 31, Appl1
5	471	100.0	4425	5 PCT-US95-04228-31	Sequence 31, Appl1
6	471	100.0	4795	1 US-08-340-011-3	Sequence 31, Appl1
7	471	100.0	4795	3 US-08-901-710-3	Sequence 3, Appl1
8	471	100.0	9108	5 PCT-US95-04228-45	Sequence 45, Appl1
9	420	89.2	6827	1 US-08-222-616-17	Sequence 17, Appl1
10	420	89.2	6827	5 PCT-US95-04228-17	Sequence 17, Appl1
11	76	16.1	160	1 US-08-223-616-5	Sequence 5, Appl1
12	76	16.1	160	5 PCT-US95-04228-5	Sequence 5, Appl1
13	26	5.5	1467	1 US-08-176-630A-3	Sequence 3, Appl1
14	26	5.5	1467	1 US-08-463-862-3	Sequence 3, Appl1
15	26	5.5	1467	2 US-08-461-985-3	Sequence 3, Appl1
16	26	5.5	1467	2 US-08-458-887-3	Sequence 3, Appl1
17	26	5.5	1467	2 US-08-932-787B-3	Sequence 3, Appl1
18	26	5.5	1467	4 US-08-932-012C-3	Sequence 3, Appl1
19	26	5.5	1467	4 US-08-888-818C-3	Sequence 3, Appl1
20	23	4.9	159	2 US-08-469-537A-19	Sequence 19, Appl1
21	23	4.9	1894	4 US-07-912-122-3	Sequence 3, Appl1
22	23	4.9	1894	5 PCT-US93-06404-3	Sequence 3, Appl1
23	23	4.9	3453	1 US-07-813-593-1	Sequence 3, Appl1
24	23	4.9	3453	1 US-07-977-451-1	Sequence 1, Appl1
25	23	4.9	3453	1 US-07-946-507-1	Sequence 1, Appl1
26	23	4.9	3453	1 US-08-252-517-1	Sequence 1, Appl1
27	23	4.9	3453	1 US-07-906-397A-1	Sequence 1, Appl1

28	23	4.9	3453	1 US-08-601-891-1	Sequence 1, Appl1
29	23	4.9	3453	2 US-09-021-324-1	Sequence 1, Appl1
30	23	4.9	3453	5 PCT-US92-02750-1	Sequence 1, Appl1
31	23	4.9	3453	5 PCT-US92-05401-1	Sequence 1, Appl1
32	23	4.9	3453	5 PCT-US92-09893-1	Sequence 1, Appl1
33	23	4.9	3521	1 US-08-232-299-1	Sequence 11, Appl1
34	23	4.9	3521	2 US-08-434-878-1	Sequence 1, Appl1
35	23	4.9	3521	5 PCT-US95-03718-1	Sequence 1, Appl1
36	23	4.9	4054	1 US-08-180-195-35	Sequence 35, Appl1
37	23	4.9	4054	1 US-08-477-329-35	Sequence 35, Appl1
38	23	4.9	4054	2 US-08-475-458-35	Sequence 35, Appl1
39	23	4.9	4054	3 US-08-980-400-35	Sequence 35, Appl1
40	23	4.9	4054	4 US-09-583-459A-35	Sequence 35, Appl1
41	23	4.9	4054	4 US-09-583-210-35	Sequence 35, Appl1
42	23	4.9	4054	4 US-09-583-449A-35	Sequence 35, Appl1
43	23	4.9	4100	1 US-08-168-917-3	Sequence 3, Appl1
44	23	4.9	4100	2 US-08-460-510-3	Sequence 3, Appl1
45	23	4.9	4100	2 US-08-460-490-3	Sequence 3, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-340-011-1  
: Sequence 1, Application US/08340011  
: Patent No. 576755  
: GENERAL INFORMATION:  
: APPLICANT: Alltalo, et al.  
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE  
: NUMBER OF SEQUENCES: 20  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: STREET: 6300 Sears Tower, 233 South Wacker Drive  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: United States of America  
: ZIP: 60606-6402  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/340,011  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/959,951  
: FILING DATE: 09-OCT-1992  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Meyers, Thomas C.  
: REGISTRATION NUMBER: 36,989  
: REFERENCE/DOCKET NUMBER: 32267  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 312/474-6300  
: TELEFAX: 312/474-0448  
: TELEX: 25-3856  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 4195 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 20..3916  
: US-08-340-011-1

Query Match 100.0% Score 471: DB 1: Length 4195;  
Best Local Similarity 100.0%: Pred. No. 1.8e-223;

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgacacatgaagaatctgtctgtacacagctccagtgccagaggaatgaagttcttg 60  
|||||  
Db 3044 CTGACCATGGAAGATCTGTCTGTACACCTCCAGGTGCCAGAGGATGAGTTCTTG 3103

QY 61 gcttccgaaagtgacatccacagagagctgtgctgcgaacatctgtctgcgaagac 120  
|||||  
Db 3104 GCTTCCGAAAGTGATCCACAGAGACCTGCTCGGAACATCTGCTGTGGAAAGC 3163

QY 121 gacgtgtgaagaatctgtacattgtgacctgtccggaacatccaaagaccctgactac 180  
|||||  
Db 3164 GACGTGTGAACATCTGTACTTTGGCTTGGCCGGGACATCTTACAAAGACCTGACATAC 3223

QY 181 gtccgaagggcagtgcccgagctgcctccctgaagtgagatgagccctgaagacatcttcag 240  
|||||  
Db 3224 GTCCGGAAGCGCAGTCCGCGGCTGCCCTGAAGTGATGGCCCTGGAAGACATCTTGAC 3233

QY 241 aaggtgtacacagcagagatgagtggtgtgcttgggtgtgcttctcgtggaagatcttc 300  
|||||  
Db 3284 AAGGTGTACACCAACCAAGATGACGTGTGCTTTGGGGTCTTCTGTGGAGATCTTC 3343

QY 301 tctctgggggacctcccgctacacctgtgagtgagatcaatgagagatctgtccagagctg 360  
|||||  
Db 3344 TCTCTGGGGGCTCCCGCTACCTGGGTGAGATGAGAGATCTGTCCAGCGGCTG 3403

QY 361 agagacggcacaagatgagtgagggcccgagctgtgacacatcccgacatgcgcatcatg 420  
|||||  
Db 3404 AGAGACGGCACAAGATGAGGGCCCGGACGTGCGCACTCCCGCATTAACGCCGATCATG 3463

QY 421 ctgaactgtgtccgagagaccccaagggagactgtgcttctgagagctg 471  
|||||  
Db 3464 CTGAACCTGTGTGCGGAGACCCCAAGCGGAGACCTGCATTTCTGGAGCTG 3514

RESULT 2  
US-08-901-710-1  
: Sequence 1, Application US/08901710  
: Patent No. 6107046  
: GENERAL INFORMATION:  
: APPLICANT: Alltalo, Karl  
: APPLICANT: Aprelikova, Olga  
: APPLICANT: Pajusola, Katri  
: APPLICANT: Armstrong, Elina  
: APPLICANT: Korhonen, Jaana  
: APPLICANT: Kaipainen, Arja  
: APPLICANT: Matikainen, Marja-Terttu  
: TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES  
: NUMBER OF SEQUENCES: 20  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
: STREET: 6300 Sears Tower, 233 South Wacker Drive  
: City: Chicago  
: STATE: Illinois  
: COUNTRY: United States of America  
: ZIP: 60606-6402  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/901,710  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/340,011  
: FILING DATE: 14-NOV-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/257,754  
: FILING DATE: 09-JUL-1994  
: PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/959,951  
FILING DATE: 09-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28113/33824  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4195 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 20..3916  
US-08-901-710-1

Query Match 100.0%; Score 471; DB 3; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 1.8e-223;  
Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctgacacatgaagaatctgtctgtacacagctccagtgccagaggaatgaagttcttg 60  
|||||  
Db 3044 CTGACCATGGAAGATCTGTCTGTACACCTCCAGGTGCCAGAGGATGAGTTCTTG 3103

QY 61 gcttccgaaagtgacatccacagagagctgtgctgcgaacatctgtctgcgaagac 120  
|||||  
Db 3104 GCTTCCGAAAGTGATCCACAGAGACCTGCTCGGAACATCTGCTGTGGAAAGC 3163

QY 121 gacgtgtgaagaatctgtacattgtgacctgtccggaacatccaaagaccctgactac 180  
|||||  
Db 3164 GACGTGTGAACATCTGTACTTTGGCTTGGCCGGGACATCTTACAAAGACCTGACATAC 3223

QY 181 gtccgaagggcagtgcccgagctgcctccctgaagtgagatgagccctgaagacatcttcag 240  
|||||  
Db 3224 GTCCGGAAGCGCAGTCCGCGGCTGCCCTGAAGTGATGGCCCTGGAAGACATCTTGAC 3283

QY 241 aaggtgtacacagcagagatgagtggtgtgcttgggtgtgcttctcgtggaagatcttc 300  
|||||  
Db 3284 AAGGTGTACACCAACCAAGATGACGTGTGCTTTGGGGTCTTCTGTGGAGATCTTC 3343

QY 301 tctctgggggacctcccgctacacctgtgagtgagatcaatgagagatctgtccagagctg 360  
|||||  
Db 3344 TCTCTGGGGGCTCCCGCTACCTGGGTGAGATGAGAGATCTGTCCAGCGGCTG 3403

QY 361 agagacggcacaagatgagtgagggcccgagagctgtgacacatcccgacatgcgcatcatg 420  
|||||  
Db 3404 AGAGACGGCACAAGATGAGGGCCCGGACGTGCGCACTCCCGCATTAACGCCGATCATG 3463

QY 421 ctgaactgtgtccgagagaccccaagggagactgtgcttctgagagctg 471  
|||||  
Db 3464 CTGAACCTGTGTGCGGAGACCCCAAGCGGAGACCTGCATTTCTGGAGCTG 3514

RESULT 3  
US-08-795-430-1  
: Sequence 1, Application US/08795430  
: Patent No. 6130071  
: GENERAL INFORMATION:  
: APPLICANT: Alltalo, Karl  
: APPLICANT: Joukov, Vladimir  
: TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
: TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
: NUMBER OF SEQUENCES: 57  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
: STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/F196/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4416 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-795-430-1

Query Match 100.0% Score 471: DB 3: Length 4416:  
Best Local Similarity 100.0% Pred. No. 1.8e-223:

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ctgacacatgaaagatcttctgtctacagcttcccaagtgagcgaaggaatgagttccctg 60  
DB 3044 CTGACCATGGAAGATCTTGTCTGTACAGCTTCACAGTGGCCGACAGCATGAGATTCTCTG 3103  
OY 61 gcttccgaagtgacatccacagagacctggtctcggaacatctgtctcgaaagc 120  
DB 3104 GCTTCCGGAAGTGACATCCACAGACACTGCGTCCGACATCTCTGTCGCAAGC 3163  
OY 121 gacgtgtagaagatctgtacttggccttgcacggagacatctacaaacacctgactac 180  
DB 3164 GACGTGTGAAGATCTGTACTTTGGCTTGGCCGGACATCTACAAAGACCTTGACTAC 3223  
OY 181 gtcgcaagggcagtgctccggctgcccctgaagtgagatgagccctaaagcatcttcgac 240  
DB 3224 GTCCGCAAGGGCAGTCCCGGCTGAGTGAAGTGATGGCCCTGAAGCATCTTTCGAC 3283  
OY 241 aaggtgtacacacgacagtgagcgtgtgctccttggggctctctctcgtggagatcttc 300  
DB 3284 AAGGTGTACACACGACAGATGACGCTGTCTTGGGCTCTTCTGTGGAGATCTTTC 3343

OY 301 tctctgggggctcccccgtaccccttg99gtgcatlcaatgaagaattctgcccagcgctg 360  
DB 3344 TCTCTGGGGGCTCCCGGTACCTGGGTGCGATGATGAGAGATTCTGCGACGGCTG 3403  
OY 361 agagacgycacaagatgagggcccgagctggccactcccgcatatgcgcgcatcag 420  
DB 3404 AGAGACGCGACAAAGATGAGGGCCCGGAGCTGGCCACTCCCGCATACGCCGATCATG 3463  
OY 421 ctgaactgtgtgctggagagccccaaggcgaagacctgcatctctggagctg 471  
DB 3464 CTGAAGTGTGTGCTGGAGACCCCAAGCGAGACTGTGATCTCGAGCTG 3514

## RESULT 4

US-08-222-616-31

; Sequence 31: Application US/08222616

; Patent No. 5635177

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,616

; FILING DATE: 4-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00586

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/826935

; FILING DATE: 22-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 821P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4425 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-222-616-31

Query Match 100.0% Score 471: DB 1: Length 4425:  
Best Local Similarity 100.0% Pred. No. 1.8e-223:

Matches 471: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 ctgacacatgaaagatcttctgtctacagcttcccaagtgagcgaaggaatgagttccctg 60  
DB 3055 CTGACCATGGAAGATCTTGTCTGTACAGCTTCACAGTGGCCGACAGGATGAGATTCTCTG 3114

OY 61 gcttccgaaagtgatcatccacagagaccgtgctcgtcgaacattctcgtcgtcgaagc 120  
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Db 3115 gcttccgaaagtgatcatccacagagaccgtgctcgtcgaacattctcgtcgtcgaagc 3174  
OY 121 gaagtgatgaagatcgtgacatttgcccttgcccgagacatctacaaagaccctgacac 180  
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Db 3175 GACCTGCTGAAGATCTGTGACTTTGGCTTGGCCGGACATCTACAAAGACCTGACTAC 3234  
OY 181 gtcgcaagagcagatgcccggccttgccctgaagtgagtgccctgaaacatcctcagac 240  
|||||  
Db 3235 GTCCCAAGGCGACGTGCCCGCTCCCTTAAGTGAATGAGCCCTCAACCATCTTCGAC 3294  
OY 241 aagtgatcacacacagcagagtgacgtgagtccttgagggtgtctccttgagagatctc 300  
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OY 301 tctctgggggctccctcgtacccctggggtgacagatcaagagatctcgtcgaagcgtg 360  
Db 3355 TCTCTGGGGCTCTCCCGTACCTGGGGTGCAGATCAATGAGAGTTCCTCCAGCGCTG 3414  
OY 361 aagagcagcacaagatgaagggcccgagcttgccacatcccgcaaacgcacatcgt 420  
Db 3415 AGAGACGGCACAAGATGAGAGGCCCGGACCTGGCCACTCCGCCATACCGCGCATCTTC 3474  
OY 421 ctgaactgtgtcgtcggagagaccacaaagcgagacgtcgtcgtcgaagcgtg 471  
Db 3475 CTGAACGTGCTGTGCGGAGACCCCAAGCGAGACTTCATCTTCGAGAGCTG 3525

RESULT 5  
PCT-US95-04228-31  
Sequence 31, Application PC/TUS9504228  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04228  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wendy M. Lee  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4425 bases

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-04228-31

Query Match 100.0%; Score 471; DB 5; Length 4425;  
Best Local Similarity 100.0%; Pred. No. 1,8e-223;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacatgaaagatctgtcgtcgtacacagcttcgaagtgagcgaagagatgagtcgtg 60  
Db 3055 CTGACCATGGAATCTTGTCTCTACAGCTTCACAGTGGCCGAGAGGATGCAATCTTCG 3114  
OY 61 gcttccgaaagtgatcatccacagagaccgtgctcgtcgaacattctcgtcgtcgaagc 120  
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OY 121 gaagtgatgaagatcgtgacatttgcccttgcccgagacatctacaaagaccctgacac 180  
Db 3175 GACCTGCTGAAGATCTGTGACTTTGGCTTGGCCGGACATCTACAAAGACCTGACTAC 3234  
OY 181 gtcgcaagagcagatgcccggccttgccctgaagtgagtgccctgaaacatcctcagac 240  
Db 3235 GTCCCAAGGCGACGTGCCCGCTCCCTTAAGTGAATGAGCCCTCAACCATCTTCGAC 3294  
OY 241 aagtgatcacacacagcagagtgacgtgagtccttgagggtgtctccttgagagatctc 300  
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OY 301 tctctgggggctccctcgtacccctggggtgacagatcaagagatctcgtcgaagcgtg 360  
Db 3355 TCTCTGGGGCTCTCCCGTACCTGGGGTGCAGATCAATGAGAGTTCGCGAGCGCTG 3414  
OY 361 aagagcagcacaagatgaagggcccgagcttgccacatcccgcaaacgcacatcgt 420  
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OY 421 ctgaactgtgtcgtcggagagaccacaaagcgagacgtcgtcgtcgaagcgtg 471  
Db 3475 CTGAACGTGCTGTGCGGAGACCCCAAGCGAGACTTCATCTTCGAGAGCTG 3525

RESULT 6  
US-08-340-011-3  
Sequence 3, Application US/08340011  
Patent No. 5776755  
GENERAL INFORMATION:  
APPLICANT: Alltalo, et al.  
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,011  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959,951  
FILING DATE: 09-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: 36,989

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? REFERENCE/DOCKET NUMBER: 32267
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6300
? TELEFAX: 312/474-0448
? TELEX: 25-3852
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4795 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 20..4111
?
US-08-340-011-3

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Query Match	100.0%	Score 471:	DB 1:	Length 4795;
Best Local Similarity	100.0%	Pred. No. 1	8e-223;	
Matches 471:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

OY	1	ctgaacatgtgaaaatctctctgctcaccagcttccaaagtgcgaaggagatgaattctctg	60
Db	3044	ctgacacatgaaatcttctctctctcactacacttccaaagtgcgaaggagatgaattctctg	310304
OY	61	gcttccccaagtgtgacatccacagagacctgctgtctcgtgaacatctctgtctcggaaagc	120
Db	3104	gctttcccgaaagtcattccacagagacctgctgtcgtcgaaacattctgtctgacgaagc	3163
OY	121	gaatgtgtgaagaatctgtgaacttggacctgtcccgaggacattctaaagaacctgactaac	180
Db	3164	gacctgtgtgaagatctgtgaacttggacctgtcccgaggacattctaaagaacctgtgacac	3223
OY	181	gtccgaagaaggacatgtgcccgctcccccgaagtgtgatgtgccccgaagaacatctctgac	240
Db	3224	gtcccgcaagggcagtgctcccgctcccccgaagtgtgatgtgccccgaagaacatcttgacac	3283
OY	241	aaagtgtataccacacgaaggatgaactgtgtgtctctcttgagggtgtctctctctggaagatctc	300
Db	3284	aaactgtgtacacacacgaaggatgaactgtgtgtctctcttgagggtgtctctctctggaagatcttc	3343
OY	301	tcctctgagggtccctcccgctaaccttgagggtgtgacatcaatgaaggaattctgtccaaacggtctg	360
Db	3344	ttctctggggggcctccctcccgctaaccttgagggtgtgacatcaatgaaggaattctgtccaaacggtctg	3403
OY	361	agagacagcgaacaagaatgaaggcccccgagactgtgccaacttccgcacatacgcgcacatcatg	420
Db	3404	acgagacagcgaacaagaatgaaggcccccgagactgtgccaacttccgcacatacgcgcacatcatg	3463
OY	421	ctgaactgtgtgtccggagagaccccaaggagagacctgcatctctcgagatcg	471
Db	3464	ctgaactgtgtgtccggagagaccccaaggagagacctgcatctctcgagatcg	3514

RESULT 7  
 US-08-901-710-3  
 : Sequence 3, Application US/08901710  
 : Patent No. 6107046  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Allitalo, Karl  
 : APPLICANT: Aprelikova, Olga  
 : APPLICANT: Pajusola, Katari  
 : APPLICANT: Armstrong, Elina  
 : APPLICANT: Korhonen, Jaana  
 : APPLICANT: Kaipainen, Arja  
 : APPLICANT: Matikainen, Marja-Terttu  
 : TITLE OF INVENTION: F14D, A RECEPTOR TYROSINE KINASE, AND USES  
 : THEREOF  
 : NUMBER OF SEQUENCES: 20  
 :  
 : CORRESPONDENCE ADDRESS:  
 :  
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 6300 Sears Tower, 233 South Wacker Drive

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1 CITY: Chicago
2 STATE: Illinois
3 COUNTRY: United States of America
4 ZIP: 60606-6402
5
6 COMPUTER READABLE FORM:
7
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/901,710
15 FILING DATE:
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/340,011
19 FILING DATE: 14-NOV-1994
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/257,754
23 FILING DATE: 09-JUL-1994
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/959,951
27 FILING DATE: 09-OCT-1992
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Gass, David A.
30 REGISTRATION NUMBER: 38,153
31 REFERENCE/DOCKET NUMBER: 28113/33824
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 312/474-6300
34 TELEFAX: 312/474-0448
35 TELEX: 25-3856
36
37 INFORMATION FOR SEO ID NO: 3:
38
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 4795 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: cDNA
45 FEATURE:
46
47 NAME/KEY: CDS
48 LOCATION: 20..4111
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50 US-08-901-710-3
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Db 3404 AGAGACGACAGCATGAGGGCCCCGAGCTGGCCACTCCCGCATACGCCGATCATG 3463  
Oy 421 ctgaactgtgtgtccggagaccacgaagcgagactgattctcggagctg 471  
Db 3464 CTGAACTGCTGTCTCCGAGACCCCAAGCGAGACCTGCTGATTCGGAGCTG 3514

## RESULT 8

PCT-US95-04228-45  
; Sequence 45, Application PC/TUS9504228  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04228  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wendy M. Lee  
; REGISTRATION NUMBER: 00,000  
; REFERENCE/DOCKET NUMBER: 821P3PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ. ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9108 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US95-04228-45

Query Match 100.0%; Score 471; DB 5; Length 9108;  
Best Local Similarity 100.0%; Pred. No. 1.7e-223;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgaccatggaagatcttctgtcacaaggtcccaagtgcccaaggaatgagttcctg 60  
Db 3987 CTGACCATGGAAGATCTTCTGTCTGCTACAGCTTCCAGGTGGCCAGAGGATGAGTCTCTG 4046  
Oy 61 gcttccgaagatgcatcacagagaccctgctgtcgaacattctgtctggaagc 120  
Db 4047 GCTTCCGAAAGTGCATCCACAGACACTGCTCGGAACATTCTGCTGCGAAGC 4106  
Oy 121 gacggtggaagatctgtgacttggccttgcggggaacatctaaagaacctgactac 180  
Db 4107 GACGTGTGAAGATCTGTGACTTTTGCCCTTCCCGGAGACATCTCAAAAGACCTGACTAC 4166  
Oy 181 gtccgaagggcagtgcccgctgcccctgaagtgaatgagccctgaagaacatcttcgac 240

Db 4167 GTCCGCAAGGGCAGTCCCGGCTGCCCCCTGAAGTGAATGCCCCCTGAAAGCATCTTGAC 4226  
Oy 241 aaggttacaccacgaagatgacgtgtgttcttgggggtctctcggagaccttc 300  
Db 4227 AAGGTACACACGACGAGATGACGTGTGCTCTTGGGTCCTCTCTCGGAATCTTC 4286  
Oy 301 tctctggggcctcccccgaacctgtgggtgcagatcaatgaagttctgcacaagcgtc 360  
Db 4287 TCTCTGGGGCTCCCGGTAACCTGGGTGCAGATCAATGAGACTTCTGCACGCGCTG 4346  
Oy 361 aagagcgcacaaagatgagggcccggaagctgtgacctccgcatacgcgcacatg 420  
Db 4347 AGAGACGGCACAAGATGAGGGCTCCGAGCTGGCCACTCCCGCATACGCCGATCATG 4406  
Oy 421 ctgaactgtgtgtccggagaccacgaagcgagactgattctcggagctg 471  
Db 4407 CTGAACTGCTGTCTCCGAGACCCCAAGCGAGACCTGCTGATTCGGAGCTG 4457

## RESULT 9

US-08-222-616-17/c  
; Sequence 17, Application US/08222616  
; Patent No. 5635177  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,616  
; FILING DATE: 4-APR-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00586  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/826935  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 821P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6827 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-616-17

Query Match 89.2%; Score 420; DB 1; Length 6827;  
Best Local Similarity 99.8%; Pred. No. 2,6e-198;  
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctggaccatggaagatctgtgtctgtacagctccagagggcgaagagatgagttctcg 60  
|||||  
DB 2749 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGCGGCAAGAGGATGAGTTCCTG 2690

QY 61 gcttcacgaagatgacatccacagagaccctgctcctcgaacatctcctcgcgaagc 120  
|||||  
DB 2689 GCTTCCCGAAGATGATCCACAGAGACTGCTCTCGGAACATTCTCTCTCGGAAGC 2630

QY 121 gacgtgtgaaagatctgtgtacattgacctgacctgacacatcaaaagacctgactac 180  
|||||  
DB 2629 GACGTGTGAAGATCTGTGACTTTGGCCTTCCCGGACATCTCAAAAGACCCGACTAC 2570

QY 181 gtccgaagagcagtgcccgctgccccctgaagtgaatgagcccttgaaagatcttcgac 240  
|||||  
DB 2569 GTCCGCAAGGCAAGTCCCGGCTGCTGTAAGTGATGAGCCCTGAAAGCATCTTCGAC 2510

QY 241 aaggtgtacacacagcagagtgacgtgtgtcccttgagggtctctcctcgcgaagcttc 300  
|||||  
DB 2509 AAGGTGTACACACAGCAGAGTGTGTCTTTGGGCTCTTCTCTGGAATCTTC 2450

QY 301 tctctgggggctcccccgtacacctgagggtgcagatcaatgagagctctcgcgaagctcg 360  
|||||  
DB 2449 TCTCTGGGGCTCCCGGTACCTGGGGTGCAATCAATGAGAGTCTCTGCGACGCGCTG 2390

QY 361 agagacgagcagaagatgagagggcccgagagctgacacatcccgacatacgccgacatcg 420  
|||||  
DB 2389 AGACACGGCACAGATGAGGGCCCCGAGCTGGCCACTGCCGCAATACGCCCGCATCATG 2330

QY 421 ctgaactgtctgtccgagagaccacgaagcgagacctgcatctcgtggaagctg 471  
|||||  
DB 2329 CTGAACGTGCTGTCGGAGAGACCCCAAGCGAGACTGCTGCTGGAAGCTG 2279

RESULT 10  
PCT-US95-04228-17/C  
Sequence 17, Application PC/TUS9504228  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04228  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wendy M. Lee  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEO ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6827 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-04228-17

Query Match 89.2%; Score 420; DB 5; Length 6827;  
Best Local Similarity 99.8%; Pred. No. 2,6e-198;  
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgacatggaagatctgtgtctgtacagctccaggtggcgaagagatgagttctcg 60  
|||||  
DB 2749 CTGACCATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGCGCAAGAGATGAGTTCCTG 2690

QY 61 gcttcacgaagatgacatccacagagaccctgctcctcgaacatctcctcgcgaagc 120  
|||||  
DB 2689 GCTTCCCGAAGATGATCCACAGAGACTGCTCTCGGAACATTCTCTCTCGGAAGC 2630

QY 121 gacgtgtgaaagatctgtgtacattgacctgacctgacacatcaaaagacctgactac 180  
|||||  
DB 2629 GACGTGTGAAGATCTGTGACTTTGGCCTTCCCGGACATCTCAAAAGACCCGACTAC 2570

QY 181 gtccgaagagcagtgcccgctgccccctgaagtgaatgagcccttgaaagacatcttcgac 240  
|||||  
DB 2569 GTCCGCAAGGCAAGTCCCGGCTGCTGTAAGTGATGAGCCCTGAAAGCATCTTCGAC 2510

QY 241 aaggtgtacacacagcagagtgacgtgtgtcccttgagggtctctcctcgcgaagcttc 300  
|||||  
DB 2509 AAGGTGTACACACAGCAGAGTGTGTCTTTGGGCTCTTCTCTGGAATCTTC 2450

QY 301 tctctgggggctcccccgtacacctgagggtgcagatcaatgagagctctcgcgaagctcg 360  
|||||  
DB 2449 TCTCTGGGGCTCCCGGTACCTGGGGTGCAATCAATGAGAGTTCCTGCGAGGCTG 2390

QY 361 agagacgagcagaagatgagagggcccgagagctgacacatcccgacatacgccgacatcg 420  
|||||  
DB 2389 AGACACGGCACAGATGAGGGCCCCGAGCTGGCCACTGCCGCAATACGCCCGCATCATG 2330

QY 421 ctgaactgtctgtccgagagaccacgaagcgagacctgcatctcgtggaagctg 471  
|||||  
DB 2329 CTGAACGTGCTGTCGGAGAGACCCCAAGCGAGACTGCTGCTGGAAGCTG 2279

RESULT 11  
US-08-222-616-5  
Sequence 5, Application US/08222616  
Patent No. 5635177  
GENERAL INFORMATION:  
APPLICANT: Genentech, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk



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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222.616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-616-5

Query Match      16.1%; Score 76; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 ggaacatctctgtcggaagcgagctgtggaagatctgtgaccttgccctggccggg 157
Db 30 GGAACATCTCTGCTCGGAAGCGAGCTGTGGAAGATCTGTGACCTTGCCCTGCCGGG 89
QY 158 acatctacaagacc 173
Db 90 ACATCTACAAAGACC 105

RESULT 12
PCT-US95-04228-5
Sequence 5, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-5
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```
Query Match      16.1%; Score 76; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 ggaacatctctgtcggaagcgagctgtggaagatctgtgaccttgccctggccggg 157
Db 30 GGAACATCTCTGCTCGGAAGCGAGCTGTGGAAGATCTGTGACCTTGCCCTGCCGGG 89
QY 158 acatctacaagacc 173
Db 90 ACATCTACAAAGACC 105
```

```
RESULT 13
US-08-176-620A-3
Sequence 3, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
```

TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1245  
US-08-176-620A-3

Query Match 5.5%: Score 26; DB 1; Length 1467;  
Best Local Similarity 100.0%: Pred. No. 0.00075;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aa:atcgtgacttgccctgcgcg 155  
|||||  
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 14  
US-08-463-862-3  
Sequence 3, Application US/08463862  
Patent No. 5776751  
GENERAL INFORMATION:  
APPLICANT: Boulton, Teri G. et al.  
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,862  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/701,544  
FILING DATE: 16-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6526-049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1467 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1245  
US-08-463-862-3

Query Match 5.5%: Score 26; DB 1; Length 1467;  
Best Local Similarity 100.0%: Pred. No. 0.00075;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatcgtgacttgccctgcgcg 155  
|||||  
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 15  
US-08-461-985-3  
Sequence 3, Application US/08461985  
Patent No. 5872006  
GENERAL INFORMATION:  
APPLICANT: Boulton, Teri G.  
APPLICANT: Cobb, Melanie H.  
APPLICANT: Yancopoulos, George D.  
APPLICANT: Nye, Steven  
APPLICANT: Panayiotatos, Nikos  
TITLE OF INVENTION: A Family of Map2 Protein Kinases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,985  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,620  
FILING DATE: 03-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6526-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1467 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1245  
US-08-461-985-3

Query Match 5.5%: Score 26; DB 2; Length 1467;  
Best Local Similarity 100.0%: Pred. No. 0.00075;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatcgtgacttgccctgcgcg 155  
|||||  
Db 655 AAGATCTGTGACTTGGCGCTTGCCCG 680

RESULT 16  
US-08-458-887-3  
Sequence 3, Application US/08458887  
Patent No. 5914261  
GENERAL INFORMATION:  
APPLICANT: Boulton, Teri G. et al.  
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas

```

: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,887
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,544
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 6526-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1467 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1245
:
US-08-458-887-3

Query Match          5.5%; Score 26; DB 2; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgacttggccttgcgcg 155
Db 655 AAGATCTGTGACTTGGCCTTGCCGC 680

RESULT 17
US-08-932-787B-3
: Sequence 3, Application US/08932787B
: Patent No. 6277963
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
: FILE REFERENCE: REG 430-A-1
: CURRENT APPLICATION NUMBER: US/08/932,787B
: CURRENT FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 08/469,547
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
:
US-08-932-787B-3
```

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: LOCATION: (1)...(1245)
: OTHER INFORMATION: ERK2 CDNA
:
US-08-932-787B-3
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Query Match          5.5%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgacttggccttgcgcg 155
Db 655 aagatctgtgacttggccttgcgcg 680
```

```

RESULT 18
US-08-932-012C-3
: Sequence 3, Application US/08932012C
: Patent No. 6297035
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: FILE REFERENCE: REG 430-Y-1
: CURRENT APPLICATION NUMBER: US/08/932,012C
: CURRENT FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 08/462,874
: PRIOR FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1245)
: OTHER INFORMATION: ERK2 CDNA
:
US-08-932-012C-3

Query Match          5.5%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgacttggccttgcgcg 155
Db 655 aagatctgtgacttggccttgcgcg 680

RESULT 19
US-08-888-818C-3
: Sequence 3, Application US/08888818C
: Patent No. 6303358
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: FILE REFERENCE: REG 430-Y-1
: CURRENT APPLICATION NUMBER: US/08/888,818C
: CURRENT FILING DATE: 1997-07-07
: PRIOR APPLICATION NUMBER: 08/478,985
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
```

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 3  
LENGTH: 1467  
TYPE: DNA  
ORGANISM: RAT  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1245)  
OTHER INFORMATION: ERK2 CDNA  
US-08-888-818C-3

Query Match 5.5%; Score 26; DB 4; Length 1467;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgacttgccg 155  
|||||  
Db 655 aagatctgacttgacttgccg 680

RESULT 20  
US-08-469-537A-19  
Sequence 19, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisompierre, et al.  
TITLE OF INVENTION: ERK AND ROR TYROSINE  
NUMBER OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USSN 08/144,992  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USSN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempier, Ph.D., Ga11 M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..159  
US-08-469-537A-19

Query Match 4.9%; Score 23; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgacttg 146  
|||||  
Db 22 gtggtgaagatctgacttg 44

RESULT 21  
US-07-912-122-3  
Sequence 3, Application US/07912122  
Patent No. 6228609  
GENERAL INFORMATION:  
APPLICANT: YANG, Zhi  
TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bertram I. Rowland  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/912,122  
FILING DATE: 19920709  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A-55931/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)789-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1894 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..1473  
US-07-912-122-3

Query Match 4.9%; Score 23; DB 4; Length 1894;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgacttg 146  
|||||  
Db 976 gtggtgaagatctgacttg 998

RESULT 22  
PCT-US93-06404-3  
Sequence 3, Application PC/TUS9306404  
GENERAL INFORMATION:  
APPLICANT: YANG, Zhi  
TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bertram I. Rowland  
STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06404  
FILING DATE: 19930707  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: FP-55931/BIR  
TELEPHONE: (415)789-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..1473  
PCT-US93-06404-3

Query Match 4.9%; Score 23; DB 5; Length 1894;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtgggaagatctgacttg 146  
|||||  
Db 976 GTGGTAAGATCTGTGACTTTGG 998

RESULT 23  
US-07-813-593-1  
Sequence 1, Application US/07813593  
Patent No. 5185438  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ihor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED  
STREET: 180 VARICK STREET  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/813,593  
FILING DATE: 19920415  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-PPP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3453 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..3009  
FEATURE:  
NAME/KEY: mat-peptide  
LOCATION: 31..3006  
US-07-813-593-1

Query Match 4.9%; Score 23; DB 1; Length 3453;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtgggaagatctgacttg 146  
|||||  
Db 2509 GTGGTAAGATCTGTGACTTTGG 2531

RESULT 24  
US-07-977-451-1  
Sequence 1, Application US/07977451  
Patent No. 5270458  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ihor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Imclone Systems Incorporated  
STREET: 180 Varick Street  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,451  
FILING DATE: 19921119  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US UNASSIGNED  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/906,397  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/05401  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TM 81102961  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:

```
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..3006
NAME/KEY: sig_peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
US-07-977-451-1

Query Match          4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgactttg 146
      |||||||
DB 2509 GTGCTGAGATCTGTGACTTTGG 2531

RESULT 25
US-07-946-507-1
Sequence 1, Application US/07946507
Patent No. 5283354
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
APPLICATION NUMBER: US/08/252,517
FILING DATE: 31-OCT-1994
CLASSIFICATION: 530
```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,507
FILING DATE: 19920917
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
NAME/KEY: mat_peptide
LOCATION: 31..3006
US-07-946-507-1

Query Match          4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgactttg 146
      |||||||
DB 2509 GTGCTGAGATCTGTGACTTTGG 2531

RESULT 26
US-08-252-517-1
Sequence 1, Application US/08252517
Patent No. 5548065
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,517
FILING DATE: 31-OCT-1994
CLASSIFICATION: 530
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; US-08-252-517-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gttgtgaagatctgtgactttg 146
Db 2509 GTGCTGAAGATCTGTGACTTTG 2531

RESULT 27
US-07-906-397A-1
; Sequence 1, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
```

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,397A
; FILING DATE: 19920626
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
; US-07-906-397A-1

Query Match 4.9%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gttgtgaagatctgtgactttg 146
Db 2509 GTGCTGAAGATCTGTGACTTTG 2531

RESULT 28
US-08-601-891-1
; Sequence 1, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
```

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated  
STREET: 180 Varick Street  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10014

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/601,891  
FILING DATE: 15-FEB-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,451  
FILING DATE: 19-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/906,397  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/05401  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TW 81102961  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/02750  
FILING DATE: 02-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,593  
FILING DATE: 24-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-7P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3453 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 112..3006  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 31..111  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..3009  
US-08-601-891-1

Query Match 4.9%; Score 23; DB 1; Length 3453;

Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 124 gtggtgaagacatctgacttgg 146  
|||||  
Db 2509 gtgtgaagatctgtgacttgg 2531

## RESULT 29

US-09-021-324-1  
Sequence 1, Application US/09021324  
Patent No. 5912133  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ihor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Imclone Systems Incorporated  
STREET: 180 Varick Street  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,451  
FILING DATE: 1992-11-19  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/906,397  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/05401  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TW 81102961  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/02750  
FILING DATE: 02-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,593  
FILING DATE: 24-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-7P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3453 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear



MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 112..3006  
FEATURE:  
NAME/KEY: s19\_peptide  
LOCATION: 31..111  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..3009  
US-09-021-324-1

Query Match 4.9%: Score 23; DB 2; Length 3453;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 124 gtggtgaagatctgtgacttgg 146  
|||||  
DB 2509 gtgtgaagatctgtgacttgg 2531

RESULT 30  
PCT-US92-02750-1  
Sequence 1, Application PC/TUS9202750  
GENERAL INFORMATION:  
APPLICANT: LEMISCHKA, ITHOR R.  
TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell  
TITLE OF INVENTION: Receptors And Their Ligands  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED  
STREET: 180 VARICK STREET  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: US  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/02750  
FILING DATE: 19920402  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FELT, IRVING N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-PPPT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3453 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..3009  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 31..3006  
PCT-US92-02750-1

Query Match 4.9%: Score 23; DB 5; Length 3453;

Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 124 gtggtgaagatctgtgacttgg 146  
|||||  
DB 2509 gtgtgaagatctgtgacttgg 2531

RESULT 31  
PCT-US92-05401-1  
Sequence 1, Application PC/TUS9205401  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ithor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED  
STREET: 180 VARICK STREET  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05401  
FILING DATE: 19920626  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-PPPT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3453 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..3009  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 31..3006  
PCT-US92-05401-1

Query Match 4.9%: Score 23; DB 5; Length 3453;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgacttgg 146  
|||||  
DB 2509 gtgtgaagatctgtgacttgg 2531

RESULT 32  
PCT-US92-09893-1  
Sequence 1, Application PC/TUS9209893  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ithor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:

```

ADDRESSER: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09893
FILING DATE: 19921116
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mal-peptide
LOCATION: 112..3006
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
PCT-US92-09893-1

Query Match          4.9%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtgtgaagatctgtacttgg 146
|||||
Db 2509 gtgtgaagatctgtacttgg 2531

RESULT 33
US-08-222-299-1
Sequence 11, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Moolle V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Seidel, Conda, Lavorgna
ADDRESSER: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
Sequence 1, Application US/08222299
Patent No. 5635388
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Mathews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-299-1

Query Match          4.9%; Score 23; DB 1; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



FILING DATE: 22-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/347,291  
FILING DATE: 02-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI J.D., David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 990008.446C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4054 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: p-alpha-17B  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 205..3471  
OTHER INFORMATION:  
US-08-180-195-35

Query Match 4.9%; Score 23; DB 1; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgacct 149  
|||||  
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 37  
US-08-477-329-35  
Sequence 35, Application US/08477329  
Patent No. 5750375  
GENERAL INFORMATION:  
APPLICANT: Sledziewski Ph.D., Andrzej Z  
APPLICANT: Bell, Lillian A.  
APPLICANT: Kindsvogel Ph.D., Wayne R.  
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,329  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 990008.446C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4054 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: p-alpha-17B  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 205..3471  
OTHER INFORMATION:  
US-08-477-329-35

Query Match 4.9%; Score 23; DB 1; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgacct 149  
|||||  
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 38  
US-08-475-458-35  
Sequence 35, Application US/08475458  
Patent No. 5843725  
GENERAL INFORMATION:  
APPLICANT: Sledziewski Ph.D., Andrzej Z  
APPLICANT: Bell, Lillian A.  
APPLICANT: Kindsvogel Ph.D., Wayne R.  
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGIC  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,458  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 990008.446D5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4054 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N

ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: p-alpha-17B  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 205..3471  
OTHER INFORMATION:  
US-08-475-458-35

Query Match 4.9%; Score 23; DB 2; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgacct 149  
|||||  
Db 2698 CTGAAGATCTGTGACTTTGGCCT 2720

RESULT 39  
US-08-980-400-35  
Sequence 35, Application US/08980400  
Patent No. 6018026  
GENERAL INFORMATION:  
APPLICANT: Sledziewski Ph.D., Andrzej Z  
APPLICANT: Bell, Lillian A.  
APPLICANT: Kindsvogel Ph.D., Wayne R.  
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/980,400  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,329  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 990008.446C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEO ID NO: 35;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4054 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: p-alpha-17B  
FEATURE:  
NAME/KEY: CDS

LOCATION: 205..3471  
OTHER INFORMATION:  
US-08-980-400-35

Query Match 4.9%; Score 23; DB 3; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatctgtgacttgacct 149  
|||||  
Db 2698 CTGAAGATCTGTGACTTTGGCCT 2720

RESULT 40  
US-09-583-459A-35  
Sequence 35, Application US/09583459A  
Patent No. 6291212  
GENERAL INFORMATION:  
APPLICANT: Sledziewski Ph.D., Andrzej Z  
APPLICANT: Bell, Lillian A.  
APPLICANT: Kindsvogel Ph.D., Wayne R.  
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS  
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/583,459A  
FILING DATE: 30-MAY-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,510  
FILING DATE: 27-DEC-1990  
APPLICATION NUMBER: US 07/146,877  
FILING DATE: 22-JAN-1988  
APPLICATION NUMBER: US 07/347,291  
FILING DATE: 02-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki J.D., David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 990008.446C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEO ID NO: 35;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4054 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: p-alpha-17B  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 205..3471

OTHER INFORMATION:  
US-09-583-459A-35

Query Match 4.9%; Score 23; DB 4; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgccct 149  
|||||  
DB 2698 GTGAAGATCTGTGACTTGCCCT 2720

## RESULT 41

US-09-583-210-35

Sequence 35, Application US/09583210

Patent No. 6291646

GENERAL INFORMATION:

APPLICANT: Sledziwski Ph.D., Andrzej Z

APPLICANT: Bell, Lillian A.

TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/583,210

FILING DATE: 30-MAY-2000

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,510

FILING DATE: 27-DEC-1990

APPLICATION NUMBER: US 07/146,877

FILING DATE: 22-JAN-1988

APPLICATION NUMBER: US 07/347,291

FILING DATE: 02-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: Maki J.D., David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.446C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 4054 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: p-alpha-17B

FEATURE:

NAME/KEY: CDS

LOCATION: 205..3471

OTHER INFORMATION:

US-09-583-210-35

Query Match 4.9%; Score 23; DB 4; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtgacttgccct 149  
|||||  
DB 2698 GTGAAGATCTGTGACTTGCCCT 2720

## RESULT 42

US-09-583-449A-35

Sequence 35, Application US/09583449A

Patent No. 6300099

GENERAL INFORMATION:

APPLICANT: Sledziwski Ph.D., Andrzej Z

APPLICANT: Bell, Lillian A.

TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/583,449A

FILING DATE: 30-MAY-2000

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,510

FILING DATE: 27-DEC-1990

APPLICATION NUMBER: US 07/146,877

FILING DATE: 22-JAN-1988

APPLICATION NUMBER: US 07/347,291

FILING DATE: 02-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: Maki J.D., David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.446C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 4054 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: p-alpha-17B

FEATURE:

NAME/KEY: CDS

LOCATION: 205..3471

OTHER INFORMATION:

US-09-583-449A-35

Query Match 4.9%; Score 23; DB 4; Length 4054;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149  
|||||  
DB 2698 GTGAAGATCTGTACTTGGCCT 2720

RESULT 43  
US-08-168-917-3

; Sequence 3, Application US/08168917  
; Patent No. 5686572

; GENERAL INFORMATION:

; APPLICANT: Wolf, David  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Fretto, Larry J.

; APPLICANT: Giese, Neil A.  
; APPLICANT: Escobedo, Jaime A.

; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND  
; STREET: Stewart Street Tower, 20th Floor \ One Market  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,917  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/650,793  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: 12418-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; MOLECULE TYPE: linear  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapiens  
; STRAIN: lambda gt10  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..3395  
; US-08-168-917-3

Query Match 4.9%; Score 23; DB 1; Length 4100;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149  
|||||  
DB 2622 GTGAAGATCTGTACTTGGCCT 2644

RESULT 44  
US-08-460-510-3

; Sequence 3, Application US/08460510  
; Patent No. 5872218

; GENERAL INFORMATION:

; APPLICANT: Wolf, David  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Fretto, Larry J.

; APPLICANT: Giese, Neil A.  
; APPLICANT: Escobedo, Jaime A.

; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and CREW  
; STREET: One Market Plaza, Stewart Street Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,510  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 012418-001430  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2422  
; TELEFAX: (415) 326-2400  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; MOLECULE TYPE: linear  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapiens  
; STRAIN: lambda gt10  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..3395  
; US-08-460-510-3

Query Match 4.9%; Score 23; DB 2; Length 4100;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 gtgaagatctgtacttggcct 149  
|||||  
DB 2622 GTGAAGATCTGTACTTGGCCT 2644

RESULT 45

US-08-460-490-3  
; Sequence 3, Application US/08460490

Patent No. 5891652  
GENERAL INFORMATION:  
APPLICANT: Wolf, David  
APPLICANT: Tomlinson, James E.  
APPLICANT: Fretto, Larry J.  
APPLICANT: Giese, Neil A.  
APPLICANT: Escobedo, Jaime A.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW  
STREET: One Market Plaza, Stewart Street Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,490  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 012418-001420  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
STRAIN: lambda gt10  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..3395  
US-08-460-490-3

Query Match 4.9%; Score 23; DB 2; Length 4100;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 127 gtcgaagatctgtacttgacct 149  
|||||  
Db 2622 GTGAGACTCTGTGACTTTGGCCT 2644

Search completed: July 15, 2002, 23:07:38  
Job time: 22991 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:09:50 : Search time 932.4 Seconds  
(without alignments)  
867.296 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514

Sequence: 1 cggaccatggaagatcttgc.....gacctgcatctcgagctg 471

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
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19: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
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23: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	471	100.0	4111	21	AAC62405	Human FLT4/VEGFR-3
2	471	100.0	4111	22	AAC68952	Human FLT4/VEGFR-3
3	471	100.0	4195	17	AAT12068	FLT4 receptor tyro
4	471	100.0	4195	21	AA37815	Human FLT4 recepto
5	471	100.0	4195	21	AA252333	Human tyrosine kin
6	471	100.0	4425	16	AA703090	Protein tyrosine-k
7	471	100.0	4795	21	AA37816	Human FLT4 recepto
8	471	100.0	4795	21	AA252334	Human tyrosine kin
9	471	100.0	9108	16	AA703104	Plasmid PRK5.tkl-1

C	10	420	89.2	6827	14	AA049753
C	11	420	89.2	6827	16	AA703101
C	12	305	64.8	4450	21	AAC62210
C	13	76	16.1	160	14	AA049747
C	14	76	16.1	160	16	AA703089
C	15	26	5.5	1047	20	AA696501
C	16	26	5.5	1467	13	AA020261
C	17	26	5.5	1815	19	AAV71031
C	18	26	5.5	1818	19	AAV71023
C	19	26	5.5	4696	17	AA713330
C	20	23	4.9	159	13	AA030721
C	21	23	4.9	159	20	AAV70215
C	22	23	4.9	1894	15	AA054036
C	23	23	4.9	3453	13	AA029954
C	24	23	4.9	3453	14	AA035502
C	25	23	4.9	3453	14	AA035549
C	26	23	4.9	3453	14	AA040914
C	27	23	4.9	3453	16	AA081012
C	28	23	4.9	3453	16	AA079068
C	29	23	4.9	3453	17	AA738733
C	30	23	4.9	3453	18	AA772118
C	31	23	4.9	3453	20	AA775114
C	32	23	4.9	3521	16	AA700801
C	33	23	4.9	4054	11	AA006869
C	34	23	4.9	6412	11	AA005989
C	35	22	4.7	4479	24	AB199406
C	36	21	4.5	2574	18	AA773125
C	37	20	4.2	20	21	AAC62208
C	38	20	4.2	1611	19	AAV62479
C	39	20	4.2	1611	19	AAV62479
C	40	20	4.2	2463	20	AA89336
C	41	20	4.2	4544	10	AA890355
C	42	20	4.2	4544	17	AA734552
C	43	20	4.2	5279	21	AA059189
C	44	20	4.2	5427	13	AA027447
C	45	20	4.2	5602	23	AA584940

#### ALIGNMENTS

RESULT 1	
ID	AAC62405 standard; cDNA; 4111 BP.
XX	XX
AC	AAC62405;
XX	XX
DT	31-JAN-2001 (first entry)
XX	XX
DE	Human FLT4/VEGFR-3 coding sequence.
XX	XX
KW	Human: FLT4: fms-like tyrosine kinase 4; lymphoedema;
KW	vascular endothelial growth factor receptor 3; VEGFR-3;
KW	Milroy-Nonne syndrome; lymphoedema praecox; ss.
OS	Homo sapiens.
XX	XX
PN	WO200058511-A1.
XX	XX
PD	05-OCT-2000.
XX	XX
PF	26-MAR-1999; 99WO-US06133.
XX	XX
PR	26-MAR-1999; 99WO-US06133.
XX	XX
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYRE-) UNIV HELSINKI LICENSING LTD OY.
PA	(UYPI-) UNIV PITTSBURGH.
XX	XX
PI	Ferrell RE, Allitalo K, Finegold DN, Karkkainen M;
XX	XX
DR	WPI: 2000-679298/66.
DR	P-PSDB: AAB29047.

PTK gene SAL-S1.  
Protein tyrosine-k  
Nucleotide sequenc  
PTK gene SAL-S1 pa  
Protein tyrosine-k  
Human extracellula  
ERK2. Rat ratius.  
Erk2-green floures  
Green flourescent  
Rat type I insulin  
Tyrosine kinase c1  
Rat orphan tyrosin  
Flk-2as gene. Mus  
Murine flk-2 cDNA.  
Murine flk-2 cDNA.  
Murine flk-2 codin  
Murine flk-2 cDNA.  
Flk2 receptor prot  
Mouse flk-2 cDNA.  
Human foetal liver  
Murine flk-2 recep  
Murine flk-2 cDNA.  
Flk2/flt3 tyrosine  
Sequence encodes P  
TR4 cDNA clone rel  
Mouse ischaemic co  
Mouse Tec tyrosine  
PCR primer used to  
Human MAP kinase.  
Human MAP kinase.  
Platelet-derived g  
cDNA encoding plat  
Platelet-derived g  
Human secreted pro  
Type B human plate  
DNA encoding novel

XX Screening a human subject for increased risk of developing a lymphatic  
PT disorder, comprises assaying a nucleic acid to determine a mutation  
PT altering the sequence of a vascular endothelial growth factor  
PT receptor-3 -

XX Claim 14: Page 46-52; 76pp: English.

XX The present sequence is the coding sequence for the human vascular  
CC endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or  
CC fms-like tyrosine kinase 4). It was used in the methods of the invention,  
CC which involve the screening of individuals to determine which VEGFR-3  
CC alleles they possess and thus their likelihood of developing hereditary  
CC lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne  
CC syndrome, which is early onset lymphoedema and lymphoedema praecox, which  
CC is late onset.

XX Sequence 4111 BP; 846 A; 1273 C; 1298 G; 694 T; 0 other:

Query Match 100.0%; Score 471; DB 21; Length 4111;  
Best Local Similarity 100.0%; Pred. No. 1e-225;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagatgagttctctg 60  
DB 3044 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagatgagttctctg 3103  
OY 61 gcttccggaagatgcatccacagaagacatgctgtctgtcgaacatctctgctggaagc 120  
DB 3104 gcttccggaagatgcatccacagaagacatgctgtctgtcgaacatctctgctggaagc 3163  
OY 121 gacgtgtgaaagatctgtactgtgcttgcctgcccgaagacatctacaaagccctgactac 180  
DB 3164 gacgtgtgaaagatctgtactgtgcttgcctgcccgaagacatctacaaagccctgactac 3223  
OY 181 gtcgcgaagggcagatgcccgcgtgcctcgaagtgaatgagtcgcccctgaaagacatcttcgac 240  
DB 3224 gtcgcgaagggcagatgcccgcgtgcctcgaagtgaatgagtcgcccctgaaagacatcttcgac 3283  
OY 241 aaggtgtacacacagaagatgagctgtgcttcttgagggtgcttctctctgaggagatcttc 300  
DB 3284 aaggtgtacacacagaagatgagctgtgcttcttgagggtgcttctctctgaggagatcttc 3343  
OY 301 tctctgggggctccctccgtacccctgagggtgacagatcaatgaagatctctgcagcgagctg 360  
DB 3344 tctctgggggctccctccgtacccctgagggtgacagatcaatgaagatctctgcagcgagctg 3403  
OY 361 aaggaagggcacaagatgagggcccgagagctgagccactccgcacatacgccgacatcatg 420  
DB 3404 aaggaagggcacaagatgagggcccgagagctgagccactccgcacatacgccgacatcatg 3463  
OY 421 ctgaacatgctgctccgagagacccaagcgagacatgcatcttcgagagctg 471  
DB 3464 ctgaacatgctgctccgagagacccaagcgagacatgcatcttcgagagctg 3514

RESULT 2

AAC68952 AAC68952 standard; cDNA; 4111 BP.

AC AAC68952:

XX 27-FEB-2001 (first entry)

XX Human Flt4/VEGFR-3 coding sequence.

XX Human: gene therapy: lymphatic disorder; hereditary lymphoedema; Flt4;  
KW vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-C; VEGF-D;  
XX fms-like tyrosine kinase 4; ss.

OS Homo sapiens.

PH Key Location/Qualifiers  
FT CDS 20..4111  
FT /\*tag= a  
FT /product= "Human Flt4/VEGFR-3"

PN CA2283470-A1.

PD 26-SEP-2000.

PF 29-SEP-1999; 99CA-2283470.

PR 26-MAR-1999; 99NC-US06133.

PR 16-AUG-1999; 99US-0375248.

PA (UYPI-) UNIV PITTSBURGH.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

PI (LUDW-) LUDWIG INST CANCER RES.

PI Altalo K, Ferrell RE, Finegold DN, Karkkainen M;

DR WPI, 2001-007762/02.

DR P-PSDB: AAB37604.

PS Claim 15: Pages 48-54; 99pp: English.

CC The present invention relates to a method for screening a human subject  
CC for an increased risk of developing a lymphatic disorder e.g. hereditary  
CC lymphoedema. The method comprises assaying nucleic acid of a human  
CC subject to determine a presence or an absence of a mutation altering the  
CC sequence or expression of vascular endothelial growth factor receptor-3  
CC (VEGFR-3)/fms-like tyrosine kinase 4 (Flt4) allele and determining an  
CC increased risk of developing lymphatic disorder from presence or absence  
CC of the mutation. The present sequence is the coding sequence for human  
CC VEGFR-3/Flt4. The presence of a mutation altering the encoded amino acid  
CC sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid  
CC correlates with an increased risk of developing a lymphatic disorder.  
CC Treatment for hereditary lymphoedema can be provided through the  
CC administration of VEGF-C and VEGF-D genes (via gene therapy) and  
CC proteins.

SO Sequence 4111 BP; 846 A; 1272 C; 1299 G; 694 T; 0 other:

Query Match 100.0%; Score 471; DB 22; Length 4111;  
Best Local Similarity 100.0%; Pred. No. 1e-225;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagatgagttctctg 60  
DB 3044 ctgacacatggaagatctgtctgtctacagcttccaggtgagcagaagatgagttctctg 3103  
OY 61 gcttccggaagatgcatccacagaagacatgctgtctgtcgaacatctctgctggaagc 120  
DB 3104 gcttccggaagatgcatccacagaagacatgctgtctgtcgaacatctctgctggaagc 3163  
OY 121 gacgtgtgaaagatctgtactgtgcttgcctgcccgaagacatctacaaagaccctgactac 180  
DB 3164 gacgtgtgaaagatctgtactgtgcttgcctgcccgaagacatctacaaagaccctgactac 3223  
OY 181 gtcgcgaagggcagatgcccgcgtgcctcgaagtgaatgagtcgcccctgaaagacatcttcgac 240  
DB 3224 gtcgcgaagggcagatgcccgcgtgcctcgaagtgaatgagtcgcccctgaaagacatcttcgac 3283  
OY 241 aaggtgtacacacagaagatgagctgtgcttcttgagggtgcttctctctgaggagatcttc 300  
DB 3284 aaggtgtacacacagaagatgagctgtgcttcttgagggtgcttctctctgaggagatcttc 3343  
OY 301 tctctgggggctccctccgtacccctgagggtgacagatcaatgaagatctctgcagcgagctg 360  
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Db 3344 tctctgggggctccctccgtacctggtgggtagcatcaatgaggagttctgcccagcgctg 3403  
QY 361 agagacggcacaagatgagtgcccgagctgagccatcccccgcataagccgcatcatg 420  
|||||  
Db 3404 agagacggcacaagatgagtgcccgagctgagccatcccccgcataagccgcatcatg 3463  
QY 421 ctgaactgtctgctcggagagaccccaagcgagacclgacatctctcgagctg 471  
|||||  
Db 3464 ctgaactgtctgctcggagagaccccaagcgagacclgacatctctcgagctg 3514

## RESULT 3

AAT12068  
ID AAT12068 standard; DNA: 4195 BP.  
XX  
AC AAT12068;  
XX  
DT 08-APR-1996 (first entry)  
XX  
DE FLT4 receptor tyrosine kinase DNA.  
XX  
XX FLT4; receptor tyrosine kinase; probe; metastasis; lymphoma;  
KM lymphangioma; immunological disease; cancer; diagnosis; therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 20..3976  
FT /tag= a  
XX  
XX W09533772-A1.  
XX  
XX 14-DEC-1995.  
XX  
XX 09-JUN-1995; 95MO-F100337.  
XX  
XX 09-JUN-1994; 94US-0257754.  
XX  
XX (ALIT/) ALITALO K.  
PA (KAIP/) KAIPAINEN A.  
PA (KARN/) KARNANI P.  
PA (KORH/) KORHONEN J.  
PA (MATI/) MATIKAINEN M.  
PA (MUST/) MUSTONEN T.  
PA (PAJU/) PAJUSOLA K.  
XX  
PI Alitalo K, Kaipainen A, Karnani P, Korhonen J, Matikainen M;  
PI Mustonen T, Pajusola K;  
XX  
XX WPI: 1996-040189/04.  
XX  
XX P-PSDB: AAR90528.  
XX  
XX Antibodies against FLT4 receptor tyrosine kinase, hybridomas and  
PT nucleic acid probes used to diagnose and treat e.g. metastatic  
PT cancers, involving alterations to lymphatic vessels.  
XX  
XX  
XX Claim 9: Page 27-33; 54pp; English.  
XX  
XX A DNA sequence (AAT12068) coding for FLT4 receptor tyrosine kinase  
CC (AAR90528) is used as a probe that specifically binds/hybridizes to  
CC DNA encoding human FLT4. Such probes are used to detect FLT4, a  
CC novel marker for lymphatic vessels and some high endothelial  
CC venules, in biological tissue for use in diagnosis and therapy of  
CC e.g. inflammatory, infectious and immunological diseases, metastatic  
CC lymph nodes and lymphangiomas.  
XX  
XX  
XX Sequence 4195 BP: 889 A; 1278 C; 1305 G; 723 T; 0 other;

Query Match 100.0%; Score 471; DB 17; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 1e-225;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgacatggaagatctgtctgtctacaagcttccaaagtggccagaaggaatgagttcttg 60  
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Db 3044 ctgacatggaagatctgtctgtctacaagcttccaaagtggccagaaggaatgagttcttg 3103  
QY 61 gcttccgaagtgatccacagagacctggtctcgcgaacatctgtctcgcgaagc 120  
Db 3104 gcttccgaagtgatccacagagacctggtctcgcgaacatctgtctcgcgaagc 3163  
QY 121 gaagtgtgaagatctgttactttgttccttgcgcggagacatctacaaagacctgactac 180  
Db 3164 gaagtgtgaagatctgttactttgttccttgcgcggagacatctacaaagacctgactac 3223  
QY 181 gtcgcgaagggcagtgctcccgctgcccctgaagtgatgagccctgaagacatctcagc 240  
Db 3224 gtcgcgaagggcagtgctcccgctgcccctgaagtgatgagccctgaagacatctcagc 3283  
QY 241 aaggtgtacacacagcagagtgacgtgtgtctcttgggtgcttctcctcgcggaagatctc 300  
Db 3284 aaggtgtacacacagcagagtgacgtgtgtctcttgggtgcttctcctcgcggaagatctc 3343  
QY 301 tctctgggggctccctccgtacctggtgggtgcagatcaatgagagttctgcccagcgctg 360  
Db 3344 tctctgggggctccctccgtacctggtgggtgcagatcaatgagagttctgcccagcgctg 3403  
QY 361 agagacggcacaagatgagtgagggcccgagctggccactcccgccataagccgcatcatg 420  
Db 3404 agagacggcacaagatgagtgagggcccgagctggccactcccgccataagccgcatcatg 3463  
QY 421 ctgaactgtctgctcggagagaccccaagcgagacclgacatctctcgagctg 471  
Db 3464 ctgaactgtctgctcggagagaccccaagcgagacclgacatctctcgagctg 3514

## RESULT 4

AA37815  
ID AA37815 standard; CDNA: 4195 BP.  
XX  
AC AA37815;  
XX  
XX 15-JAN-2001 (first entry)  
XX  
XX  
XX Human FLT4 receptor tyrosine kinase short form coding sequence.  
DE  
XX  
XX Human; FLT4 receptor tyrosine kinase; antibody; extracellular domain;  
KM lymphatic vessel detection; lymphatic tissue; lymph node tissue;  
KM endothelial venule; diagnosis; lymphoma; short form; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX  
XX Key Location/Qualifiers  
XX  
XX FT CDS 20..3916  
XX  
XX FT /tag= a  
XX  
XX FT /product= FLT4 receptor tyrosine kinase short form  
XX  
XX US6107046-A.  
XX  
XX 22-AUG-2000.  
XX  
XX 28-JUL-1997; 97US-0901710.  
XX  
XX 09-OCT-1992; 92US-0959951.  
XX  
XX 09-JUN-1994; 94US-0257754.  
XX  
XX 14-NOV-1994; 94US-0340011.  
XX  
XX (ORIN ) ORION CORP.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX  
XX Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;  
PI Matikainen M, Pajusola K.  
XX  
XX WPI: 2000-571323/53.  
XX  
XX P-PSDB: AAY90365.



[illegible]

PT	domain and Ig constant domain, useful for studying, and therapeutic
PT	modulation of, cell growth and differentiation
XX	
PS	Disclosure: Fig 15A-F; 125pp; English.
XX	
CC	DNA probes based on protein tyrosine-kinase (PTK) sequences were used
CC	to screen cDNA libraries to identify novel PTK genes. The S&L-S1
CC	gene (see also AAT03101) was isolated from several megakaryocytic cell
CC	libraries. The gene can be used to produce recombinant S&L-S1 or its
CC	fragments, to detect related genes, and to design drugs, peptides
CC	or antisense nucleotides that modulate PTK activity.
XX	
SQ	Sequence 4425 BP: 939 A; 1348 C; 1361 G; 777 T; 0 other;
Query Match 100.0%; Score 471; DB 16; Length 4425;	
Best Local Similarity 100.0%; Pred. No. 1e-225;	
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ctgaccatggaagatcttctgtctacagctcccaagtgccagagagatctctcg 60
DB	3055 ctgaccatggaagatcttctgtctacagctcccaagtgccagagagatctctcg 3114
QY	61 gcttcccgaaagtgcataccacagagaccctgctgtcctcggaacatctgtctcgaaagc 120
DB	3115 gcttcccgaaagtgcataccacagagaccctgctgtcctcggaacatctgtctcgaaagc 3174
QY	121 gacgttggtgaagatctgtgaacttggccttgcctcgcgagacatctacaagaaccctgaatac 180
DB	3175 gacgttggtgaagatctgtgaacttggccttgcctcgcgagacatctacaagaaccctgaatac 3234
QY	181 gtcccgaaagggcagtgcccggtctgcctccctgaagtgaatggccctgaagaagatcttgac 240
DB	3235 gtcccgaaagggcagtgcccggtctgcctccctgaagtgaatggccctgaagaagatcttgac 3294
QY	241 aaggtgtacaccacgcagagatgacgtgtgtctctcttgagggtctctctcggaagatctctc 300
DB	3295 aaggtgtacaccacgcagagatgacgtgtgtctctcttgagggtctctctcggaagatctctc 3354
QY	301 tctctggggggtctcccgtaaccttgggtgtgcagatcaatgaagaattctctgcacggctgtg 360
DB	3355 tctctggggggtctcccgtaaccttgggtgtgcagatcaatgaagaattctctgcacggctgtg 3414
QY	361 agagacgagacaaagatgagggcccgagctgcgcactcccgcatcagccgatacgccgatacg 420
DB	3415 agagacgagacaaagatgagggcccgagctgcgcactcccgcatcagccgatacgccgatacg 3474
QY	421 ctgaactctgtgtccgagagaccacaaggcgagacctgtacatctcggagctg 471
DB	3475 ctgaactctgtgtccgagagaccacaaggcgagacctgtacatctcggagctg 3525
RESULT 7	
AAA37816	
ID	AAA37816 standard; cDNA: 4795 BP.
XX	AAA37816;
AC	
XX	
DT	15-JAN-2001 (first entry)
XX	
DE	Human FLT4 receptor tyrosine kinase long form coding sequence.
XX	
KM	Human; FLT4 receptor tyrosine kinase; antibody; extracellular domain;
KW	lymphatic vessel detection; lymphatic tissue; lymph node tissue;
KW	endothelial venule; diagnosis; lymphoma; long form; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	CDS 20..4111
FT	/*tag=
FT	/product= FLT4 receptor tyrosine kinase long form

PN US6107046-A.  
XX  
PD 22-AUG-2000.  
XX  
PF 28-JUL-1997; 97US-0901710.  
XX  
PR 09-OCT-1992; 92US-0959951.  
XX 09-JUN-1994; 94US-0257754.  
PR 14-NOV-1994; 94US-0340011.  
XX  
PA (ORIN ) ORION CORP.  
PA (LUDM-) LUDWIG INST CANCER RES.  
XX  
XX Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;  
P1 Melikainen M, Pajusola K;  
XX  
XX WPI: 2000-571323/53.  
XX P-PSDB: AAY90366.  
XX  
XX Anticbody to extracellular domain of or to an epitope unique to a  
PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing  
PT lymphoma and imaging lymphatic vessels or high endothelial venules in  
PT tissue  
XX  
XX Disclosure: Column 55-66; 66pp; English.  
XX  
XX This sequence encodes the human Flt4 receptor tyrosine kinase long  
CC form protein. The invention relates to an antibody (I) specific to the  
CC extracellular domain of or to an epitope unique to a vertebrate Flt4  
CC receptor tyrosine kinase protein (II). A composition comprising (I) is  
CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph  
CC node tissue or high endothelial venules in an organism preferably mammal  
CC especially human. The method comprises administering the composition and  
CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high  
CC endothelial venules. (I) is also useful for screening a biological sample  
CC for the presence of (II) or diagnosing a disease state. The diagnosing  
CC method of the disease state preferably lymphoma comprises obtaining a  
CC tissue sample on a vertebrate organism suspected of being in a diseased  
CC state characterised by in Flt4 expression in lymphatic cells or high  
CC endothelial venules and screening the diseased state utilising (I).  
CC (I) is also useful for imaging lymphatic vessels or high endothelial  
CC venules in a tissue by contacting the tissue with (I) and imaging the  
CC vessels by detecting (I) bound to the tissues.  
XX  
XX Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;  
SQ

Query Match 100.0%; Score 471; DB 21; Length 4795;  
Best Local Similarity 100.0%; Pred. No. 1e-225;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgacacatggaagatctgtctgtctacacgtcccaagtgccagagagatgagttctctg 60  
DB 3044 ctgacacatggaagatctgtctgtctacacgtcccaagtgccagagagatgagttctctg 3103  
OY 61 gcttcccgaaagtgacatccacagagacctggtctcgcgaacattctgtctcgaaagc 120  
DB 3104 gcttcccgaaagtgacatccacagagacctggtctcgcgaacattctgtctcgaaagc 3163  
OY 121 gacgtgtgtaagatctgtgacttgccttgccttcgacgagacatacaaaacctgactac 180  
DB 3164 gacgtgtgtaagatctgtgacttgccttgccttcgacgagacatacaaaacctgactac 3223  
OY 181 gtcgcgaaggaagtgccggtctgacctgaagtgaatgagccctgaagacatctctcgac 240  
DB 3224 gtcgcgaaggaagtgccggtctgacctgaagtgaatgagccctgaagacatctctcgac 3283  
OY 241 aaggtgtacacacgaagtgagtggttcccttgggtgctctctcgcggaagatcttc 300  
DB 3284 aaggtgtacacacgaagtgagtggttcccttgggtgctctctcgcggaagatcttc 3343  
OY 301 tctctgggggacctcccgctacccctgggtgacagatcaaatgaagatcttcgacagggctg 360  
|||||

DB 3344 tctctgggggacctcccgctacccctgggtgacagatcaaatgaagatcttcgacagggctg 3403  
OY 361 agagacgagcaacaagatgtagggcccgagcttgccactccgcatacgcgcacatg 420  
DB 3404 agagacgagcaacaagatgtagggcccgagcttgccactccgcatacgcgcacatg 3463  
OY 421 ctgaactgctgtgtccgagagaccccaaggcgagacgtcattctcggagctg 471  
DB 3464 ctgaactgctgtgtccgagagaccccaaggcgagacgtcattctcggagctg 3514

RESULT 8  
AA252334  
ID AA252334 standard; CDNA; 4795 BP.  
XX  
XX AA252334;  
AC  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human tyrosine kinase receptor Flt4-long form cDNA.  
XX  
KW Human: receptor tyrosine kinase: RTK; Flt4; fms-like tyrosine kinase 4;  
KW VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;  
KW cytosolic; tumour imaging; anti-tumour therapy; treatment; diagnosis;  
KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;  
KW sarcoma; malignancy; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 20..4111  
FT /tag="a  
FT /product="Flt4 receptor-long form"  
XX  
XX WO200021560-A1.  
XX  
XX 20-APR-2000.  
XX  
XX 08-OCT-1999; 99WO-US23525.  
XX  
XX 09-OCT-1998; 98US-0169079.  
XX  
XX (LUDM-) LUDWIG INST CANCER RES.  
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
XX  
XX Alitalo K, Kaipainen A, Vailtoila R, Jussila L;  
PI WPI: 2000-317850/27.  
XX P-PSDB: AAY70747.  
XX  
XX Treating neoplastic diseases such as lymphoma, carcinomas, melanomas  
PT and sarcomas, involves administering a compound capable of inhibiting  
PT binding of ligand proteins to fms-like tyrosine kinase-4 receptor -  
XX  
XX Disclosure: Page 120-127; 148pp; English.  
XX  
XX The patent discloses a method to treat neoplastic disease characterised  
CC by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also  
CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in  
CC endothelial cells of blood vessels adjacent to malignant neoplasm. The  
CC method involves administering a compound that inhibits binding of a  
CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular  
CC endothelial cells. The compound is useful for treating neoplastic disease  
CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas  
CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used  
CC for manufacturing medicament useful for diagnostic screening, imaging and  
CC treatment of malignancies characterised by Flt4-expressing blood cells.  
CC The present sequence is a cDNA encoding the long form of Flt4 receptor  
CC from an oligo-dT primed human erythroleukemia cell line (HEL) cDNA  
CC library in bacteriophage lambda gt11. The Flt4 gene maps to chromosome 1  
CC region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in  
CC their 3' sequences and are differentially expressed in HEL and DAPI cell  
CC lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases

CC (RTKs). It is used as a target for tumour imaging and anti-tumour  
CC therapy.

Sequence 4795 BP: 977 A; 1490 C; 1494 G; 834 T; 0 other:

Query Match 100.0%; Score 471; DB 21; Length 4795;  
Best Local Similarity 100.0%; Pred. No. 1e-225;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgaccatggaagatctgtctgtctacagctccaggtgagcagagatgagttcccg 60
Db 3044 ctgaccatggaagatctgtctgtctacagctccaggtgagcagagatgagttcccg 3103
OY 61 gcttcccgaaagatgcatccacagagacctgtgctcggaaacatctgtctgcygaagc 120
Db 3104 gcttcccgaaagatgcatccacagagacctgtgctcggaaacatctgtctgcygaagc 3163
OY 121 gacgtggtgaagatctgtgacttggccttgcgcggagacatctacaagaacctgactac 180
Db 3164 gacgtggtgaagatctgtgacttggccttgcgcggagacatctacaagaacctgactac 3223
OY 181 gtcgcaaggagcagtgcccggtctgccttgaaagtgaatgcccctgaaagcatcttcgac 240
Db 3224 gtcgcaaggagcagtgcccggtctgccttgaaagtgaatgcccctgaaagcatcttcgac 3283
OY 241 aaggtgtacacacgacgaagtgactgtgtctcttgggggtgctctctggaagatcttc 300
Db 3284 aaggtgtacacacgacgaagtgactgtgtctcttgggggtgctctctggaagatcttc 3343
OY 301 tctctgggggctccctcccttacccctgggggtgacatcaatgaggaattctgcacagcgctg 360
Db 3344 tctctgggggctccctcccttacccctgggggtgacatcaatgaggaattctgcacagcgctg 3403
OY 361 agagacgycacaaagatgagggcccggagctgagcactccgcacatagcgcgcatcag 420
Db 3404 agagacgycacaaagatgagggcccggagctgagcactccgcacatagcgcgcatcag 3463
OY 421 ctgaactgtctgtccgagagaccccaaggcgaagactgcatctctggagctg 471
Db 3464 ctgaactgtctgtccgagagaccccaaggcgaagactgcatctctggagctg 3514
```

RESULT 9  
AAT03104  
ID AAT03104 standard; DNA: 9108 BP.

AC AAT03104:

DT 14-FEB-1996 (first entry)

DE Plasmid pRK5.tki-1.1 encoding Sal S-1.

KW Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;

KM differentiation; pRK5.tki-1.1; ss.

OS Chimeric synthetic;  
OS Chimeric Homo sapiens.

PN W09527061-A1.

PD 12-OCT-1995.

PF 04-APR-1995; 95MO-US04228.

PR 04-APR-1994; 94US-0222616.

PA (GETH ) GENENTECH INC.

PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP.

XX Wood WI;  
XX MPI: 1995-366160/47.

XX Agonist antibodies which activate specific protein tyrosine  
PT kinase(s) - also activate chimeric proteins of kinase extracellular  
PT domain and Ig constant domain, useful for studying, and therapeutic  
PT modulation of, cell growth and differentiation

XX Example 7; Page 102-111; 125pp; English.

XX PCR primers given in AAT03102-03 were used to amplify plasmid  
CC PRK5.tki-1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.  
CC The product was used to construct a fusion of the SAL-S1  
CC extracellular domain and human IgG1 Fc domain, which was expressed  
CC in 293 and COS7 cells and used to raise antibodies having  
CC protein tyrosine-kinase agonist activity.

XX Sequence 9108 BP: 2086 A; 2554 C; 2491 G; 1977 T; 0 other:

Query Match 100.0%; Score 471; DB 16; Length 9108;  
Best Local Similarity 100.0%; Pred. No. 9.9e-226;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3987 ctgaccatggaagatctgtctgtctacagctccaggtgagcagagatgagttcccg 4046
OY 61 gcttcccgaaagatgcatccacagagacctgtgctcggaaacatctgtctgcygaagc 120
Db 4047 gcttcccgaaagatgcatccacagagacctgtgctcggaaacatctgtctgcygaagc 4106
OY 121 gacgtggtgaagatctgtgacttggccttgcgcggagacatctacaagaacctgactac 180
Db 4107 gacgtggtgaagatctgtgacttggccttgcgcggagacatctacaagaacctgactac 4166
OY 181 gtcgcaaggagcagtgcccggtctgccttgaaagtgaatgcccctgaaagcatcttcgac 240
Db 4167 gtcgcaaggagcagtgcccggtctgccttgaaagtgaatgcccctgaaagcatcttcgac 4226
OY 241 aaggtgtacacacgacgaagtgactgtgtctcttgggggtgctctctggaagatcttc 300
Db 4227 aaggtgtacacacgacgaagtgactgtgtctcttgggggtgctctctggaagatcttc 4286
OY 301 tctctgggggctccctcccttacccctgggggtgacatcaatgaggaattctgcacagcgctg 360
Db 4287 tctctgggggctccctcccttacccctgggggtgacatcaatgaggaattctgcacagcgctg 4346
OY 361 agagacgycacaaagatgagggcccggagctgagcactccgcacatagcgcgcatcag 420
Db 4347 agagacgycacaaagatgagggcccggagctgagcactccgcacatagcgcgcatcag 4406
OY 421 ctgaactgtctgtccgagagaccccaaggcgaagactgcatctctggagctg 471
Db 4407 ctgaactgtctgtccgagagaccccaaggcgaagactgcatctctggagctg 4457
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RESULT 10  
AAQ49753/c  
ID AAQ49753 standard; DNA: 6827 BP.

AC AAQ49753:

DT 10-MAR-1994 (first entry)

DE PTK gene SAL-S1.

KW PTK: protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;

KM fetal liver kinase; megakaryocyte; amplification; primer;

XX polymerase chain reaction; PCR; ds.

XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS complement (1877..2923)

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FT      /*tag= d
FT      /note= "bases illegible in the specification"
XX
XX      WO9315201-A.
XX      05-AUG-1993.
XX
XX      22-JAN-1993: 93WO-0500586.
XX
XX      22-JAN-1992: 92US-0826935.
XX
XX      (MDEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
XX      Avraham H, Cowley S, Groopman J, Scadden D;
XX
XX      WPI: 1993-320330/40.
XX      P-PSDB: AAR41940.
XX
XX      New protein tyrosine kinase genes and proteins encoded by genes -
XX      are of human mega-karyocytic origin
XX
XX      Claim 2: Fig 4: 60pp; English.
XX
XX      PTK genes were identified using two sets of degenerative
XX      oligonucleotide primers: a first set which amplifies all PTK DNA
XX      segments (AA049743-44), and a second set which amplifies highly
XX      conserved sequences present in the catalytic domain of the c-kit
XX      subgroup of PTKs (AA049745-46). The PTK genes identified are described
XX      in AA049747-57 and AAR41997-02.
XX      SAL-S1 is expressed in several megakaryocytic cell lines, but not
XX      in erythroid cell lines. The SAL-S1 expression prod. exhibited
XX      significant sequence homology with known protein tyrosine kinases
XX      of the FLT/FLK family. The partial and full-length SAL-S1 gene
XX      sequences are given in AA049747 and AA049753 respectively.
XX
XX      Sequence 6827 BP; 1555 A; 1868 C; 1740 G; 1660 T; 4 other:
SQ
Query Match      89.2%; Score 420; DB 14; Length 6827;
Best Local Similarity 99.8%; Pred. No. 3.2e-200;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 ctgaccatggaagatctgtctgtctacagcttcagtgagcagagatgagatctcgtg 60
DB      2749 CTGACCATGCAAGATCTGTCTGTCTACAGCTTCACAGTGGCCAGAGGATGCAATTCCTG 2690
OY      61 gcttccgaaagtgcattcctcagacagagacctggtctctcggaacatctctgtctcgaaagc 120
DB      2689 GCTTCCCGAAAGTGCATCCACAGACCTGCTCGAATCTGTGCTCGAAAGC 2630
OY      121 gactgtgtgaagatctgtgacttctgaccttgcccgagacatcaaaaacctgactac 180
DB      2629 GACGTGCTGAAGATCTGTGACTTTGGCTTGGCTTGGCCGACATCTACAAAGCCCGACTAC 2570
OY      181 gtccgcaaggcagtgcccgctgcccctgaaagtgaatgagcccttgaagacatcttcgac 240
DB      2569 GTCCCGCAAGGCGCATGCCCCGCTGCCCTGAGTGAATGATGAGCCCTGAACGATCTTCGAC 2510
OY      241 aaagtgtgacacacagagatgacgtgtgtgtcttctgtgggtgtcttctctcgagagatcttc 300
DB      2509 AAGGTGTACACCAAGCAGATGACGTGTGTGCTTTGGGTGCTTCTGTGCGGATCTTC 2450
OY      301 tctctgaggacctcccgtaaccttgagggtgacatcaatgaagatcttcgacagcgagctg 360
DB      2449 TCTCTGGGGCGCTTCCCGTACCTCGGGGTGCACATCAATGAGCAATTCCTCCAGCGCTG 2390
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OY      361 agagacggcacaaagatgaggcccgagagcttgcacactccgcatacagcgcatcatg 420
DB      2389 AGAGACGGCACAAAGATGAGAGGCGCCCGAGACTGACCTCCGCCATACGCCGATCATG 2330
OY      421 ctgaactgtctgtctcgagagaccccaaggcagagaccctgcatctcggagctg 471
DB      2329 CTGAAGCTGTGTGTCGAGACCCCAAGCGGAGACATTCATTCGAGCTG 2279
RESULT 11
AA03101/C
ID      AA03101 standard; DNA: 6827 BP.
XX
XX      AA03101;
AC      XX
XX      14-FEB-1996 (first entry)
DT      XX
XX      Protein tyrosine-kinase SAL-S1 gene.
DE      XX
XX      Protein tyrosine-kinase; PTK; SAL-S1; agonist; cell growth;
KW      XX
XX      differentiation; ss.
OS      XX
XX      Homo sapiens.
FH      Key      Location/Qualifiers
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FT      /*tag= a
FT      /note= "base n at position 3026 is not identified
FT      in the specification"
XX
XX      PN      WO9527061-A1.
XX      PD      12-OCT-1995.
XX
XX      PF      04-APR-1995: 95WO-US04228.
XX
XX      PR      04-APR-1994: 94US-0222616.
XX
XX      PA      (GENE) GENENTECH INC.
XX
XX      PI      Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX      PI      Wood WI;
XX
XX      WPI: 1995-366160/47.
XX      P-PSDB: AAR85938.
XX
XX      DR      Agonist antibodies which activate specific protein tyrosine
XX      kinase(s) - also activate chimeric proteins of kinase extracellular
XX      domain and Ig constant domain, useful for studying, and therapeutic
XX      modulation of, cell growth and differentiation
XX
XX      PS      Disclosure: Page 39-46; 125pp; English.
XX
XX      CC      DNA probes based on protein tyrosine-kinase (PTK) sequences were used
XX      to screen cDNA libraries to identify novel PTK genes. The SAL-S1
XX      gene (see also AA03090) was isolated from several megakaryocytic cell
XX      libraries. The gene can be used to produce recombinant SAL-S1 or its
XX      fragments, to detect related genes, and to design drugs, peptides
XX      or antisense nucleotides that modulate PTK activity.
XX
XX      SQ      Sequence 6827 BP; 1558 A; 1870 C; 1738 G; 1660 T; 1 other:
Query Match      89.2%; Score 420; DB 16; Length 6827;
Best Local Similarity 99.8%; Pred. No. 3.2e-200;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 ctgaccatggaagatctgtctgtctacagcttcagtgagcagagagatgagctcgtg 60
DB      2749 CTGACCATGGAAGATCTTGTCTGTACAGCTTCAGGTGGCCAGAGGATGAGTTCCTG 2690
OY      61 gcttccgaaagtgcattcctcagacagagacctggtctctcggaacatctctgtctcgaaagc 120
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Db 2689 GCTTCCCAAGTGCATTCACAGACCTGCTCTCGAATTCCTCTCGAAGC 2630
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Db 2639 GACGTGCTGAAGATCTGTGACTTTTGCCCTTCCGGGACATCTACAAAGACCCGACTAC 2570
Oy 181 gtccgcaaggcaatgcccgcgtgcctcgaagtgaatgagccctgaagatcttcgac 240
Db 2569 CTCCGCAACGGCAGTGCCTCCGCTCCCTGAAATGATGCCCTGAAAGACATCTTCAC 2510
Oy 241 aaggtgtacacacagcagatgtagctgtgtccttgggtgtctctctcgtggaatcttc 300
Db 2509 AAGGTGTACACGACGACAGTACGTGTGCTTTGGGGCTTCTCTCGAATCTTC 2450
Oy 301 tctctgggggctcccccgtaccctcgtgggtgagatcaatgaagatctctgcacgagctg 360
Db 2449 TCTCTGGGGGCTCTCCCTTACCCTTGCGGTGAGATCAATGACATCTTCCGACGCTG 2330
Oy 361 agagagcagacaagatgagggcccgagactggtccactccgcacatagcgcgacatg 420
Db 2389 AGACACGCGCACAGCATGAGGCGCCCGACGCTGGCCACTCCGCCATACGCCCATCATG 2330
Oy 421 ctgaactgtctgtccggagaccccaaggcagagactgtgactctctcgtgagctg 471
Db 2329 CTGAATCTCTGCTCGGAGACCCCAAGCGACGACCTGCTGCTCGAGCTG 2279

RESULT 12
AAC62210
ID AAC62210 standard; DNA: 4450 BP.
XX
AC AAC62210;
XX
DT 06-MAR-2001 (first entry)
XX
DE Nucleotide sequence of the human flt-4 gene.
XX
KW Antisense oligonucleotide; flt-4; receptor type tyrosine kinase;
KM lymphangiogenesis; prostate cancer; prostate cell; ss.
OS Homo sapiens.
XX
XX Location/Qualifiers
FH key 22..3918
FT CDS
FT /product= "flt-4"
FT /transl_except= (pos: 55..57, aa: Trp)
FT /transl_except= (pos: 58..60, aa: Leu)
FT /transl_except= (pos: 61..63, aa: Cys)
FT /transl_except= (pos: 64..66, aa: Leu)
FT /transl_except= (pos: 67..69, aa: Gly)
FT /transl_except= (pos: 70..72, aa: Leu)
FT /transl_except= (pos: 73..75, aa: Leu)
FT /transl_except= (pos: 76..78, aa: Asp)
FT /transl_except= (pos: 79..81, aa: Gly)
FT /transl_except= (pos: 82..84, aa: Leu)
FT /transl_except= (pos: 85..87, aa: Val)
FT /transl_except= (pos: 88..90, aa: Ser)
FT /transl_except= (pos: 91..93, aa: Asp)
FT /transl_except= (pos: 94..96, aa: Tyr)
FT /transl_except= (pos: 97..99, aa: Ser)
FT /transl_except= (pos: 1639..1641, aa: Lys)
FT /transl_except= (pos: 2236..2238, aa: Arg)
FT /transl_except= (pos: 3508..3510, aa: Ser)
FT /transl_except= (pos: 3598..3600, aa: Ser)
FT /transl_except= (pos: 3796..3798, aa: Phe)
XX
XX MO200062063-A1.
XX
XX 19-OCT-2000.
XX
XX 13-APR-1999; 99MO-US08079.
```

```
XX
PR 13-APR-1999; 99MO-US08079.
XX
PA (MMBL-) NORTHWEST BIOTHEAPUTICS INC.
XX
PI Su SL:
DR WPI: 2000-687067/67.
XX P-PSDB: AAB30542.
PT Detecting metastatic potential, diagnosing metastatic prostate cancer
PT or determining the prognosis of a subject with prostate cancer
PT comprises detecting the expression of flt-4 in a prostate cell
XX
PS Claim 6: Fig 1A-F: 78pp; English.
XX
CC The present sequence encodes human flt-4. Flt-4 is a receptor type
CC tyrosine kinase with 7 Ig-like domains similar to other VEGF receptors.
CC Flt-4 may play a role in lymphangiogenesis. Antisense oligonucleotides
CC can be used for detecting the metastatic potential, diagnosing
CC metastatic prostate cancer or determining the prognosis of a subject
CC with prostate cancer. The method comprises identifying the prostate
CC cell in a body fluid sample and detecting the expression of flt-4 in
CC the cell. Expression of flt-4 in a prostate cell indicates that the
CC cell is a cancerous prostate cell that has metastatic potential or is
CC a secondary tumour metastasis of a primary prostate tumour.
XX
SQ Sequence 4450 BP; 968 A; 1352 C; 1349 G; 781 T; 0 other:
XX
Query Match 64.8%; Score 305; DB 21; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1..1e-142;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ctgaccatggaagatctgtctgtctacagcttccagtgagcagagagatgttctc 60
Db 3046 ctgaccatggaagatctgtctgtctacagcttccagtgagcagagagatgttctc 3105
Oy 61 gcttccccaagatgcatccacaagagacctgtgctctcgaaacatctcgtcggaaagc 120
Db 3106 gcttccccaagatgcatccacaagagacctgtgctctcgaaacatctcgtcggaaagc 3165
Oy 121 gaagtgatgaagatctgtgacttggccttgcgggacatccaaagacctgactac 180
Db 3166 gaagtgatgaagatctgtgacttggccttgcgggacatccaaagacctgactac 3225
Oy 181 gtccgcaaggcagtgcccggtgcctcgaagtgaatgagccctgaagacatcttgac 240
Db 3226 gtccgcaaggcagtgcccggtgcctcgaagtgaatgagccctgaagacatcttgac 3285
Oy 241 aaggtgtacacacagcagatgtagctgtgctcttgggtgctctctcgtggaatctc 300
Db 3286 aaggtgtacacacacagcagatgtagctgtgctcttgggtgctctctcgtggaatctc 3345
Oy 301 tctctgggggctcccccgtacacctgggggtgcagatcaatgaagatctgcacg 356
Db 3346 tctctgggggctcccccgtacacctgggggtgcagatcaatgaagatctgcacg 3401

RESULT 13
AA049747
ID AA049747 standard; DNA: 160 BP.
XX
AC AA049747;
XX
DT 10-MAR-1994 (first entry)
XX
DE PTK gene SAL-sI partial sequence.
XX
XX PTK: protein tyrosine kinase; catalytic domain; c-Kit; FLT/FLK;
KM fetal liver kinase; megakaryocyte; amplification; primer;
KM polymerase chain reaction; PCR; ss.
```

OS	Homo sapiens.	Location/Qualifiers
XX		
FH	Key	2..160
FT	CDS	/tag= a
FT		1..21
FT	misc_feature	/tag= b
FT		/note= "PTK1/3 primers"
FT	misc_feature	136..160
FT		/tag= C
FT		/note= "PTK1W primer"
XX		
PN	WO9315201-A.	
PD	05-AUG-1993.	
XX		
XX		
PF	22-JAN-1993:	93WO-US00586.
XX		
PR	22-JAN-1992:	92US-0826935.
XX		
PA	(NEW-) NEW ENGLAND DEACONESS HOSPITAL.	
XX		
P1	Avraham H, Cowley S, Groopman J, Scadden D:	
XX		
DR	WPI: 1993-320330/40.	
DR	P-PSDB: AAR41894.	
XX		
PT	New protein tyrosine kinase genes and proteins encoded by genes -	
PT	are of human mega-karyocytic origin	
XX		
PS	Claim 2: Fig 1: 60pp: English.	
XX		
CC	PTK genes were identified using two sets of degenerative	
CC	oligonucleotide primers: a first set which amplifies all PTK DNA	
CC	segments (AAQ49743-44), and a second set which amplifies highly	
CC	conserved sequences present in the catalytic domain of the c-kit	
CC	subgroup of PTKs (AAQ49745-46). The PTK genes identified are described	
CC	in AAQ49747-57 and AAR41897-02.	
CC	SL-SI is expressed in several megakaryocytic cell lines, but not	
CC	in erythroid cell lines. The SAL-SI expression prod. exhibited	
CC	significant sequence homology with known protein tyrosine kinases	
CC	of the Fln/Flk family. The partial and full-length SAL-SI gene	
CC	sequences are given in AAQ49747 and AAQ49753 respectively.	
XX		
SO	Sequence 160 BP: 35 A: 44 C: 47 G: 34 T: 0 other:	
Query Match 16.1%; Score 76; DB 14; Length 160;		
Best Local Similarity 100.0%; Pred. No. 4.2e-28;		
Matches 76: Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	98 ggaacatctcgtcgtcgcgaagcgacgctggtgaagatctgtgacctgacctgccggg	157
Db	30 ggaacatctcgtcgtcgcgaagcgacgctggtgaagatctgtgacctgacctgccggg	89
Oy	158 acatctacaagacc 173	
Db	90 acatctacaagacc 105	
RESULT 14		
AA703089		
ID	AA703089 standard: DNA: 160 BP.	
XX	AA703089:	
XX		
DT	14-FEB-1996 (first entry)	
XX		
DE	Protein tyrosine-kinase SAL-SI DNA fragment.	
XX		
KW	Protein tyrosine-kinase; PTK; SAL-SI; agonist; cell growth;	
KW	differentiation; ss.	
XX		

OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	20..160
FT		/*tag= a
XX		
PN	W09527061-A1.	
XX		
PD	12-OCT-1995.	
XX		
PF	04-APR-1995;	95WO-US04228.
XX		
PR	04-APR-1994;	94US-0222616.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP,	
PI	Wood WI;	
XX		
DR	WPI: 1995-366160/47.	
XX	P-PSDB: AAR85922.	
XX		
PT	Agonist antibodies which activate specific protein tyrosine	
PT	kinase(s) - also activate chimeric proteins of kinase extracellular	
PT	domain and Ig constant domain, useful for studying, and therapeutic	
PT	modulation of, cell growth and differentiation	
XX		
PS	Disclosure: Page 35; 125pp; English.	
XX		
CC	DNA probes based on protein tyrosine-kinase (PTK) sequences were used	
CC	to screen cDNA libraries to identify novel PTK genes. A SAL-SI gene	
CC	fragment (AA03088) was isolated from several megakaryocytic cell lines	
CC	(see AA03090 for the full-length sequence).	
XX		
SQ	Sequence 160 BP; 35 A; 44 C; 47 G; 34 T; 0 other;	
	Query Match	16.1%; Score 76; DB 16; Length 160;
	Best Local Similarity	100.0%; Pred. No. 4.2e-28;
	Matches 76; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	98 ggaacatctcgtcgtcgcgaaagcgacgctgtgaagatcgtgacttggccttgcgcg99	157
DB		
	30 ggaacatctcgtcgtcgcgaaagcgacgctgtgaagatcgtgacttggccttgcgcg99	89
QY	158 acatctacaagaagcc 173	
DB	90 acatctacaagaagcc 105	
	RESULT 15	
	ABA96501	
ID	ABA96501 standard; cDNA: 1047 BP.	
XX		
XX	ABA96501;	
XX		
DT	12-MAR-2002 (first entry)	
XX		
DE	Human extracellular signal-regulated protein kinase-2 (erk-2) cDNA.	
XX		
KW	Human; extracellular signal-regulated protein kinase-2; erk-2;	
KW	recombinant production; Escherichia coli; HeLa cell; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1047
FT		/*tag= a
FT		/product= "Human erk-2"
XX		
PN	KR98022142-A.	
XX		
DD	25-JUN-1998.	

XX PF 20-SEP-1996: 96KR-0041219.  
 XX XX 20-SEP-1996: 96KR-0041219.  
 XX PA (GLDS ) LG CHEM LTD.  
 XX PI Kim CH, Cho JM, Chung HH, Lee JH;  
 XX DR WPI: 1999-300710/25.  
 XX P-PSDB: AAM52700.  
 XX PT Process for preparing extracellular signal-regulated protein kinase-2  
 XX from E. coli .  
 XX PS Example 2; Flg 1a-c; 9pp: Korean.  
 XX CC The invention relates to a process for the recombinant production  
 CC of human extracellular signal-regulated protein kinase-2 (erk-2) in  
 CC Escherichia coli. The present sequence represents cDNA encoding human  
 CC erk-2 initially isolated from HeLa cells.  
 XX SO Sequence 1047 BP: 303 A: 255 C: 225 G: 264 T: 0 other;

Query Match 5.5%; Score 26; DB 20; Length 1047;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgctgctgccc 155  
 |||||||  
 Db 454 aagatctgacttgctgctgccc 479

## RESULT 16

AAO20261  
 ID AAO20261 standard: DNA: 1467 BP.  
 XX AC AAO20261:  
 XX DT 31-MAR-1992 (first entry)  
 XX DE ERK2.  
 KW Microtubule-associated protein 2: central nervous system;  
 KW extracellular signal-regulated kinase; ERK; CNS; MAP2; ss  
 XX OS Rat rattus.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..1248  
 FT /\*tag= a  
 FT /label= ERK2  
 FT 172..174  
 FT /\*tag= b  
 FT /label= initiation\_codon  
 FT 202..204  
 FT /\*tag= c  
 FT /label= initiation\_codon  
 FT 1246..1248  
 FT /\*tag= d  
 XX PN MO9119008-A.  
 XX PD 12-DEC-1991.  
 XX PF 03-JUN-1991: 91MO-US03894.  
 XX PR 16-MAY-1991: 91US-0701544.  
 XX PR 01-JUN-1990: 90US-0532004.  
 XX PA (REGC-) REGENERON PHARM INC.  
 XX (TEXA ) UNIV OF TEXAS SYSTEM.

XX PI Boulton TG, Cobb MH, Yancopoulos GD, Nye S, Panayotatos N;  
 XX DR WPI: 1992-007489/01.  
 XX DR P-PSDB: AAR20104.  
 XX PT DNA encoding MAP2 kinase enzyme and vectors or host cells - are  
 XX PT for assaying cellular factor (e.g. NGF), and drug screening  
 XX PS Disclosure; Fig 3A; 9pp; English.

CC The identification of a family of protein serine/threonine kinases  
 CC which phosphorylate microtubule-associated protein 2 (MAP2) is  
 CC based, in part, on the cloning and characterisation of MAP2 kinases  
 CC designated extracellular signal-regulated kinase 1, 2 and 3 (ERK1,  
 CC ERK2 and ERK3) which are expressed in the central nervous system,  
 CC and on the identification of another ERK family member, ERK4, with  
 CC anlsera.  
 CC CC ERK1-3 are represented in AAO20260-62.  
 XX SO Sequence 1467 BP: 365 A: 382 C: 355 G: 365 T: 0 other;

Query Match 5.5%; Score 26; DB 13; Length 1467;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgctgctgccc 155  
 |||||||  
 Db 655 aagatctgacttgctgctgccc 680

## RESULT 17

AAV71031  
 ID AAV71031 standard: cDNA: 1815 BP.  
 XX AC AAV71031:  
 XX DT 08-FEB-1999 (first entry)  
 XX DE Erk2-green fluorescent protein fusion product.  
 KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;  
 KW Intracellular signalling; Chimera; ss.  
 XX OS Chimeric - Aequorea victoria.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..1815  
 FT /\*tag= a  
 XX PN MO9845704-A2.  
 XX PD 15-OCT-1998.  
 XX PF 07-APR-1998: 98WO-DK00145.  
 XX PR 07-APR-1997: 97DK-0000392.  
 XX PA (NOVO ) NOVO-NORDISK AS.  
 XX PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;  
 XX PI Tullin S;  
 XX DR WPI: 1998-594491/50.  
 XX DR P-PSDB: AAM85016.  
 XX PT Determining effect on signalling pathways in live cells from  
 XX PT redistribution of luminophores - specifically fusions of green  
 XX PT fluorescent protein with a signalling component, and new apparatus,  
 XX PT particularly for identifying toxins and potential therapeutic agents

PS Claim 63: Pages 122-125; 326pp; English.

XX The present sequence encodes a rat Erk2-green fluorescent

CC protein fusion product. The fusion protein is used in an assay

CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light

CC emitted from a lumiphore present in the cells. The variation in light

CC emission is processed to provide information that correlates spatial

CC distribution to the degree of the molecule. The method is used to

CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and

CC to identify new drug targets.

SO Sequence 1815 BP; 480 A; 506 C; 451 G; 378 T; 0 other;

Query Match 5.5%; Score 26; DB 19; Length 1815;  
Best Local Similarity 100.0%; Pred. No. 0.0041;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgccgcg 155  
Db 484 aagatctgacttgagcttgccgcg 509

RESULT 18  
AAV71023  
ID AAV71023 standard; cDNA; 1818 BP.

AC AAV71023;

DT 08-FEB-1999 (first entry)

DE Green fluorescent protein-Erk2 fusion product.

KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;  
KW Intracellular signalling; chimera; ss.

OS Chimeric - Rattus sp.

XX Chimeric - Rattus sp.

XX Key Location/Qualifiers  
FH CDS 1..1818  
FT /\*tag= a

PN MO9845704-A2.

XX 15-OCT-1998.

PD 07-APR-1998; 98WO-DK00145.

PF 07-APR-1997; 97DK-0000392.

PR (NOVO ) NOVO-NORDISK AS.

PA Kasper A. Petersen Bjorn S. Scudder K. Thastrup O;  
PI Tullin S;  
PI WPI; 1998-594491/50.  
DR P-PSDB; AAW85007.

XX Determining effect on signalling pathways in live cells from  
PT redistribution of lumiphores - specifically fusions of green  
PT fluorescent protein with a signalling component, and new apparatus,  
PT particularly for identifying toxins and potential therapeutic agents

PS Claim 63: Pages 71-74; 326pp; English.

XX The present sequence encodes a green fluorescent protein (GFP)-rat  
CC Erk2 fusion product. The fusion protein is used in an assay  
CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light

CC emitted from a lumiphore present in the cells. The variation in light

CC emission is processed to provide information that correlates spatial

CC distribution to the degree of the molecule. The method is used to

CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and

CC to identify new drug targets.

SO Sequence 1818 BP; 482 A; 505 C; 451 G; 380 T; 0 other;

Query Match 5.5%; Score 26; DB 19; Length 1818;  
Best Local Similarity 100.0%; Pred. No. 0.0041;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgacttgagcttgccgcg 155  
Db 1225 aagatctgacttgagcttgccgcg 1250

RESULT 19  
AAT13330  
ID AAT13330 standard; cDNA to mRNA; 4696 BP.

AC AAT13330;

DT 09-JUL-1996 (first entry)

DE Rat type I insulin-like growth factor receptor cDNA.

KW Insulin-like growth factor I receptor; IGF 1R; somatomedin C;  
KW smooth muscle; cell growth; cell proliferation; healing;  
KW nerve regeneration; angiogenesis; antisense RNA; atherosclerosis;  
KW tumour; restenosis; ds.

OS Rattus norvegicus strain Sprague-Dawley.

XX Rattus norvegicus strain Sprague-Dawley.

XX Key Location/Qualifiers  
FH CDS 46..4158  
FT /\*tag= a  
FT sig-peptide 46..135  
FT /\*tag= b 136..4155  
FT mat-peptide /\*tag= C

PN WO9610401-A1.

XX 11-APR-1996.

PD 27-SEP-1995; 95WO-US12563.

PF 04-OCT-1994; 94US-0317898.

PR (UYEM-) UNIV EMORY.

PA Delafontaine P;  
PI WPI; 1996-209180/21.  
DR P-PSDB; AAR91430.

XX Insulin-like growth factor I receptor anti-sense RNA and  
PT ATG-directed sense oligo:nucleotide(s) - useful for regulating  
PT growth factor receptor gene expression for e.g. wound healing and  
PT atherosclerosis

PS Claim 18: Page 36-42; 73pp; English.

XX A cDNA clone (AAT13330) codes for rat insulin-like growth factor  
CC I receptor (IGF 1R) (AAR91430). It was obtd. from a rat brain cell  
CC cDNA library by PCR amplification (see AAT1332-33). IGF 1R plays  
CC a crucial role in vascular smooth muscle cell (VSMC) proliferative

CC responses. The gene provides the basis for antisense methods  
CC (see AAT1325 and AAT1328) to down-regulate IGF 1R gene expression  
CC and retard VSMC growth, e.g. to treat restenosis and atherosclerosis,  
CC and also for ATP-directed sense oligonucleotide (see AAT1336)  
CC methods to stimulate VSMC growth e.g. for healing wounds and burns.  
XX  
50 Sequence 4696 BP: 1151 A; 1268 C; 1241 G; 1036 T; 0 other:

Query Match	5.5%	Score 26:	DB 17:	Length 4696:
Best Local Similarity	100.0%	Pred. No.	0.0039:	
Matches 26:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

Qy	77	102
Db	3443	3468

RESULT	20
AAQ30721	
ID	AAQ30721 standard; DNA; 159 BP.

	Key	Location/Qualifiers
FH	CDS	1.159
FT		/*tag= a
FT		

PN W09218149-A.

PD 29-OCT-1992.

PF 23-APR-1992; 92WO-US03376.

PR 23-APR-1991; 91US-0690199.

**XX**

XXXXXX

PI P, Maisson-Pierre PC, Squinto SP, Stilt T, Yancopoulos GD;

DR WPI; 1992-381778/46.

XX  
XX

PT Assaying neurotrophin activity using cells that express trkB - also  
PT for identifying agonists and antagonists, and new recombinant cells,  
PT and nucleic acid producing trkB, for diagnosis and treatment of  
PT neurological disease

PS Disclosure; Fig 12C; 156pp; English.

CC The sequence is that of tyrosine kinase clone RTK-6, isolated  
CC from adult or embryonic (E13) rat brain cDNA, which shows  
CC homology to the known tyrosine kinase molecules h kit, h csfr,  
CC hpcck1phar and mcsfr. It may be of use in the treatment of  
CC neurodegenerative disease/neurotrauma including motor neuron  
CC disorders such as amyotrophic lateral sclerosis, Werdnig-Hoffman  
CC disease, chronic proximal spinal muscular atrophy and Guillain-Barre  
CC syndrome. It may also be of use in the treatment of neurological  
CC disorders associated with diabetes, Parkinson's disease,  
CC Alzheimer's disease and Huntington's chorea.

50 Sequence 159 BP; 38 A; 36 C; 50 G; 35 T; 0 other;

Query Match	4.9%	Score 23;	DB 13;	Length 159;
Best Local Similarity	100.0%	Pred. No. 0.14;		
Matches	23;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0.

OY 124 gtgtgaagatctgtgacttgg 14  
 |||||  
 Db 22 gtgtgaagatctgtgacttgg 44

RESULT	21
AAV70215	
ID	AAV70215 standard; DNA; 159 BP

XX	11-FEB-1999 (first entry)
DT	
XX	
XX	
DE	Rat orphan tyrosine kinase receptor peptide clone RTK-6 encoding DNA.
XX	
KW	Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; neurotrophin activity; trkb; proto-oncogene; tyrosine kinase receptor; binding protein; BDNF; NT-3; diagnosis; ss.

05	Synthetic.
05	Rattus sp.

PN US5843749-A.

PD 01-DEC-1998.

PF 06-JUN-1995; 95US-0469537.

PR 17-MAR-1995; 95US-0406247.

PR 28-OCT-1993; 93US-0144992.

XX  
XX  
DECEMBER TWENTY TWO  
1944[illegible]

XX  
DB 1999-044594 /04  
WBT:

DR P-PSDB; AAW83155.  
XX

PT DNA encoding receptor tyrosine kinase

XX  
XX

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CC for-2, ehk-1 and ehk-2. AISC  
CC for-1; for-2; ehk-1; and Ehb

CC The present invention describes nucleic acid molecules for *ror-1*,  
CC *ror-2*, *ehk-1* and *ehk-2*. Also described are the corresponding proteins:  
CC *Ror-1*, *Ror-2*, *Ehk-1* and *Ehk-2*. The proteins are orphan receptor  
CC tyrosine kinases. The present sequence encodes a rat orphan tyrosine  
CC kinase receptors peptide clone from the present invention.

50 sequence 159 BP; 38 A; 36 C; 51 G; 34 T; 0 other,

```
Query Match      4.9%; Score 23; DB 20; Length 159;
Best Local Similarity 100.0%; Pred. NO. 0.14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY	124	gtgtgtgaagatctgtgacttgg	14
Db	22	gtgtgtgaagatctgtgacttgg	44

RESULT	22
AAQ54036	
ID	AAQ54036 standard; cDNA; 1894 BP
XX	

```

AC  AA054036:
XX  12-JUL-1994 (first entry)
XX  FLK-2ws gene.
DE
XX  Polymerase chain reaction: primer: amplify; PCR: fetal liver kinase-2;
XX  FLK-2; nested: mouse; mFLK-2; PCLIT: inhibition; binding;
XX  ligand; receptor; modulation; growth; haematopoietic progenitor cell;
XX  antibody; ss.
XX  Mus musculus.
XX
XX  Key Location/Qualifiers
XX  CDS 31..1476
XX  /tag- a
XX  /product= Soluble FLK-2
XX
XX  W09401576-A.
XX
XX  20-JAN-1994.
XX
XX  07-JUL-1993: 93WO-US06404.
XX
XX  09-JUL-1992: 92US-0912122.
XX
XX  (SYST-) SYSTEMIX INC.
XX
XX  Yang Z;
XX
XX  WPI: 1994-035079/04.
XX  P-PSDB: AAR47579.
XX
XX  New soluble and human foetal liver kinase-2 DNA sequences - used
XX  for obtaining prods. for modulating the growth of haematopoietic
XX  progenitor cells
XX
XX  Claim 1: Page 11-14: 21pp: English.
XX
XX  This sequence encodes murine soluble foetal liver kinase-2 (FLK-2ws).
XX  This sequence was isolated using the primer sequences given in AA054034-
XX  35. Primer PCLIT corresponds to mFLK-2 nucleotide positions 1-24,
XX  except that at position 2, C is changed to A, and primer PCLI
XX  corresponds to mFLK-2 nucleotide positions 341-3428 (sic). This
XX  sequence may be used in the production of FLK-2 protein. The
XX  resulting proteins may be used in culture and in vivo for inhibiting
XX  binding of the FLK-2 ligand to the FLK-2 receptor. Therefore they may
XX  be used for modulating the growth of haematopoietic progenitor cells.
XX  The proteins may also be used for producing antibodies for identifying
XX  cells carrying FLK-2, removing soluble FLK-2 from culture fluids or
XX  natural fluids, purifying FLK-2 or assaying for the presence of
XX  FLK-2.
XX
XX  Sequence 1894 BP; 494 A; 459 C; 500 G; 441 T; 0 other;
XX
XX
XX  Query Match 4.9%; Score 23; DB 15; Length 1894;
XX  Best Local Similarity 100.0%; Pred. No. 0.13;
XX  Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 124 gtggtgaagatctgtgactcttg 146
XX  |||||||
XX  Db 976 gtggtgaagatctgtgactcttg 998
XX
XX  RESULT 23
XX  ID AA029954 standard; cDNA: 3453 BP.
XX
XX  AC AA029954;
XX
XX  DT 15-MAR-1993 (first entry)
XX

```

```

DE  Murine flk-2 cDNA sequence.
XX
XX  Thymidine kinase; TK; haematopoietic; stem cells; proliferation;
XX  differentiation; progenitor cells; foetal liver kinase; ss.
XX
XX  Mus musculus.
XX
XX  Key Location/Qualifiers
XX  CDS 31..3009
XX  /tag- a
XX
XX  W09217486-A.
XX
XX  15-OCT-1992.
XX
XX  02-APR-1992: 92WO-US02750.
XX
XX  02-APR-1991: 91US-0679666.
XX  28-JUN-1991: 91US-0728913.
XX  15-NOV-1991: 91US-0793065.
XX  24-DEC-1991: 91US-0813593.
XX
XX  (UYPR-) UNIV PRINCETON.
XX
XX  Lemischka IR;
XX
XX  WPI: 1992-366185/44.
XX  P-PSDB: AAR28038.
XX
XX  Stimulating proliferation and/or differentiation of primitive
XX  mammalian haematopoietic stem cells - using ligand that binds
XX  thymidine kinase and flk-1 and flk-2
XX
XX  Claim 6: Fig 1a: 94pp: English.
XX
XX  The murine foetal liver kinase (flk) -2 clone was isolated by
XX  standard PCR techniques from stem-cell receptor-contg. tissue cDNA
XX  libraries. Suitable tissues include foetal liver, spleen or thymus
XX  cells or adult marrow or brain cells. The PCR primers used are based
XX  on known sections of the flk-2 gene. The murine flk-2 clone may be
XX  used in a vector to transform haematopoietic cells. The thymidine
XX  kinase encoded by flk-2 is expressed in primitive but not mature
XX  haematopoietic cells. Ligand binding to the TK may be prepd. which
XX  can stimulate proliferation and/or differentiation of primitive
XX  haematopoietic cells in vivo. The ligands can stimulate the
XX  proliferation of additional primitive stem cells, differentiation into
XX  more mature progenitor cells, or both.
XX  See also AA029955-7.
XX
XX  Sequence 3453 BP; 946 A; 822 C; 876 G; 809 T; 0 other;
XX
XX
XX  Query Match 4.9%; Score 23; DB 13; Length 3453;
XX  Best Local Similarity 100.0%; Pred. No. 0.13;
XX  Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 124 gtggtgaagatctgtgactcttg 146
XX  |||||||
XX  Db 2509 gtggtgaagatctgtgactcttg 2531
XX
XX  RESULT 24
XX  ID AA053502 standard; cDNA: 3453 BP.
XX
XX  AC AA053502;
XX
XX  DT 27-JUN-1994 (first entry)
XX
XX  DE Murine flk-2 cDNA.
XX
XX  KW Receptor protein tyrosine kinase; PTK family; foetal liver kinase;
XX  mfk; primitive; totipotent; haematopoietic cell; stem cell;
XX

```

```

KM proliferation; stromal cell; ds.
XX
OS Mus musculus.
XX
FH Key location/Qualifiers
FT CDS 31..3009 /*tag= a
FT sig_peptide 31..111
FT mat_peptide 112..3006 /*tag= b
FT /*tag= c
XX
PN US5270458-A.
XX
PD 14-DEC-1993.
XX
PE 02-APR-1991; 91US-0679666.
XX
PR 02-APR-1991; 91US-0679666.
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 26-JUN-1992; 92US-0906397.
PR 12-NOV-1992; 92US-0975049.
PR 19-NOV-1992; 92US-0977451.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
DR WPI; 1993-405021/50.
DR P-PSDB; AAR44994.
XX
PT isolated nucleic acid molecules of hematopoietic stem cell
PT receptor flk-2 - encoding mammalian receptor protein tyrosine
PT kinases expressed in primitive haematopoietic cells
XX
PS Claim 2: Fig 1a: 60pp: English.
XX
CC Nucleic acid sequences coding for murine flk-2 and specified
CC subfragments of it are claimed. The flk-2 polypeptide is a protein
CC tyrosine kinase expressed only in primitive haematopoietic cells.
CC The CDNA can be used to recombinantly produce flk-2 for stimulating
CC self-renewal of totipotent stem cells and development of all
CC haematopoietic cells.
XX
SQ Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
XX

```

Query Match 4.9%; Score 23; DB 14; Length 3453;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgacttgg 146  
 |||||||||||||||||||||  
 DB 2509 gtggtgaagatctgtgacttgg 2531

```

RESULT 25
AAQ35249
ID AAQ35249 standard; cDNA: 3453 BP.
XX
AC AAQ35249;
XX
DT 25-JUN-1993 (first entry)
XX
DE Murine flk-2 coding sequence.
XX
KM Murine; receptor; protein; tyrosine kinase; PTK; primitive; mammalian;
KM hematopoietic cell; PTK; mature; mHC; fetal; liver kinase 2; flk-2;
KM liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
KM multipotential; T-lymphoid; lineage; ss.
XX

```

```

OS Mus musculus.
XX
FH Key location/Qualifiers
FT CDS 31..3009 /*tag= a
FT misc_RNA 31..111
FT /*tag= b
FT /*note= "hydrophobic leader"
XX
PN W09300349-A.
XX
PD 07-JAN-1993.
XX
PE 26-JUN-1992; 92WO-US05401.
XX
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 02-APR-1992; 92WO-US02750.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
DR WPI; 1993-036323/04.
DR P-PSDB; AAR31375.
XX
PT Nucleic acid encoding receptor protein tyrosine kinase - allows
PT development of ligands to stimulate proliferation and/or
PT differentiation of mammalian haematopoietic stem cells
XX
PS Claim 5; Fig 1a: 78pp: English.
XX
CC This sequence encodes a murine receptor protein tyrosine kinase which
CC belongs to a new functional class of protein tyrosine kinases (PTKs).
CC PTKs in this class are expressed in primitive mammalian hematopoietic
CC (PBC) cells but not in mature hematopoietic cells (mHC). The protein
CC encoded by this sequence is an example of a receptor PTK and is called
CC fetal liver kinase 2 (flk-2). flk-2 is expressed in fetal liver,
CC spleen and thymus, and adult brain and marrow. Expression of flk-2
CC mRNA occurs in the most primitive thymocyte subset, which is believed
CC to be uncommitted. Therefore, thymocytes expressing flk-2 may be
CC multipotential. flk-2 is the first receptor tyrosine kinase known to
CC be expressed in the T-lymphoid lineage.
XX
SQ Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
XX

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Query Match 4.9%; Score 23; DB 14; Length 3453;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 gtggtgaagatctgtgacttgg 146  
 |||||||||||||||||||||  
 DB 2509 gtggtgaagatctgtgacttgg 2531

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RESULT 26
AAQ40914
ID AAQ40914 standard; cDNA: 3453 BP.
XX
AC AAQ40914;
XX
DT 19-OCT-1993 (first entry)
XX
DE Murine flk-2 cDNA.
XX
KM Murine; receptor; protein; tyrosine kinase; PTK; flk-2; primitive;
KM hematopoietic cell; mature; family; conserved; region;
KM catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;
KM thymus; adult; brain; bone marrow; multipotential; CFU-blast colony;
KM hierarchy; transduction; T-lymphoid; lineage; ss.
XX

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OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 31..3009
FT sig_peptide /tag= a
FT /product= Flk2 receptor protein-tyrosine-kinase
FT /tag= b
FT /note= "Hydrophobic leader sequence"
FT mat_peptide 112..3006
FT /tag= c
XX
XX WO9310136-A.
XX
XX 27-MAY-1993.
XX
XX
XX 16-NOV-1992. 92WO-US09893.
XX
XX 15-NOV-1991. 91US-0793065.
XX
XX (UYP- ) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI: 1993-182479/22.
XX
XX P-PSDB: AAR37502.
XX
XX Tolipotent haematopoietic stem cell receptors, their ligands and
XX DNA sequences - for treating anaemia(s) and bone marrow damage
XX due to e.g. cancer chemotherapy or radiotherapy
XX
XX Claim 6: Fig 1a: 127pp: English.
XX
XX This sequence encodes the murine receptor protein tyrosine kinase
XX (PTK), flk-2. This nucleic acid is expressed in primitive hema-
XX topoietic cells and not in mature hematopoietic cells. Members of
XX this family of PTK's can be recognised by the conserved amino acid
XX regions in the catalytic domain. This family of PTK's also contains
XX c-Kit. These new receptors are termed fetal liver kinases (Flk's)
XX after the tissue in which they were discovered. Flk-2 is also
XX expressed in fetal spleen, fetal thymus, adult brain and adult
XX bone marrow. flk-2 is expressed in individual multipotential CFU-
XX blast colonies capable of generating numerous multilineage colonies
XX upon replating. It is likely therefore, that flk-2 is expressed in
XX the entire primitive portion of the Hematopoietic hierarchy. This is
XX consistent with flk-2 being important in transducing putative self-
XX renewal signals from the environment. flk-2 is the first receptor
XX PTK known to be expressed in the T-lymphoid lineage.
XX
XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX
XX Query Match 4.9%; Score 23; DB 14; Length 3453;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX Oy 124 gtgtgaagatctgtgacttgg 146
XX |||||||||||||||||||
XX Db 2509 gtgtgaagatctgtgacttgg 2531
XX
XX
XX RESULT 27
XX ID AA081012 standard; cDNA: 3453 BP.
XX
XX AC AA081012;
XX
XX 16-AUG-1995 (first entry)
XX
XX Flk2 receptor protein-tyrosine-kinase cDNA.
XX
XX Mouse flk2; receptor protein-tyrosine-kinase; primitive
XX hematopoietic cell; fetal liver kinase; ds.
XX
XX

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OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 31..3009
FT sig_peptide /tag= a
FT /product= Flk2 receptor protein-tyrosine-kinase
FT /tag= b
FT mat_peptide 112..3006
FT /tag= c
XX
XX WO9500554-A.
XX
XX 05-JAN-1995.
XX
XX
XX 17-JUN-1994. 94WO-US06944.
XX
XX 18-JUN-1993. 93US-0080244.
XX
XX 21-JUN-1993. 93US-0081508.
XX
XX 23-NOV-1993. 93US-0157490.
XX
XX (UYP- ) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI: 1995-052014/07.
XX
XX P-PSDB: AAR67815.
XX
XX Ligand for receptor protein tyrosine kinase - useful for the
XX stimulation of primitive haematopoietic stem cells causing
XX proliferation and/or differentiation
XX
XX Disclosure: Fig 1a: 131pp: English.
XX
XX The sequence corresponds to a cDNA encoding a mouse Flk2 (fetal
XX liver kinase) receptor protein-tyrosine-kinase. Flk2 is expressed
XX in primitive hematopoietic cells but not in mature hematopoietic
XX cells. The gene product is useful in isolation of receptor ligands,
XX which have applications in diagnosis of bone marrow disorders and in
XX stimulating proliferation and/or differentiation of primitive
XX hematopoietic stem cells.
XX
XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX
XX Query Match 4.9%; Score 23; DB 16; Length 3453;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX Oy 124 gtgtgaagatctgtgacttgg 146
XX |||||||||||||||||||
XX Db 2509 gtgtgaagatctgtgacttgg 2531
XX
XX
XX RESULT 28
XX ID AA079068 standard; cDNA: 3453 BP.
XX
XX AC AA079068;
XX
XX 04-JUL-1995 (first entry)
XX
XX Mouse flk-2 cDNA.
XX
XX Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
XX hematopoiesis; stem cell; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 58..3039
XX sig_peptide /tag= a
XX 58..138
XX

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FT      mat_peptide      /*tag= b
FT      139..3036
FT      /*tag= c
PN      US5367057-A.
XX      22-NOV-1994.
PD      02-APR-1991: 91US-0679666.
XX      02-APR-1991: 91US-0679666.
PR      02-APR-1991: 91US-0679666.
PR      28-JUN-1991: 91US-0728913.
PR      15-NOV-1991: 91US-0793065.
PR      24-DEC-1991: 91US-0813593.
PR      26-JUN-1992: 92US-0906397.
PR      12-NOV-1992: 92US-0975049.
PR      19-NOV-1992: 92US-0977451.
PR      30-APR-1993: 93US-0055269.
XX      (UYP- ) UNIV PRINCETON.
XX      Lemischka IR:
XX      WPI: 1995-005894/01.
XX      P-PSDB: AAR67535.
XX      Murine flk-2 receptor protein tyrosine kinase - used to stimulate
PT      proliferation and/or stimulation of primitive mammalian
PT      haematopoietic stem cells in vitro or in vivo.
XX      Disclosure: Fig. 1A-1F: 69pp: English.
XX      CC      CDNA5 encoding receptor protein tyrosine-kinases, mouse foetal liver
CC      kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAG79068-70,
CC      respectively, and the deduced amino acid sequences in AAR67535-37,
CC      respectively.
XX      SO      Sequence 3453 BP; 946 A; 822 C; 876 G; 809 T; 0 other:
Query Match      4.9%; Score 23; DB 16; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      124 gtggtgaagatctgactcttg 146
DB      2509 gtggtgaagatctgactcttg 2531
RESULT 29
AAT38733
ID      AAT38733 standard; cDNA: 3453 BP.
XX      AC      AAT38733:
XX      DT      11-DEC-1996 (first entry)
XX      DE      Human foetal liver kinase 2 cDNA.
XX      KW      Human; foetal liver kinase 2; flk-2; protein tyrosine kinase;
KW      monoclonal; antibody; extracellular domain; receptor assay;
KW      haematopoietic stem cell; ligand; stimulation; proliferation;
KW      differentiation; treatment; anaemia; bone marrow damage;
KW      cancer chemotherapy; radiation; ds.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
FT      CDS      31..3009
FT      sig_peptide /*tag= a
FT      31..111
FT      mat_peptide /*tag= b
FT      112..3006

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FT      US5448065-A.      /*tag= c
XX      20-AUG-1996.
PD      02-APR-1991: 91US-0679666.
XX      02-APR-1991: 91US-0679666.
PR      19-NOV-1992: 92US-0977451.
PR      02-APR-1991: 91US-0679666.
PR      28-JUN-1991: 91US-0728913.
PR      15-NOV-1991: 91US-0793065.
PR      24-DEC-1991: 91US-0813593.
PR      26-JUN-1992: 92US-0906397.
PR      12-NOV-1992: 92US-0975049.
PR      30-APR-1993: 93US-0055269.
PR      31-OCT-1994: 94US-0252517.
XX      (UYP- ) UNIV PRINCETON.
XX      Lemischka IR:
XX      WPI: 1996-392678/39.
XX      P-PSDB: AAR97418.
XX      Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
PT      for isolating haematopoietic stem cells expressing receptor and for
PT      obtaining ligands
XX      Disclosure: Columns 27-34: 50pp: English.
XX      CC      The present sequence encodes human foetal liver kinase 2 (flk-2), a
CC      protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
CC      raised against the extracellular portion of flk-2 can be used to
CC      assay for flk receptors on the surface of primitive haematopoietic
CC      stem cells, and to isolate positive cells. The antibodies can also
CC      be used as, or to obtain ligands, which stimulate the proliferation
CC      and/or differentiation of stem cells. The ligands can be used, e.g.
CC      for treating anaemia, or bone marrow damage resulting from cancer
CC      chemotherapy, or radiation.
XX      SO      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
Query Match      4.9%; Score 23; DB 17; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      124 gtggtgaagatctgactcttg 146
DB      2509 gtggtgaagatctgactcttg 2531
RESULT 30
AAT72118
ID      AAT72118 standard; cDNA: 3453 BP.
XX      AC      AAT72118:
XX      DT      19-AUG-1997 (first entry)
XX      DE      Murine flk-2 receptor coding sequence.
XX      KW      Human; foetal liver kinase 2; flk2; receptor protein tyrosine kinase;
KW      PTK; liver; spleen; thymus; adult; brain; bone marrow/primitive portion;
KW      haematopoietic hierarchy; extracellular domain; soluble form; ligand;
KW      proliferation; differentiation; mammalian; haematopoietic stem cell;
KW      macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse; ss.
XX      OS      Mus musculus.
XX      FH      Key      Location/Qualifiers
FT      CDS      31..3009

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FT      /*tag= a
FT      /product= Murine_flk-2
FT      sig_peptide 31..111
FT      /*tag= b
FT      mat_peptide 112..3006
FT      /*tag= c
XX
XX      US5621090-A.
XX
XX      15-APR-1997.
XX
XX      02-APR-1991: 91US-0679666.
XX
XX      26-JUN-1992: 92US-0906397.
XX      02-APR-1991: 91US-0679666.
XX      28-JUN-1991: 91US-0728913.
XX      15-NOV-1991: 91US-0793065.
XX      24-DEC-1991: 91US-0813593.
XX
XX      (UYP- ) UNIV PRINCETON.
XX
XX      Lemischka IR:
XX
XX      WPI: 1997-235228/21.
XX      P-PSDB: AAM19874.
XX
XX      Protein containing the extracellular domain of human flk-2 - used
XX      for identification of primitive haematopoietic cell proliferation
XX      and differentiation stimulatory ligands, e.g. for treating anaemia
XX
XX      Disclosure: Fig 1A: 55pp; English.
XX
XX      This sequence encodes the murine fetal liver kinase 2 (flk2). flk-2 is
XX      a receptor protein tyrosine kinase (PTK) and is important in transducing
XX      putative self-renewal signals from the environment. flk-2 is expressed
XX      in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
XX      and it is thought that flk-2 is expressed in the entire primitive portion
XX      of the haematopoietic hierarchy. The invention concerns a recombinant
XX      nucleic acid, preferably mRNA, which encodes a protein containing only
XX      the extracellular domain of human flk-2 and lacking the flk-2 intra-
XX      cellular catalytic domain. The resultant protein represents a soluble
XX      form of flk-2 which is used to isolate specific ligands for flk-2. These
XX      ligands can be used to stimulate proliferation and/or differentiation of
XX      mammalian hematopoietic stem cells, in vivo or in vitro, e.g. for
XX      treatment of macrocytic or aplastic anaemia or bone marrow damage caused
XX      by cancer treatment or radiation.
XX
XX      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX      Query Match 4.9%; Score 23; DB 18; Length 3453;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy      124 gtggtgaagatcgtgacttgg 146
Oy      |||
Db      2509 gtggtgaagatcgtgacttgg 2531

```

## RESULT 31

AAAX77514  
ID AAX77514 standard; cDNA; 3453 BP.

AAAX77514:

05-AUG-1999 (first entry)

Murine flk-2 cDNA.

Murine: flk-2; flk-1; cell isolation; fetal liver kinase; receptor;

monoclonal; polyclonal; antibody; tyrosine kinase; ds.

Mus sp.

```

XX      XX      Location/Qualifiers
XX      Key 31..3009
XX      CDS /*tag= a
XX      /*product= "flk-2"
XX
XX      US5912133-A.
XX
XX      15-JUN-1999.
XX
XX      10-FEB-1998: 98US-0021324.
XX
XX      19-NOV-1992: 92US-0977451.
XX      02-APR-1991: 91US-0679666.
XX      28-JUN-1991: 91US-0728913.
XX      15-NOV-1991: 91US-0793065.
XX      24-DEC-1991: 91US-0813593.
XX      26-JUN-1992: 92US-0906397.
XX      12-NOV-1992: 92US-0975049.
XX      30-APR-1993: 93US-0055269.
XX      31-OCT-1994: 94US-0252498.
XX      15-FEB-1996: 96US-0601891.
XX
XX      (UYP- ) UNIV PRINCETON.
XX
XX      Lemischka IR:
XX
XX      WPI: 1999-357194/30.
XX      P-PSDB: AAY08616.
XX
XX      Isolating hematopoietic cells expressing fetal liver kinase 1
XX      receptors
XX
XX      Disclosure: Fig 1a: 59pp; English.
XX
XX      This invention describes a novel method of isolating cells expressing
XX      fetal liver kinase 1 (flk-1) receptors on their surface and comprises
XX      binding the cells to a polyclonal or monoclonal antibody specific to
XX      the flk-1 receptor and isolating the cells that have bound to the
XX      antibody. The method can be used to isolate hematopoietic stem cells in
XX      any mammal but preferably a rat, mouse, rabbit or human. The proteins of
XX      the invention belong to the receptor protein family. This sequence
XX      encodes the murine flk-2 protein which is used in the method of the
XX      invention.
XX
XX      Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:
XX
XX      Query Match 4.9%; Score 23; DB 20; Length 3453;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy      124 gtggtgaagatcgtgacttgg 146
Oy      |||
Db      2509 gtggtgaagatcgtgacttgg 2531

```

## RESULT 32

AAT00801  
ID AAT00801 standard; DNA; 3521 BP.

AAT00801:

29-FEB-1996 (first entry)

Flk2/flt3 tyrosine kinase receptor gene.

Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;

haematopoiesis; hypoplasemia; anaemia; thrombocytopenia; stem cell; ss.

Mus sp.

Key Location/Qualifiers



XX genes -  
 P1 Matsui T, Aaronson SA, Pierce JH;  
 XX WPI: 1990-290306/38.  
 DR P-PSDB: AAR06910.  
 XX  
 XX Type alpha platelet-derived growth factor receptor gene - useful  
 PT for transforming cells to express novel protein receptor and also  
 PT susceptible to genetic engineering.  
 XX  
 PS Claim 3: Fig 3: 64pp: English.  
 XX  
 CC The 7K4 clone is the largest cDNA clone related to the T11 genomic  
 CC clone, isolated from a library prep. from human thymus DNA. The  
 CC T4 cDNA clone was isolated from a M426 human embryo fibroblast  
 CC cDNA library. The exons shown were determined from the T11  
 CC genomic clone. The gene has been mapped to chromosome 4 at  
 CC location q 11-12, which is within the same region as the c-kit  
 CC proto-oncogene. The coding region can be introduced into the pSV2  
 CC gpt vector with a simian sarcoma virus LTR as a promoter and  
 CC expressed in a host. The resulting protein is a novel PDGF  
 CC receptor designated type alpha (the known receptor is designated  
 CC type beta). The cDNA can be used also to investigate the  
 CC mechanisms of PDGF regulatory processes or in bioassays for detect-  
 CC ing related genes, particularly for identification of classes of  
 CC tumour cells or of genetic defects in connective tissue and/or  
 CC healing response.  
 XX  
 SQ Sequence 6412 BP; 1885 A; 1299 C; 1443 G; 1785 T; 0 other;

Query Match 4.9%; Score 23; DB 11; Length 6412;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 gtgaagatcgtgacttgacct 149  
 |||||||  
 Db 2632 gtgaagatcgtgacttgacct 2654

RESULT 35  
 ARI99406  
 ID ARI99406 standard; cDNA: 4479 BP.  
 XX  
 AC ARI99406;  
 XX  
 DT 07-MAR-2002 (first entry)  
 XX  
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:321.  
 XX  
 KM Mouse: ischaemia; compressive ischaemia; occlusive ischaemia;  
 KM vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200188188-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 18-MAY-2001: 2001WO-JP04192.  
 XX  
 PR 18-MAY-2000: 2000JP-0145977.  
 XX  
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 XX  
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 XX  
 DR WPI: 2002-034733/04.  
 DR P-PSDB: ABB57136.  
 XX  
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or  
 PT by determining the expression profile of a gene group comprising these

PT genes -  
 XX Claim 2: Page 876-884; 2690pp: English.  
 PS  
 XX The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
 CC the protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The  
 CC expression levels or expression profiles produced by these genes are  
 CC used as an indicator when screening for ischaemic condition-improving  
 CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914  
 CC represent PCR primers for a mouse ischaemic condition related sequence,  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 4479 BP; 978 A; 1249 C; 1294 G; 958 T; 0 other;

Query Match 4.7%; Score 22; DB 24; Length 4479;  
 Best Local Similarity 100.0%; Pred. No. 0.4;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 gagactgctgctcggaacat 104  
 |||||||  
 Db 2309 gagactgctgctcggaacat 2330

RESULT 36  
 AAT73125  
 ID AAT73125 standard; cDNA: 2574 BP.  
 XX  
 AC AAT73125;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Mouse Tec tyrosine kinase gene.  
 XX  
 KM 5'-flanking region: mouse; murine; Tec; tyrosine kinase; promoter;  
 KM gene expression; haematopoietic stem cell; liver cell;  
 KM gene therapy; ds.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9734007-A1.  
 XX  
 PD 18-SEP-1997.  
 XX  
 PF 10-MAR-1997: 97WO-JP00741.  
 XX  
 PR 12-MAR-1996: 96JP-0054294.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Hasegawa M, Mano H, Sakata T;  
 XX  
 DR WPI: 1997-470886/43.  
 XX  
 PT DNA with Tec tyrosine kinase promoter activity - for expression of  
 PT foreign genes in e.g. haematopoietic stem cells and liver cells  
 XX  
 PS Example 3: Pages 8-10; 17pp: Japanese.  
 XX  
 CC The present sequence is the mouse Tec tyrosine kinase gene, whose  
 CC associated 5'-flanking region has Tec gene promoter activity. It  
 CC allows high levels of expression of foreign genes in  
 CC haematopoietic stem and liver cells, for use in gene therapy.  
 XX  
 SQ Sequence 2574 BP; 770 A; 539 C; 651 G; 614 T; 0 other;

Query Match 4.5%; Score 21; DB 18; Length 2574;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 catcacagagacctgctgc 95  
|||||  
DB 1566 catcacagagacctgctgc 1586

## RESULT 37

AAC62208  
ID AAC62208 standard; DNA: 20 BP.

AC AAC62208;

DT 06-MAR-2001 (first entry)

DE PCR primer used to amplify cDNA encoding flt-4.

XX Antisense oligonucleotide; flt-4; receptor type tyrosine kinase;  
KM lymphangioemesis; prostate cancer; prostate cell; PCR primer: ss.  
XX

OS Homo sapiens.

XX WO200062063-A1.

PN 19-OCT-2000.

PD 13-APR-1999; 99WO-US08079.

PF 13-APR-1999; 99WO-US08079.

PR 13-APR-1999; 99WO-US08079.

PT (NMBI-) NORTHWEST BIOTHERAPEUTICS INC.

XX Su SL:

PI WPI: 2000-687067/67.

XX Detecting metastatic potential, diagnosing metastatic prostate cancer  
PT or determining the prognosis of a subject with prostate cancer  
PS comprises detecting the expression of flt-4 in a prostate cell

XX Example; Page 50; 78pp; English.

CC PCR primers AAC62208-09 were used to amplify cDNA encoding flt-4. Flt-4  
CC is a receptor type tyrosine kinase with 7 Ig-like domains similar to  
CC other VEGF receptors. Flt-4 may play a role in lymphangioemesis.  
CC Antisense oligonucleotides can be used for detecting the metastatic  
CC potential, diagnosing metastatic prostate cancer or determining the  
CC prognosis of a subject with prostate cancer. The method comprises  
CC identifying the prostate cell in a body fluid sample and detecting the  
CC expression of flt-4 in the cell. Expression of flt-4 in a prostate cell  
CC indicates that the cell is a cancerous prostate cell that has metastatic  
CC potential or is a secondary tumour metastasis of a primary prostate  
CC tumour.  
XX  
XX Sequence 20 BP: 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match 4.2%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 agaggagtgagctctgc 62  
|||||  
DB 1 agaggagtgagctctgc 20

## RESULT 38

AAV62479  
ID AAV62479 standard; CDNA: 1611 BP.  
XX

AC AAV62479;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Human MAP kinase, ERK-2 cDNA sequence.

XX ERK-1; ERK-2; mitogen-activated protein kinase; MAP kinase; human;  
KM inhibition; malignant; neoplastic growth; epithelial cell; mammal;  
KM endothelial cell; antisense oligonucleotide; primary cancer;  
KM metastatic cancer; breast cancer; prostate cancer; angiosarcoma;  
KM endocrine tissue cancer; ds.  
XX

OS Homo sapiens.

XX WO9844101-A1.

PN 08-OCT-1998.

PD 19-MAR-1998; 98WO-US05471.

PF 12-AUG-1997; 97US-0909742.

PR 28-MAR-1997; 97US-0827520.

PR 01-APR-1997; 97US-0831994.

XX (UYNV ) UNIV NEW YORK STATE RES FOUND.

XX Malbon CC, Sivaraman VS, Wang H;

PI WPI: 1998-557109/47.

XX Treatment of e.g. breast or prostate cancer or angiosarcoma - by  
PT administering antisense oligonucleotides to genes encoding  
PT mitogen-activating protein kinases ERK1 and ERK2

XX Disclosure; Page 12; 59pp; English.

XX This represents the cDNA sequence of the human ERK-2, a  
CC mitogen-activated protein (MAP) kinase. The invention provides a method  
CC of inhibiting malignant neoplastic growth of epithelial or endothelial  
CC cell in a mammal which comprises administering to the mammal an effective  
CC amount of an oligonucleotide complementary to part of the mRNA for the  
CC MAP kinases, ERK-1 or ERK2 which is over-expressed in the mammal. Also  
CC provided is a method for identifying and monitoring potentially malignant  
CC neoplastic cells by measuring the levels of ERK1 and ERK2 mRNA in  
CC epithelial or endothelial cells and comparing it to the levels from  
CC normal cells of the same origin. Administration of the ERK1 and ERK2  
CC antisense oligonucleotides (AAV62480 and AAV62481) to neoplastic  
CC endothelial or epithelial cells inhibits over-expression of ERK1 and  
CC ERK2. This can be used to treat epithelial and endothelial malignancies  
CC including primary or metastatic cancers of e.g. the breast, prostate,  
CC other endocrine tissue or angiosarcoma.  
XX  
XX Sequence 1611 BP: 403 A; 421 C; 407 G; 380 T; 0 other;

Query Match 4.2%; Score 20; DB 19; Length 1611;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgacttgacct 149  
|||||  
DB 817 aagatctgacttgacct 836

## RESULT 39

AAV62479/C  
ID AAV62479 standard; CDNA: 1611 BP.

AC AAV62479;

XX 18-JAN-1999 (first entry)

XX Human MAP kinase, ERK-2 cDNA sequence.  
DE

KW	ERK-1; ERK-2; mitogen-activated protein kinase; MAP kinase; human;
KW	inhibitor; malignant; neoplastic growth; epithelial cell; mammal;
KW	endothelial cell; antisense oligonucleotide; primary cancer;
KW	metastatic cancer; breast cancer; prostate cancer; angiosarcoma;
KX	endocrine tissue cancer; ds.
XX	
OS	Homo sapiens.
PN	MO9844101.v1.
PD	08-OCT-1998.
PF	19-MAR-1998; 98MO-US05471.
PR	12-AUG-1997; 97US-0909742.
PR	28-MAR-1997; 97US-0827520.
PK	01-APR-1997; 97US-0831994.
PA	(UYNV ) UNIV NEW YORK STATE RES FOUND.
PI	Malbon CC, Sivaraman VS, Wang H;
DR	WPI: 1998-557109/47.
PT	Treatment of e.g. breast or prostate cancer or angiosarcoma - by
PT	administering antisense oligonucleotides to genes encoding
PT	mitogen-activating protein kinases ERK1 and ERK2
PS	Disclosure: Page 12: 59pp; English.
XX	
CC	This represents the cDNA sequence of the human ERK-2, a
CC	mitogen-activated protein (MAP) kinase. The invention provides a method
CC	of inhibiting malignant neoplastic growth of epithelial or endothelial
CC	cell in a mammal which comprises administering to the mammal an effective
CC	amount of an oligonucleotide complementary to part of the mRNA for the
CC	MAP kinases, ERK-1 or ERK2 which is over-expressed in the mammal. Also
CC	provided is a method for identifying and monitoring potentially malignant
CC	neoplastic cells by measuring the levels of ERK1 and ERK2 mRNA in
CC	epithelial or endothelial cells and comparing it to the levels from
CC	normal cells of the same origin. Administration of the ERK1 and ERK2
CC	antisense oligonucleotides (AAV62480 and AAV62481) to neoplastic
CC	endothelial or epithelial cells inhibits over-expression of ERK1 and
CC	ERK2. This can be used to treat epithelial and endothelial malignancies
CC	including primary or metastatic cancers of e.g. the breast, prostate,
CC	other endocrine tissue or angiosarcoma.
XX	
SQ	Sequence 1611 BP; 403 A; 421 C; 407 G; 380 T; 0 other:
XX	
Query Match	4.2%; Score 20; DB 19; Length 1611;
Best Local Similarity	100.0%; Pred. No. 4.1;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Y	130 aagatcgtgacttgacct 149
D	
B	109 AAGATCTGTGACTTGGCCT 90
RESULT 40	
AAX89336	
ID	AAX89336 standard; CDNA to mRNA; 2463 BP.
XX	
AAX89336;	
DT	27-SEP-1999 (first entry)
DE	Platelet-derived growth factor beta receptor gene sequence.
KW	Chlmera gene; chromosome translocation; t(5;14)(q33;q32); CEV14 gene;
KW	platelet-derived growth factor beta receptor; PDGFR-beta; ds.
OS	Homo sapiens.

XX	JP11187085-A.
PN	13-JUL-1999.
XX	26-DEC-1997;
PF	97JP-0361020.
XX	26-DEC-1997;
PR	97JP-0361020.
XX	(MTP ) MITSUBISHI YUKA BCL KK.
PA	WIPI: 1999-451550/38.
DR	P-PSDB; AAY28935.
XX	New DNA - and sensitive method for its detection
PT	Claim 6; Page 10-13; 13pp; Japanese.
XX	The invention describes a new DNA containing a chimera gene specific to
PS	the chromosome translocation t(5;14)(q33;q32) formed by fusing the CEV14
CC	gene (1-2287 basepairs of the present sequence) with a platelet-derived
CC	growth factor beta receptor (PDGFR-beta) gene. A method for the detection
CC	of a chimera gene produced by t(5;14)(q33;q32) in a sample by preparing
CC	cDNA from the DNA or mRNA in the sample as the template and using an
CC	oligonucleotide designed to bind the CEV14 gene region of the above
CC	chimera and an oligonucleotide designed to bind the PDGFR gene region as
CC	the primers and detecting the amplified product formed by the PCR is also
CC	provided. The method can detect a gene specific to the presence of
CC	t(5;14)(q33;q32) specifically at a high sensitivity. The present sequence
CC	represents the PDGFR-beta gene sequence.
XX	Sequence 2463 BP; 681 A; 631 C; 629 G; 522 T; 0 other;
SQ	
Query Match	4.2%; Score 20; DB 20; Length 2463;
Best Local Similarity	100.0%; Pred. No. 4;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	130 aaagatctgacttgacct 149 
Db	1810 aaagatctgtgacttggcct 1829
RESULT	41
AAN90355	ID AAN90355 standard; CDNA; 4544 BP.
XX	AAN90355;
AC	01-NOV-1989 (first entry)
XX	CDNA encoding platelet derived growth factor receptor.
DE	Platelet derived growth factor receptor; human;
XX	ligand binding receptor analogues; isoforms; assays; antibodies;
KW	atherosclerosis; wound healing; peptide dimer; CDNA.
OS	Homo sapiens.
XX	Key Location/Qualifiers
FH	CDS 354
FT	/tag= a
XX	EPJ25224-A.
PM	26-JUL-1989.
XX	18-JAN-1989;
PF	89EP-0100787.
XX	22-JAN-1988;
PR	88US-0146877.
XX	(ZYMO ) ZYMOGENETICS INC.
PA	
XX	

PI	Sledziewski AZ, Bell LA, Kindsvogel WR;
XX	
DR	WPI: 1989-214434/30.
DR	P-PSDB: AAP90127.
XX	
PT	Secreted ligand-binding receptor analogues eg PDGF receptor
PT	- used in assays. In purifications and as, or with,
PT	therapeutic agents.
XX	
PS	Claim 2; fig 1; 45pp: English.
XX	
CC	CDNA encoding platelet derived growth factor receptor (see corresp.
CC	AAP90127). Used in the invention to make analogues that are secreted
CC	(pref. Ile-29 - Met-44, and Ile-29 - Lys-53); see specification for
CC	details). These analogues are easily purified, produced in large
CC	quantities recombinantly, used to produce antibodies, to screen ligands,
CC	as imaging agents, as (ant.)agonists, or therapeutically for
CC	atherosclerosis and wound healing, and assays.
XX	
SO	Sequence 4544 BP; 947 A; 1398 C; 1263 G; 936 T; 0 other;
OY	Query Match 4.2%; Score 20; DB 10; Length 4544;
	Best Local Similarity 100.0%; Pred. No. 4;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	130 aaagatctgtgacttgacct 149
	2874 aaagatctgtgacttgacct 2893
RESULT 42	
AAT34552	
ID	AAT34552 standard; CDNA: 4544 BP.
XX	
AC	AAT34552;
XX	
DT	11-OCT-1996 (first entry)
XX	
DE	Platelet-derived growth factor receptor cDNA.
XX	
KW	Platelet-derived growth factor receptor; PDGF-R; peptide dimer;
KW	protein secretion; agonist; antagonist; ss.
XX	
OS	Homo sapiens.
XX	
PI	Key Location/Qualifiers
FT	CDS 354..3674
FT	/*tag= a
XX	
PN	EP721983-A1.
XX	
PD	17-JUL-1996.
XX	
PF	18-JAN-1989; 89EP-0100787.
XX	
PR	22-JAN-1988; 88US-0146877.
XX	
PA	(Zymo ) ZYMOGENETICS INC.
XX	
PI	Bell LA, Kindsvogel WR, Sledziewski AZ;
XX	
DR	WPI: 1996-322833/33.
DR	P-PSDB: AAR99690.
XX	
PT	Prodn. of biologically active peptide dimers, esp. platelet-derived
PT	growth factor receptor analogues - useful for systematic designing
PT	of novel (ant.)agonists
XX	
PS	Disclosure: fig 1; 45pp: English.
XX	
CC	A CDNA sequence (AAT34552) codes for human platelet-derived growth
CC	factor receptor (PDGF-R) (AAR99690). It was obt'd. from a human

CC	diploid dermal fibroblast library using probes (see also
CC	AAt34555-57) complementary to sequences of the mouse PDGF-R.
CC	The cDNA can be used in novel constructs that allow the prodn.
CC	of secreted biologically active PDGF-R analogues. This may
CC	comprise linking a sequence coding for PDGF-R, or the ligand-
CC	binding domain of the PDGF-R extracellular region, to a protein
CC	secretion signal (e.g. SUC2) and promoter, and expression in
CC	transformed host cells, esp. Saccharomyces cerevisiae. The
CC	secreted PDGF-R analogues are used in ligand screening procedures,
CC	to screen for (ant)agonists, and in diagnostic assays.
SQ	Sequence 4544 BP: 948 A; 1397 C; 1263 G; 936 T; 0 other;
	Query Match                 4.2% Score 20; DB 17; Length 4544;
	Best Local Similarity      100.0%; Pred. No. 4;
	Matches     20; Conservative   0; Mismatches    0; Indels     0; Gaps     0
OY	130 aaagatcgtgacttgacct 149 
Db	2874 aagatctgacttgcct 2893
RESULT 43	
AAC59189	
ID	AAC59189 standard; cDNA; 5279 BP.
XX	
AC	AAC59189;
XX	
DT	30-JAN-2001 (first entry)
XX	
DE	Human secreted protein cDNA sequence #33.
XX	
KM	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KM	antiallergic; hepatoprotective; antidiabetic; antiinflammatory; anticancer;
KM	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM	cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM	neurological disease; infection; human; secreted protein; ss.
OS	Homo sapiens.
XX	
PN	WO200055201-A1.
PD	
XX	21-SEP-2000.
PF	09-MAR-2000; 2000WO-US06059.
XX	
PR	12-MAR-1999; 99US-0124096.
PR	03-DEC-1999; 99US-0168622.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Rosen CA, Ruben SM, Komatsoulis G;
XX	
DR	WPI: 2000-628182/60.
XX	P-PSDB: AAB27714.
PT	Novel human secreted proteins useful for diagnosis, prevention and
PT	treatment of disorders including neurological, cell proliferative,
PT	cardiovascular, autoimmune/inflammatory disorders and microbial
PT	infections -
XX	
PS	Claim 1: Page 355-356; 427pp: English.
XX	
XX	
CC	The invention relate to the isolation of genes AAC59157-C59205 encoding
CC	49 human secreted proteins AAB27682-B27730. The genes can be used to
CC	generate fusion proteins by linking to the gene for the human
CC	immunoglobulin G Fc portion for increasing the stability of
CC	the fusion protein as compared to the human protein only. The genes and
CC	proteins are useful for preventing, ameliorating or treating medical
CC	conditions, e.g. by protein or gene therapy. The genes are isolated
CC	from a range of human tissues disclosed in the specification. The
CC	nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)  
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
XX  
SQ Sequence 5279 BP; 1404 A; 1145 C; 1121 G; 1596 T; 13 other:

Query Match 4.2%; Score 20; DB 21; Length 5279;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgacct 149  
Db 547 aagatctgtacttgacct 566

RESULT 44  
AAO27447  
ID AAO27447 standard; DNA: 5427 BP.  
XX  
AC AAO27447:  
XX  
DT 09-FEB-1993 (first entry)  
XX  
DE Type B human platelet-derived growth factor receptor.  
XX  
KM PGCF: PDGF-R; mesenchyme; tyrosine kinase; ligand binding region: ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 187..3507  
FT /\*tag= a  
XX  
PN WO9213867-A.  
XX  
PD 20-AUG-1992.  
XX  
PF 28-JAN-1992: 92WO-US00730.  
XX  
PR 31-JAN-1991: 91US-0650793.  
XX  
PA (COR-) COR THERAPEUTICS INC.  
XX  
PI Escobedo JA, Fretto LJ, Glese NA, Tomlinson JE, Williams LT;  
PI Wolf D;  
XX  
DR MPI: 1992-289970/36.  
DR P-PSDB: AAR26205.  
XX  
PT Platelet derived growth factor receptor (PDGF-R) polypeptide(s)  
PT - useful as therapeutic and diagnostic agents e.g. for assaying  
PT PDGF activity in sample  
XX  
PS Disclosure: Page 75; 109pp; English.  
XX  
CC The sequence given encodes one allele of type B human platelet-  
CC derived growth factor (PDGF) receptor (PDGF-R). This receptor is  
CC typically found on cells of mesenchymal origin. It acts while in  
CC the form of two transmembrane glycoproteins, each of which is about  
CC 180 kD. This receptor has three major regions. The first is a  
CC transmembrane region, which spans the membrane once, separating the  
CC regions of the receptor exterior to the cell from those interior to  
CC the cell. The second region is an extracellular region which  
CC contains the domains which bind the PDGF. The third region is an  
CC intracellular region which possesses a tyrosine kinase activity.

CC This tyrosine kinase domain is notable in having an insert of approx.  
CC 100 amino acids, as compared with most other receptor tyrosine kinase  
CC domains which are contiguous or have shorter insert sequences.  
CC Fragments of this sequence between 8 and 400 amino acids comprising  
CC one or more PDGF ligand binding region from the extracellular domain  
CC may be used to bind a PDGF ligand.  
XX  
SQ Sequence 5427 BP; 1177 A; 1604 C; 1494 G; 1152 T; 0 other:

Query Match 4.2%; Score 20; DB 13; Length 5427;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtacttgacct 149  
Db 2707 aagatctgtacttgacct 2726

RESULT 45  
AAS84940  
ID AAS84940 standard; CDNA: 5602 BP.  
XX  
AC AAS84940:  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #20744.  
XX  
KM Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder: ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001: 2001WO-US08631.  
XX  
PR 31-MAR-2000: 2000US-0540217.  
XX  
PR 23-AUG-2000: 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
PI  
XX  
DR MPI: 2001-639362/73.  
DR P-PSDB: ABG20753.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
PS Claim 1; SEQ ID NO 20744; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and



CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 5602 BP; 1201 A; 1682 C; 1539 G; 1180 T; 0 other;

Query Match 4.2%; Score 20; DB 23; Length 5602;  
Best Local Similarity 100.0%; Pred No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 aagatctgtgacttggcct 149  
|||||  
DB 2877 aagatctgtgacttggcct 2896

Search completed: July 15, 2002, 23:10:10  
Job time: 18428 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:25:30 ; Search time 9532.94 Seconds

(without alignments)  
1033.931 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3044\_3514

Perfect score: 471

Sequence: 1 ctgacatcgaagatctgt.....gacctgcatctcggagctg 471

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 segs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
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2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_r:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_scs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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1	471	100.0	4195	6	AR016568	AR016568 Sequence
2	471	100.0	4195	6	AR106405	AR106405 Sequence
3	471	100.0	4416	6	AR112506	AR112506 Sequence
4	471	100.0	4416	6	HSE1r4	HSE1r4
5	471	100.0	4425	6	I44520	I44520 Sequence 31
6	471	100.0	4425	6	HSU43143	U43143 Human recep
7	471	100.0	4795	6	AR016569	AR016569 Sequence
8	471	100.0	4795	6	AR106406	AR106406 Sequence
9	420	89.2	6827	6	I44515	I44515 Sequence 17
10	305	64.8	4450	9	HSE1r4X	HSE1r4X
11	305	64.8	4450	9	AC022095	AC022095
12	113	24.0	127488	2	AC108083	AC108083
13	113	24.0	130129	2	AC025336	AC025336 Homo sapi
14	113	24.0	168347	2	AC106813	AC106813 Homo sapi
15	103	21.9	173341	2	AC108083	AC108083 Homo sapi
16	76	16.1	160	6	I44509	I44509 Sequence 5
17	31	6.6	5284	10	MUSPRKA	MUSPRKA
18	31	6.6	260266	2	AL646088	AL646088 Mus muscu
19	19	5.9	534	4	AB017155	AB017155 Oryctolag
20	27	5.7	2753	5	XELXFGFRA2	M62322 Xenopus lae
21	27	5.7	3634	5	XLU24491	U24491 Xenopus lae
22	27	5.7	3815	5	XELX1EGFR	M55163 Xenopus lae
23	27	5.7	4254	10	AF402786	AF402786 Rattus no
24	27	5.7	4360	10	AF402785	AF402785 Rattus no
25	27	5.7	161580	2	AC098957	AC098957 Rattus no
26	26	5.5	1256	10	MMMPK42	X58712 Mouse MAPK
27	26	5.5	1467	6	AR016532	AR016532 Sequence
28	26	5.5	1467	6	AR036245	AR036245 Sequence
29	26	5.5	1467	6	AR171291	AR171291 Sequence
30	26	5.5	1467	6	AR172792	AR172792 Sequence
31	26	5.5	1467	6	I34200	I34200 Sequence 3
32	26	5.5	1467	10	RATERRK2	M64300 Rat extrace
33	26	5.5	1534	5	S65207	S65207 endothe1a1
34	26	5.5	1747	10	MUSERK2	D10939 Mouse mRNA
35	26	5.5	1815	6	AB4443	AB4443 Sequence 58
36	26	5.5	1818	6	AB4425	AB4425 Sequence 40
37	26	5.5	4617	5	CCOUERK2	X83287 C.cotturmix
38	26	5.5	4696	10	RAT1G1R1T	I29232 Rattus norv
39	25	5.3	786	10	D8726454	D87267 Mus musculu
40	23	4.9	159	6	AR062728	AR062728 Sequence
41	23	4.9	272	9	D50001S13	D50013 Human DNA f
42	23	4.9	429	10	MUS3RKT	I36163 Mus musculu
43	23	4.9	1525	5	AP178759	AP178759 Dantio rer
44	23	4.9	1894	6	AR149571	AR149571 Sequence
45	23	4.9	2538	14	AC2TRKSEA	M25158 Avian retro

## ALIGNMENTS

RESULT 1	AR016568	AR016568	4195 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR016568	Sequence 1 from patent US 5776755.				
ACCESSION	AR016568					
VERSION	AR016568.1	GI:3972845				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 4195)					
AUTHORS	Altaiio,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J. and Kaipainen,A.					
TITLE	FLR4, a receptor tyrosine kinase					
JOURNAL	Patent: US 5776755-A 1 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..4195					
BASE COUNT	889 a	1279 c	1305 g	722 t		
ORIGIN	/organism="unknown"					

Query Match	100.0%	Score 471:	DB 6:	Length 4195:
-------------	--------	------------	-------	--------------

Best Local Similarity 100.0%; Pred. No. 2,1e-263;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatgaagatctgtctgtctacagcttcccaagtgccagagagatgagcttctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCTTG 3103
OY 61 gcttccgaaagatgcatccacagagaccttgctgcttcgaaacatctgctgctggaagc 120
Db 3104 GCTTCCGAAAGTGCATCCACAGACCTGCTGCTCGAAGATTCGTCTGCGAAGC 3163
OY 121 gacgtgtaagatctgtactgtgcttgcctgcgagacatctacaagaccctgaactac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTGCCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgcaaggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttgac 240
Db 3224 GTCCGCAAGGCACTGCCGCTGCCCTGAGTGTGAGTGCCTCGAAGACATCTTCGAC 3283
OY 241 aaggtgtaacacacagcagagtgagctgtgcttcttgagggtactctctggaagatcttc 300
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTCTTGGGAGTCTTCTGCGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgggtgagatcaatgaagagatctctgcagcagctg 360
Db 3344 TCTCTGGGGCTCCCGTACCTCGGCTGACATCAATGAGAGTCTCTGCGAGCTTCG 3403
OY 361 agagacgacacaaagatgagagggcccgagctgacaccccgcaataagccgacatg 420
Db 3404 AGAGACGACACAAAGATGAGAGGGCCCGGAGCTGCGACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccacaaagcgagacatctctcgagagc 471
Db 3464 CTGAAGTGTGCTGCTGCGAGACCCCAAGCGAGACCTGCATTCTCGAGCTG 3514

RESULT 2
ARI06405 4195 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6107046.
ACCESSION ARI06405
VERSION ARI06405.1 GI:12820935
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4195)
AUTHORS Allitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 1 22-AUG-2000;
FEATURES
source 1..4195
location/Qualifiers
BASE COUNT 889 a 1279 c 1305 g 722 t
ORIGIN
```

Query Match 100.0%; Score 471; DB 6; Length 4195;  
Best Local Similarity 100.0%; Pred. No. 2,1e-263;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ctgacacatgaagatctgtctgtctacagcttcccaagtgccagagagatgagcttctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCTTG 3103
OY 61 gcttccgaaagatgcatccacagagaccttgctgcttcgaaacatctgctgctggaagc 120
Db 3104 GCTTCCGAAAGTGCATCCACAGACCTGCTGCTCGAAGATTCGTCTGCGAAGC 3163
OY 121 gacgtgtaagatctgtactgtgcttgcctgcgagacatctacaagaccctgaactac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTGCCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgcaaggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttgac 240
Db 3224 GTCCGCAAGGCACTGCCGCTGCCCTGAGTGTGAGTGCCTCGAAGACATCTTCGAC 3283
OY 241 aaggtgtaacacacagcagagtgagctgtgcttcttgagggtactctctggaagatcttc 300
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTCTTGGGAGTCTTCTGCGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgggtgagatcaatgaagagatctctgcagcagctg 360
Db 3344 TCTCTGGGGCTCCCGTACCTCGGCTGACATCAATGAGAGTCTCTGCGAGCTTCG 3403
OY 361 agagacgacacaaagatgagagggcccgagctgacaccccgcaataagccgacatg 420
Db 3404 AGAGACGACACAAAGATGAGAGGGCCCGGAGCTGCGACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccacaaagcgagacatctctcgagagc 471
Db 3464 CTGAAGTGTGCTGCTGCGAGACCCCAAGCGAGACCTGCATTCTCGAGCTG 3514
```

```
OY 181 gtccgcaaggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttgac 240
Db 3224 GTCCGCAAGGCACTGCCGCTGCCCTGAGTGTGAGTGCCTCGAAGACATCTTCGAC 3283
OY 241 aaggtgtaacacacagcagagtgagctgtgcttcttgagggtactctctggaagatcttc 300
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTCTTGGGAGTCTTCTGCGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgggtgagatcaatgaagagatctctgcagcagctg 360
Db 3344 TCTCTGGGGCTCCCGTACCTCGGCTGACATCAATGAGAGTCTCTGCGAGCTTCG 3403
OY 361 agagacgacacaaagatgagagggcccgagctgacaccccgcaataagccgacatg 420
Db 3404 AGAGACGACACAAAGATGAGAGGGCCCGGAGCTGCGACCTCCGCAATACCCCGCATCATG 3463
OY 421 ctgaactgtgctgcgagagaccacaaagcgagacatctctcgagagc 471
Db 3464 CTGAAGTGTGCTGCTGCGAGACCCCAAGCGAGACCTGCATTCTCGAGCTG 3514
```

```
RESULT 3
ARI12506 4416 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6130071.
ACCESSION ARI12506
VERSION ARI12506.1 GI:14092406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4416)
AUTHORS Allitalo,K. and Joukov,V.
TITLE Vascular endothelial growth factor C (VEGF-C). DELTA.Cys.sub.156
JOURNAL Protein and gene, and uses thereof
FEATURES
source 1..4416
location/Qualifiers
BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN
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Query Match 100.0%; Score 471; DB 6; Length 4416;  
Best Local Similarity 100.0%; Pred. No. 2,1e-263;  
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ctgacacatgaagatctgtctgtctacagcttcccaagtgccagagagatgagcttctg 60
Db 3044 CTGACCATGACAGATCTTGTCTGTCTACAGCTTCAGCTGCCAGAGAGATGAGATTCTTG 3103
OY 61 gcttccgaaagatgcatccacagagaccttgctgcttcgaaacatctgctgctggaagc 120
Db 3104 GCTTCCGAAAGTGCATCCACAGACCTGCTGCTCGAAGATTCGTCTGCGAAGC 3163
OY 121 gacgtgtaagatctgtactgtgcttgcctgcgagacatctacaagaccctgaactac 180
Db 3164 GACGTGTGAAGATCTGTGACTTTGGCTTGCCCGGACATCTACAAAGACCTGACTTAC 3223
OY 181 gtccgcaaggcagtgccgagctgccttgaaatgagtgagccctgaagacatcttgac 240
Db 3224 GTCCGCAAGGCACTGCCGCTGCCCTGAGTGTGAGTGCCTCGAAGACATCTTCGAC 3283
OY 241 aaggtgtaacacacagcagagtgagctgtgcttcttgagggtactctctggaagatcttc 300
Db 3284 AAGGTGTACACACAGCAGATGACGTGTGCTCTTGGGAGTCTTCTGCGAGATCTTC 3343
OY 301 tctctggggcctcccgtaacctgggtgagatcaatgaagagatctctgcagcagctg 360
Db 3344 TCTCTGGGGCTCCCGTACCTCGGCTGACATCAATGAGAGTCTCTGCGAGCTTCG 3403
OY 361 agagacgacacaaagatgagagggcccgagctgacaccccgcaataagccgacatg 420
Db 3464 AGAGACGACACAAAGATGAGAGGGCCCGGAGCTGCGACCTCCGCAATACCCCGCATCATG 3463
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds  
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2.195 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3150\_3150

Perfect score: 1 t 1

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: gb\_ba:\*  
2: gb\_htg:\*  
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11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
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30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Query Length	DB ID	Description
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C	1	100.0	2	6	AX081326	AX081326 Sequence
C	2	100.0	2	6	AX081327	AX081327 Sequence
C	3	100.0	2	6	AX081328	AX081328 Sequence
C	4	100.0	2	6	AX092440	AX092440 Sequence
C	5	100.0	2	6	AX092441	AX092441 Sequence
C	6	100.0	2	6	AX092442	AX092442 Sequence
C	7	100.0	2	6	AX092443	AX092443 Sequence
C	8	100.0	2	6	AX092444	AX092444 Sequence
C	9	100.0	2	6	AX092445	AX092445 Sequence
C	10	100.0	2	6	AX092446	AX092446 Sequence
C	11	100.0	2	6	AX092447	AX092447 Sequence
C	12	100.0	2	6	AX092448	AX092448 Sequence
C	13	100.0	2	6	AX092451	AX092451 Sequence
C	14	100.0	2	6	AX092452	AX092452 Sequence
C	15	100.0	2	6	AX092453	AX092453 Sequence
C	16	100.0	2	6	AX092454	AX092454 Sequence
C	17	100.0	2	6	AX092455	AX092455 Sequence
C	18	100.0	2	6	AX092528	AX092528 Sequence
C	19	100.0	2	6	AX092530	AX092530 Sequence
C	20	100.0	2	6	AX092538	AX092538 Sequence
C	21	100.0	2	6	AX092539	AX092539 Sequence
C	22	100.0	2	6	AX175286	AX175286 Sequence
C	23	100.0	2	6	AX175287	AX175287 Sequence
C	24	100.0	2	6	AX235098	AX235098 Sequence
C	25	100.0	2	6	AX235098	AX235098 Sequence
C	26	100.0	2	6	BD001933	BD001933 Sequence
C	27	100.0	2	8	CNS01C93	AL115237 Sensilize
C	28	100.0	3	2	AC079635	AC079635 Mus muscu
C	29	100.0	3	2	AC079635	AC079635 Mus muscu
C	30	100.0	3	5	CHKNACM5	M23994 Chicken car
C	31	100.0	3	6	AX092456	AX092456 Sequence
C	32	100.0	3	6	AX092457	AX092457 Sequence
C	33	100.0	3	6	AX092458	AX092458 Sequence
C	34	100.0	3	6	AX092459	AX092459 Sequence
C	35	100.0	3	6	AX092459	AX092459 Sequence
C	36	100.0	3	6	AX092460	AX092460 Sequence
C	37	100.0	3	6	AX092461	AX092461 Sequence
C	38	100.0	3	6	AX092462	AX092462 Sequence
C	39	100.0	3	6	AX092463	AX092463 Sequence
C	40	100.0	3	6	AX092463	AX092463 Sequence
C	41	100.0	3	6	AX092464	AX092464 Sequence
C	42	100.0	3	6	AX092465	AX092465 Sequence
C	43	100.0	3	6	AX092466	AX092466 Sequence
C	44	100.0	3	6	AX092467	AX092467 Sequence
C	45	100.0	3	6	AX092467	AX092467 Sequence

## ALIGNMENTS

RESULT	1	2	DNA	linear	PAT	27-FEB-2001
AX081326/c	AX081326	2 bp				
LOCUS	Sequence 5 from Patent WO0108707.					
DEFINITION	AX081326					
ACCESSION	AX081326.1					
VERSION	GI:13170168					
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct.					
REFERENCE	synthetic construct					
AUTHORS	1 (bases 1 to 2)					
TITLE	Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.					
JOURNAL	Conjugates and methods for the production thereof, and their use					
FEATURES	for transporting molecules via biological membranes					
SOURCE	Patent: WO 0108707-A 5 08-FEB-2001;					
	Aventis Pharma Deutschland GmbH (DE)					
	Location/Qualifiers					
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	/note="Oligonucleotide"					
	1 a	0 c	0 g	0 t	1 others	
	BASE COUNT					
	ORIGIN					

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 2  
AX081327/c  
LOCUS Sequence 6 from Patent WO0108707.  
DEFINITION  
ACCESSION AX081327  
VERSION AX081327.1 GI:13170169  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..2  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

BASE COUNT 1 a 0 c 0 g 0 t 1 others  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 3  
AX081328/c  
LOCUS Sequence 7 from Patent WO0108707.  
DEFINITION  
ACCESSION AX081328  
VERSION AX081328.1 GI:13170170  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

BASE COUNT 1 a 0 c 0 g 0 t 1 others  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 4  
AX092440/c  
LOCUS Sequence 1 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092440  
VERSION AX092440.1 GI:13444535  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 2 a 0 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 4  
AX092440/c  
LOCUS Sequence 1 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092440  
VERSION AX092440.1 GI:13444535  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 2 a 0 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 2 T 2

RESULT 5  
AX092441/c  
LOCUS Sequence 2 from Patent WO0116366.  
DEFINITION  
ACCESSION AX092441  
VERSION AX092441.1 GI:13444536  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide"

BASE COUNT 1 a 1 c 0 g 0 t  
ORIGIN



DEFINITION Sequence 8 from Patent WO0116366.  
ACCESSION AX092447  
VERSION AX092447.1 GI:13444542  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 2 T 2

RESULT 11  
AX092448/C  
LOCUS Sequence 9 from Patent WO0116366.  
DEFINITION AX092448  
ACCESSION AX092448  
VERSION AX092448.1 GI:13444543  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 2 T 2

RESULT 12  
AX092451  
LOCUS Sequence 12 from Patent WO0116366.  
DEFINITION AX092451  
ACCESSION AX092451  
VERSION AX092451.1 GI:13444546

KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 12 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 T 1

RESULT 13  
AX092452  
LOCUS Sequence 13 from Patent WO0116366.  
DEFINITION AX092452  
ACCESSION AX092452  
VERSION AX092452.1 GI:13444547  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 13 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source Location/Qualifiers  
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/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 T 1

RESULT 14  
AX092452/C  
LOCUS Sequence 13 from Patent WO0116366.  
DEFINITION AX092452  
ACCESSION AX092452  
VERSION AX092452.1 GI:13444547  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

unclassified.  
1 (bases 1 to 2)  
REFERENCE Kless, H.  
AUTHORS  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 13 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1  
Db 2 t 2

RESULT 15  
AX092453 2 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092453  
DEFINITION Sequence 14 from Patent WO0116366.  
ACCESSION AX092453  
VERSION AX092453.1 GI:13444548  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE Kless, H.  
AUTHORS 1 (bases 1 to 2)  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 14 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 1 c 0 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1  
Db 1 t 1

RESULT 16  
AX092454 2 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092454  
DEFINITION Sequence 15 from Patent WO0116366.  
ACCESSION AX092454  
VERSION AX092454.1 GI:13444549  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE Kless, H.  
AUTHORS 1 (bases 1 to 2)

TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 15 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1  
Db 1 t 1

RESULT 17  
AX092455 2 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092455  
DEFINITION Sequence 16 from Patent WO0116366.  
ACCESSION AX092455  
VERSION AX092455.1 GI:13444550  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE Kless, H.  
AUTHORS 1 (bases 1 to 2)  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 16 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 0 g 2 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1  
Db 1 t 1

RESULT 18  
AX092528 2 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092528/c  
DEFINITION Sequence 89 from Patent WO0116366.  
ACCESSION AX092528  
VERSION AX092528.1 GI:13444523  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE Kless, H.  
AUTHORS 1 (bases 1 to 2)  
TITLE Template-dependent nucleic acid polymerization using  
JOURNAL oligonucleotide triphosphates building blocks  
Patent: WO 0116366-A 89 08-MAR-2001;



YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1

Db 2 T 2

RESULT 19  
AX092530/c 2 bp DNA linear PAT 21-MAR-2001

LOCUS AX092530  
DEFINITION Sequence 91 from Patent WO0116366.  
ACCESSION AX092530  
VERSION AX092530.1 GI:13444625  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 91 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 0 c 1 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1

Db 1 T 1

RESULT 20  
AX092538 2 bp DNA linear PAT 21-MAR-2001

LOCUS AX092538  
DEFINITION Sequence 99 from Patent WO0116366.  
ACCESSION AX092538  
VERSION AX092538.1 GI:13444633  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 99 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
Location/Qualifiers

source 1..2  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1

Db 2 T 2

RESULT 21  
AX092539/c 2 bp DNA linear PAT 21-MAR-2001

LOCUS AX092539  
DEFINITION Sequence 100 from Patent WO0116366.  
ACCESSION AX092539  
VERSION AX092539.1 GI:13444634  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 100 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 2 a 0 c 0 g 0 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
1

Db 2 T 2

RESULT 22  
AX175286 2 bp DNA linear PAT 03-JUL-2001

LOCUS AX175286  
DEFINITION Sequence 50 from Patent WO0144465.  
ACCESSION AX175286  
VERSION AX175286.1 GI:14598654  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial construct.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Phillips,N.C. and Fillion,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;  
Bloniche Life Sciences Inc. (CA)

FEATURES  
source 1..2  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 2 T 2

RESULT 23  
AX175287  
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 51 from Patent WO0144465.  
ACCESSION AX175287  
VERSION AX175287.1 GI:14598655  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Phillips,N.C. and Filion,M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)  
FEATURES  
source location/Qualifiers  
1..2  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 T 1

RESULT 24  
AX235098  
LOCUS AX235098 2 bp DNA linear PAT 11-SEP-2001  
DEFINITION Sequence 55 from Patent WO0163540.  
ACCESSION AX235098  
VERSION AX235098.1 GI:15593746  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Bureau,T.  
TITLE Method for identifying transposons from a nucleic acid database  
JOURNAL Patent: WO 0163540-A 55 30-AUG-2001;  
MCGILL UNIVERSITY (CA)  
FEATURES  
source location/Qualifiers  
1..2  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="sequence from g1 3243214"  
BASE COUNT 1 a 0 c 0 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1

Db 2 T 2

RESULT 25  
AX235098/c  
LOCUS AX235098 2 bp DNA linear PAT 11-SEP-2001  
DEFINITION Sequence 55 from Patent WO0163540.  
ACCESSION AX235098  
VERSION AX235098.1 GI:15593746  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Bureau,T.  
TITLE Method for identifying transposons from a nucleic acid database  
JOURNAL Patent: WO 0163540-A 55 30-AUG-2001;  
MCGILL UNIVERSITY (CA)  
FEATURES  
source location/Qualifiers  
1..2  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="sequence from g1 3243214"  
BASE COUNT 1 a 0 c 0 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 T 1

RESULT 26  
BD001933  
LOCUS BD001933 2 bp DNA linear PAT 31-JAN-2002  
DEFINITION Sensitized method for detecting DNA.  
ACCESSION BD001933  
VERSION BD001933.1 GI:18628673  
KEYWORDS JP 2000146894-A/2.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 2)  
AUTHORS Takenaka,S. and Takagi,M.  
TITLE Sensitized method for detecting DNA  
JOURNAL Patent: JP 2000146894-A 2 26-MAY-2000;  
FUJI PHOTO FILM CO LTD  
COMMENT  
OS Artificial Sequence  
PN JP 2000146894-A/2  
PD 26-MAY-2000  
PF 04-NOV-1998 JP 1998328872  
PI SHIGEO TAKENAKA,MAKOTO TAKAGI  
PC G01N27/327,C12N15/09,C12Q1/68,G01N33/483,G01N33/50,G01N27/30,  
PC C12N15/00  
CC  
FH  
CC  
FH  
FT  
FT

FEATURES  
source location/Qualifiers  
1..2  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 0 a 0 c 0 g 1 t 1 others  
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 t 1  
Db 1 t 1

RESULT 27  
CNS01C99  
LOCUS  
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.  
ACCESSION AL115237.1 GI:5829856  
KEYWORDS cDNA library; nitrogen deprivation.  
SOURCE Botryotinia fuckelliana.  
ORGANISM Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 2)  
AUTHORS Bilton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France  
REFERENCE 2 (bases 1 to 2)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBS11 vector.

FEATURES  
source  
1..2  
/organism="Botryotinia fuckelliana"  
/strain="T4"  
/db\_xref="taxon:40559"  
/note="Genoscope sequence ID : W04F091"

BASE COUNT 0 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 t 1  
Db 2 t 2

RESULT 28  
AC079635  
LOCUS  
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC079635.3 GI:14647267  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3)  
AUTHORS McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Ballja, V., Dedhia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchhoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vill, M.D. and Zutavern, T.  
TITLE Mouse Genomic Sequence

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3)  
AUTHORS McCombie, W.R.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA  
COMMENT On Jul 10, 2001 this sequence version replaced gi:14595773.  
\* NOTE: This record contains 1 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1  
\* 3: contig of 3 bp in length.  
This entry has been temporarily removed. An update for RP23-152L20 will be submitted as soon as it becomes available.

FEATURES  
source  
1..3  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="RP23-152L20"

BASE COUNT 1 a 0 c 1 g 1 t  
ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 t 1  
Db 3 t 3

RESULT 29  
AC079635/c  
LOCUS  
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC079635.3 GI:14647267  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3)  
AUTHORS McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Ballja, V., Dedhia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchhoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vill, M.D. and Zutavern, T.  
TITLE Mouse Genomic Sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3)  
AUTHORS McCombie, W.R.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA  
COMMENT On Jul 10, 2001 this sequence version replaced gi:14595773.  
\* NOTE: This record contains 1 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.

\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 3: contig of 3 bp in length.  
This entry has been temporarily removed. An update for RP23-152L20  
will be submitted as soon as it becomes available.

## FEATURES

## source

1..3  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="RP23-152L20"

## BASE COUNT

1 a 0 c 1 g 1 t

## Query Match

100.0%; Score 1; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

1 t 1  
2 t 2

## RESULT 30

## LOCUS

CHKNCAMC5 3 bp DNA linear VRT 17-JUL-2000

## DEFINITION

CHICKEN CARDIAC NEURAL CELL ADHESION (NCAM) GENE, EXON 12D.

## ACCESSION

M23994 J04140

## VERSION

M23994.1 GI:212442

## KEYWORDS

## SEGMENT

## SOURCE

## ORGANISM

5 of 6  
chicken.  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 3)  
Prediger, E.A., Hoffman, S., Edelman, G.M. and Cunningham, B.A.  
Four exons encode a 93-base-pair insert in three neural cell  
adhesion molecule mRNAs specific for chicken heart and skeletal  
muscle

## REFERENCE

## AUTHORS

## TITLE

JOURNAL, PROC. NATL. ACAD. SCI. U.S.A. 85 (24), 9616-9620 (1988)  
MEDLINE 89071747  
PUBMED 3200847

## COMMENT

Exon 12D represents a very small exon.

## FEATURES

## source

1..3  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="PEC101B"  
/issue\_type="cardiac muscle"  
/dev\_stage="day 10 embryo"  
1..3  
/gene="NACM"  
/number=12

## BASE COUNT

2 a 0 c 1 g 0 t

## ORIGIN

Query Match 100.0%; Score 1; DB 5; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

1 t 1  
2 t 2

## RESULT 31

## LOCUS

AX092456/c 3 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 17 from Patent WO0116366.  
ACCESSION AX092456  
VERSION AX092456.1 GI:13444551

## KEYWORDS

unidentified.

## SOURCE

unclassified.

## ORGANISM

1 (bases 1 to 3)

## REFERENCE

1 (bases 1 to 3)

## AUTHORS

Kless, H.

## TITLE

Template-dependent nucleic acid polymerization using

## JOURNAL

Oligonucleotide triphosphates building blocks

## DEFINITION

Patent: WO 0116366-A 17 08-MAR-2001;

## ACCESSION

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar

## VERSION

(IL)

## FEATURES

Location/Qualifiers

## source

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

## BASE COUNT

3 a 0 c 0 g 0 t

## ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

1 t 1  
3 t 3

## RESULT 32

## LOCUS

AX092457/c 3 bp DNA linear PAT 21-MAR-2001

## DEFINITION

Sequence 18 from Patent WO0116366.

## ACCESSION

AX092457

## VERSION

AX092457.1 GI:13444552

## KEYWORDS

unidentified.

## SOURCE

unclassified.

## ORGANISM

1 (bases 1 to 3)

## REFERENCE

1 (bases 1 to 3)

## AUTHORS

Kless, H.

## TITLE

Template-dependent nucleic acid polymerization using

## JOURNAL

Oligonucleotide triphosphates building blocks

## DEFINITION

Patent: WO 0116366-A 18 08-MAR-2001;

## ACCESSION

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar

## VERSION

(IL)

## FEATURES

Location/Qualifiers

## source

1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

## BASE COUNT

2 a 1 c 0 g 0 t

## ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

1 t 1  
2 t 2

## RESULT 33

## LOCUS

AX092458/c 3 bp DNA linear PAT 21-MAR-2001

## DEFINITION

Sequence 19 from Patent WO0116366.

## ACCESSION

AX092458

## VERSION

AX092458.1 GI:13444553

KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT  
2 a 0 c 1 g 0 t

ORIGIN  
1 t 1  
2 t 2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34  
AX092459  
LOCUS AX092459 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 20 from Patent WO0116366.  
ACCESSION AX092459  
VERSION AX092459.1 GI:13444554  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 20 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT  
2 a 0 c 0 g 1 t

ORIGIN  
1 t 1  
3 t 3

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35  
AX092459/C  
LOCUS AX092459 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 20 from Patent WO0116366.  
ACCESSION AX092459  
VERSION AX092459.1 GI:13444554  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 20 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT  
2 a 0 c 0 g 1 t

ORIGIN  
1 t 1  
2 t 2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 36  
AX092460  
LOCUS AX092460 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 21 from Patent WO0116366.  
ACCESSION AX092460  
VERSION AX092460.1 GI:13444555  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT  
2 a 1 c 0 g 0 t

ORIGIN  
1 t 1  
3 t 3

Query Match  
Best Local Similarity 100.0%; Score 1; DB 6; Length 3;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 37  
AX092461/C  
LOCUS AX092461 3 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 22 from Patent WO0116366.  
ACCESSION AX092461  
VERSION AX092461.1 GI:13444556  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.

TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 22 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 38  
AX092462/c 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092462  
DEFINITION Sequence 23 from Patent WO0116366.  
ACCESSION AX092462  
VERSION AX092462.1 GI:13444557  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 39  
AX092463 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092463  
DEFINITION Sequence 24 from Patent WO0116366.  
ACCESSION AX092463  
VERSION AX092463.1 GI:13444558  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 40  
AX092463/c 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092463  
DEFINITION Sequence 24 from Patent WO0116366.  
ACCESSION AX092463  
VERSION AX092463.1 GI:13444558  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
source 1..3  
Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t

Query Match 100.0%; Score 1; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
|  
Db 1 t 1

RESULT 41  
AX092464 3 bp DNA linear PAT 21-MAR-2001  
LOCUS AX092464  
DEFINITION Sequence 25 from Patent WO0116366.  
ACCESSION AX092464  
VERSION AX092464.1 GI:13444559  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3)  
AUTHORS Kless,H.  
TITLE Template-dependent nucleic acid polymerization using  
oligonucleotide triphosphates building blocks  
JOURNAL Patent: WO 0116366-A 25 08-MAR-2001;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar  
(IL)

FEATURES  
Location/Qualifiers

```
source 1..3
        /organism="unidentified"
        /db_xref="taxon:32644"
        /note="synthetic oligonucleotide:"
BASE COUNT      2 a      0 c      1 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
    |
Db 3 T 3

RESULT 42
AX092465/c      3 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION      Sequence 26 from Patent WO0116366.
ACCESSION      AX092465
VERSION      AX092465.1 GI:13444560
KEYWORDS
SOURCE      .
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 3)
AUTHORS      Kless,H.
TITLE      "Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
            Patent: WO 0116366-A 26 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)"
FEATURES
source 1..3
        /organism="unidentified"
        /db_xref="taxon:32644"
        /note="synthetic oligonucleotide:"
BASE COUNT      1 a      1 c      1 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 t 1
    |
Db 1 T 1

RESULT 43
AX092466/c      3 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION      Sequence 27 from Patent WO0116366.
ACCESSION      AX092466
VERSION      AX092466.1 GI:13444561
KEYWORDS
SOURCE      .
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 3)
AUTHORS      Kless,H.
TITLE      "Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
            Patent: WO 0116366-A 27 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)"
FEATURES
source 1..3
        /organism="unidentified"
        /db_xref="taxon:32644"
        /note="synthetic oligonucleotide:"
```

```
BASE COUNT      1 a      0 c      2 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1
    |
Db 1 T 1

RESULT 44
AX092467      3 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION      Sequence 28 from Patent WO0116366.
ACCESSION      AX092467
VERSION      AX092467.1 GI:13444562
KEYWORDS
SOURCE      .
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 3)
AUTHORS      Kless,H.
TITLE      "Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
            Patent: WO 0116366-A 28 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)"
FEATURES
source 1..3
        /organism="unidentified"
        /db_xref="taxon:32644"
        /note="synthetic oligonucleotide:"
BASE COUNT      1 a      0 c      1 g      1 t
ORIGIN

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 t 1
    |
Db 3 T 3

RESULT 45
AX092467/c      3 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION      Sequence 28 from Patent WO0116366.
ACCESSION      AX092467
VERSION      AX092467.1 GI:13444562
KEYWORDS
SOURCE      .
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 3)
AUTHORS      Kless,H.
TITLE      "Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
            Patent: WO 0116366-A 28 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)"
FEATURES
source 1..3
        /organism="unidentified"
        /db_xref="taxon:32644"
        /note="synthetic oligonucleotide:"
BASE COUNT      1 a      0 c      1 g      1 t
ORIGIN
```

Query Match 100.0%: Score 1; DB 6; Length 3;  
 Best Local Similarity 100.0%: Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L 1  
 1 1  
 db 1 + 1

Search completed: July 15, 2002, 23:28:08  
 Job time: 24541 sec



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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds  
(without alignments)  
1.098 Million cell updates/sec

Title: US-09-375-248-1\_COPY\_3150\_3150  
Perfect score: 1  
Sequence: 1 t 1

Scoring table: OLIGO-MUC  
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/lna/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/lna/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/lna/PTCDS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/lna/Backfile1.seq: \*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	1	US-08-457-274A-16
C 2	1	100.0	2	3	US-09-016-520-35
C 3	1	100.0	2	4	US-09-130-973-35
C 4	1	100.0	2	4	US-09-477-902-35
C 5	1	100.0	2	5	PCT-US95-05758-16
C 6	1	100.0	3	1	US-07-791-213D-46
C 7	1	100.0	3	1	US-07-791-213D-62
C 8	1	100.0	3	1	US-08-268-679B-7
C 9	1	100.0	3	1	US-08-295-743-22
C 10	1	100.0	3	1	US-08-602-036A-2
C 11	1	100.0	3	1	US-08-293-150A-46
C 12	1	100.0	3	1	US-08-293-150A-62
C 13	1	100.0	3	2	US-08-502-374A-2
C 14	1	100.0	3	2	US-08-542-407A-2
C 15	1	100.0	3	4	US-08-793-634B-12
C 16	1	100.0	3	4	US-08-793-634B-12
C 17	1	100.0	3	4	US-08-793-634B-13
C 18	1	100.0	3	4	US-08-793-634B-13
C 19	1	100.0	3	4	US-08-973-568-55
C 20	1	100.0	4	1	US-07-755-462-2
C 21	1	100.0	4	1	US-07-755-462-2
C 22	1	100.0	4	1	US-07-630-288A-7
C 23	1	100.0	4	1	US-07-630-288A-11
C 24	1	100.0	4	1	US-07-630-288A-11
C 25	1	100.0	4	1	US-07-630-288A-34
C 26	1	100.0	4	1	US-07-630-288A-34
C 27	1	100.0	4	1	US-08-188-943-1

C 28	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl1
C 29	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
C 30	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl1
C 31	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
C 32	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl1
C 33	1	100.0	4	1	US-08-393-219-11	Sequence 9, Appl1
C 34	1	100.0	4	1	US-08-510-032A-9	Sequence 9, Appl1
C 35	1	100.0	4	1	US-08-510-032A-9	Sequence 7, Appl1
C 36	1	100.0	4	1	US-08-468-049-7	Sequence 11, Appl1
C 37	1	100.0	4	1	US-08-468-049-11	Sequence 11, Appl1
C 38	1	100.0	4	1	US-08-468-049-11	Sequence 34, Appl1
C 39	1	100.0	4	1	US-08-468-049-34	Sequence 5, Appl1
C 40	1	100.0	4	1	US-08-468-015B-5	Sequence 12, Appl1
C 41	1	100.0	4	1	US-08-468-015B-12	Sequence 3, Appl1
C 42	1	100.0	4	1	US-08-351-365-3	Sequence 4, Appl1
C 43	1	100.0	4	1	US-08-351-365-3	Sequence 4, Appl1
C 44	1	100.0	4	1	US-08-351-365-4	Sequence 4, Appl1
C 45	1	100.0	4	1	US-08-351-365-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1  
US-08-457-274A-16/c  
; Sequence 16, Application US/08457274A  
; Patent No. 5734086  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Jeffrey G.  
; TITLE OF INVENTION: Cyclochrome P4501pr Gene and Its Uses  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: P. O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,274A  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1304  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Musca domestica  
; STRAIN: Learn-Pyr  
; DEVELOPMENTAL STAGE: Adult  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: Chromosome 1  
; US-08-457-274A-16

Query Match 100.0%; Score 1; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 2 t 2

## RESULT 2

US-09-016-520-35  
Sequence 35, Application US/09016520A

Patent No. 6127533

GENERAL INFORMATION:

APPLICANT: Cook, Phillip D

APPLICANT: Manoharan, Muthiah

APPLICANT: Kawasaki, Andrew

TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides

FILE REFERENCE: ISIS2824

CURRENT APPLICATION NUMBER: US/09/016,520A

CURRENT FILING DATE: 1998-01-30

EARLIER APPLICATION NUMBER: 60/037,143

EARLIER FILING DATE: 1997-02-14

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35

LENGTH: 2

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

NAME/KEY: misc\_feature

LOCATION: (1)..(2)

OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy

US-09-016-520-35

Query Match 100.0%; Score 1; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 t 1

## RESULT 3

US-09-130-973-35  
Sequence 35, Application US/09130973

Patent No. 6172209

GENERAL INFORMATION:

APPLICANT: Manoharan, Muthiah

APPLICANT: Cook, Phillip Dan

APPLICANT: Prakash, Thazna P

APPLICANT: Kawasaki, Andrew M

TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For

FILE REFERENCE: ISIS2955

CURRENT APPLICATION NUMBER: US/09/130,973

CURRENT FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35

LENGTH: 2

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: NAME/KEY: misc\_feature

LOCATION: (1)..(2)

OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)

OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1

OTHER INFORMATION: Sequence  
US-09-130-973-35

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 t 1

## RESULT 4

US-09-477-902-35

Sequence 35, Application US/09477902

Patent No. 6194598

GENERAL INFORMATION:

APPLICANT: Cook, Phillip D

APPLICANT: Manoharan, Muthiah

APPLICANT: Kawasaki, Andrew

TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides

FILE REFERENCE: ISIS2824

CURRENT APPLICATION NUMBER: US/09/477,902

CURRENT FILING DATE: 2000-01-05

PRIOR APPLICATION NUMBER: 09/016,520

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/037,143

PRIOR FILING DATE: 1997-02-14

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35

LENGTH: 2

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

NAME/KEY: misc\_feature

LOCATION: (1)..(2)

OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy

US-09-477-902-35

Query Match 100.0%; Score 1; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 t 1

## RESULT 5

PCT-US95-05758-16/c  
Sequence 16, Application PC/TUS9505758

GENERAL INFORMATION:

APPLICANT: Cornell Research Foundation, Inc.

TITLE OF INVENTION: Cytochrome P4501p Gene and Its

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: P. O. Box 1051, Clinton Square

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05758  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1304  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Musca domestica  
STRAIN: learn-pyr  
DEVELOPMENTAL STAGE: Adult  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Chromosome 1  
PCT-US95-05758-16

Query Match 100.0%; Score 1; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 t 1  
Db 2 T 2

RESULT 6  
US-07-791-213D-46  
Sequence 46, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 t 1  
Db 1 T 1

RESULT 7  
US-07-791-213D-62  
Sequence 62, Application US/07791213D  
Patent No. 5409895  
GENERAL INFORMATION:  
APPLICANT: MORISHITA, Hideaki  
APPLICANT: KANAMORI, Toshinori  
APPLICANT: NOBUHARA, Masahiro  
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
TREATING USING THE SAME  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,213D  
FILING DATE: 13-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 2-306745  
FILING DATE: 13-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 029650-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 t 1  
Db 1 t 1

RESULT 8  
US-08-268-679B-7/C  
; Sequence 7, Application US/08268679B  
; Patent No. 5674729  
; GENERAL INFORMATION:  
; APPLICANT: WIMMER, ECKARD; MOLIA,  
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.  
; TITLE OF INVENTION: DE NOVO CELL-FREE  
; TITLE OF INVENTION: SYNTHESIS PICOINAVIRUS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVE.  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/268,679B  
; FILING DATE: 30-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07\846,914  
; FILING DATE: 06-MAR-1992  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 07\719,761  
; FILING DATE: 24-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MARIA C.H. LIN  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 0887-4095 US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6845  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE:  
; DESCRIPTION: OLIGONUCLEOTIDE  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE: N.A.  
; POSITION IN GENOME: N.A.  
; US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 t 1

RESULT 9  
US-08-295-743-22

; Sequence 22, Application US/08295743  
; Patent No. 5719271  
; GENERAL INFORMATION:  
; APPLICANT: ISIS Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Covalently Cross-Linked  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; ADDRESSEE: and No. 5719271is  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 720 Kb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/295,743  
; FILING DATE: 30-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 846,376  
; FILING DATE: 05-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph Luccl  
; REGISTRATION NUMBER: 33,307  
; REFERENCE/DOCKET NUMBER: ISIS-1006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
; OTHER INFORMATION: hexylamine modified uridine  
; OTHER INFORMATION: moiety  
; US-08-295-743-22

Query Match 100.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 t 1

RESULT 10  
US-08-602-036A-2  
; Sequence 2, Application US/08602036A  
; Patent No. 5789248  
; GENERAL INFORMATION:  
; APPLICANT: Oeystein, Fodstad  
; APPLICANT: Hoyt, Eivind  
; APPLICANT: Engebraten, Olav  
; APPLICANT: Maelandsmo, Gunhild H.  
; APPLICANT: Agrawal, Sudhir  
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND  
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE AND DORR LLP  
; STREET: 60 State Street

```

: CITY: Boston
: STATE: MA
: COUNTRY: United States of America
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/602,036A
: FILING DATE: 16-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerner, Ann-Louise
: REGISTRATION NUMBER: 33,523
: REFERENCE/DOCKET NUMBER: HY2-039CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 526-6000
: TELEFAX: (617) 526-5000
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: US-08-602-036A-2

Query Match      100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 2 u 2

RESULT 11
US-08-293-150A-46
: Sequence 46, Application US/08293150A
: Patent No. 5792629
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshinori
: APPLICANT: NOBUHARA, Masahito
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: TITLE OF INVENTION: TREATING USING THE SAME
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-AUG-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
```

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-293-150A-46
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Query Match      100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1
Db 1 t 1
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```

RESULT 12
US-08-293-150A-62
: Sequence 62, Application US/08293150A
: Patent No. 5792629
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshinori
: APPLICANT: NOBUHARA, Masahito
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: TITLE OF INVENTION: TREATING USING THE SAME
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-AUG-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
```

LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-293-150A-62

Query Match  
Best Local Similarity 100.0%; Score 1; DB 1; Length 3;  
Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1 t 1  
Db 1 t 1

RESULT 13  
US-08-502-374A-2  
Sequence 2, Application US/08502374A  
Patent No. 5872007  
GENERAL INFORMATION:  
APPLICANT: Fodstad, Oegstedein  
APPLICANT: Hovig, Eivind  
APPLICANT: Engestraten, Olav  
APPLICANT: Maeldams, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502.374A  
FILING DATE: 14-Jul-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-526-6000  
TELEFAX: 617-526-5000  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-502-374A-2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;  
Pred. No. 0;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1 t 1  
Db 2 u 2

RESULT 14  
US-08-642-407A-2  
Sequence 2, Application US/08642407A  
Patent No. 5877308  
GENERAL INFORMATION:  
APPLICANT: Oegstedein, Fodstad  
APPLICANT: Hovig, Eivind  
APPLICANT: Engestraten, Olav  
APPLICANT: Maeldams, Gunhild H.  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND  
METHODS OF INHIBITING METASTATIC CANCER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642.407A  
FILING DATE: 03-May-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-039CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-642-407A-2

Query Match  
Best Local Similarity 100.0%; Score 1; DB 2; Length 3;  
Pred. No. 0;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1 t 1  
Db 2 u 2

RESULT 15  
US-08-793-634B-12  
Sequence 12, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
APPLICANT: Marshall, Jerry S.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 1 T 1

RESULT 16  
US-08-793-634B-12/C  
Sequence 12, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
APPLICANT: Marchall, Jerry S.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B

FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 t 1  
Db 3 T 3

RESULT 17  
US-08-793-634B-13  
Sequence 13, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Surin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W.G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
APPLICANT: Marchall, Jerry S.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA  
US-08-793-634B-13

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 1 t 1

RESULT 18  
US-08-793-634B-13/C  
Sequence 13, Application US/08793634B  
Patent No. 6211431  
GENERAL INFORMATION:  
APPLICANT: Boevink, Petra C.  
APPLICANT: Sutin, Brian P.  
APPLICANT: Keese, Paul K.  
APPLICANT: Chu, Paul W. G.  
APPLICANT: Waterhouse, Peter M.  
APPLICANT: Khan, Rafiqul I.  
APPLICANT: Larkin, Philip J.  
APPLICANT: Taylor, William C.  
APPLICANT: Matchall, Jerry S.  
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
City: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,634B  
FILING DATE: June 9, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-793-634B-13

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

RESULT 19  
US-08-973-568-55/C

Sequence 55, Application US/08973568B  
Patent No. 6277634  
GENERAL INFORMATION:  
APPLICANT: McCall, Maxine J.  
APPLICANT: Hendry, Philip  
APPLICANT: Lockett, Trevor  
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF  
FILE REFERENCE: 47203bpcplus  
CURRENT APPLICATION NUMBER: US/08/973,568B  
CURRENT FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO: 55  
LENGTH: 3  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
OTHER INFORMATION: Synthetic Ribozyme or portion thereof  
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and  
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
1  
Db 3 t 3

RESULT 20  
US-07-755-462-2  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Cathoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
City: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:



LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
|  
Db 3 T 3

RESULT 21  
US-07-755-462-2/C  
Sequence 2, Application US/07755462  
Patent No. 5273881  
GENERAL INFORMATION:  
APPLICANT: Sena, Elissa P.  
APPLICANT: Calhoun, Cornelia J.  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop  
TITLE OF INVENTION: Formation  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,462  
FILING DATE: 19910904  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520,321  
FILING DATE: 07-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4255-0001.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Cleavage site for DpnI  
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
|  
Db 2 T 2

RESULT 22  
US-07-630-288A-7/C  
Sequence 7, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2430  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-7

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
|  
Db 4 T 4

RESULT 23  
US-07-630-288A-11  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use

NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 3 t 3

RESULT 24  
US-07-630-288A-11/C  
Sequence 11, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 t 1  
Db 2 t 2

RESULT 25  
US-07-630-288A-34  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glessner  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Glessner, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 1 u 1

RESULT 26  
US-07-630-288A-34/c  
Sequence 34, Application US/07630288A  
Patent No. 5472840  
GENERAL INFORMATION:  
APPLICANT: Stefano, James E.  
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Giesser  
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/630,288A  
FILING DATE: 17-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/370,218  
FILING DATE: 06-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/252,243  
FILING DATE: 30-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Giesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 58190 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 717-2443  
TELEFAX: (708) 717-2430  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 3 t 3

RESULT 27  
US-08-188-943-1  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
TITLE OF INVENTION: Rapid Assays for Amplification  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,943  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,602  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370068-3630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 t 1  
Db 2 t 2

RESULT 28  
US-08-188-943-1/c  
Sequence 1, Application US/08188943  
Patent No. 5635347  
GENERAL INFORMATION:  
APPLICANT: Link, John R.  
APPLICANT: Gudibande, Satyanarayana R.  
APPLICANT: Kenten, John H.  
TITLE OF INVENTION: Rapid Assays for Amplification